

SEIR Model for Transmission of Dengue Fever

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Abstract— In this paper, we study a system of differential equations that models the population dynamics of SEIR vector transmission of dengue fever. The model studied mathematical analysis by reviewing the fixed points and eigen values to determine the dynamic behaviour of system. The Simulations on the model for some parameter values were performed and the breeding rates results showed a state become either endemic or non-endemic. The SEIR model can be potential for modelling using real data.

Keywords— Dengue fever; Endemic; SEIR model; Stability; Threshold parameter.

I. INTRODUCTION

After the Second World War; Dengue fever is regarded as a serious infectious disease that risks about 2.5 billion people all over the world, especially in the tropical countries and became a major epidemic disease occurred in Southeast Asia. Such epidemic arises due to climate change and a lack of people knowledge and awareness on dengue fever so that the dengue fever possibly becomes an endemic for a long time.

The mathematical models for dengue fever found that compartmental dynamics such as Susceptible, Infected, Removed (SIR) and Susceptible, Exposed, Infected, Removed (SEIR). Particularly, in SIR models [2, 3, 4, 7, 9, 11] and SEIR model [5] had been published. The difference of the both model is in the SIR model, latent period is excluded as one of the variables whereas in the SEIR model, the latent period is included as adding variable which examines the spreading of dengue fever. Latent period is very important and crucial because of the unpredictable climate changing as one of the global warming consequences [1] nowadays. Hence, in this SEIR model, we constructed and analysed a mathematical model for its transmission dynamics. Simulation of the model by using parameter values which is calculated by ODESOLVE.

A. Dengue Fever

Dengue fever is caused by four serotypes and they are closely related as a family of dengue virus 1 (DEN1), virus 2

(DEN2), virus 3 (DEN3) and virus 4 (DEN4). These viruses carried by two kinds of mosquitoes that are *Aedes aegypti* and *Aedes albopictus* which spread through the mosquitoes bite. According to WHO (2009) [10], *Aedes albopictus* is a kind of mosquito that can transmit the dengue virus and the presence of the species was detected in Asia in recent years. However, *Aedes aegypti* is still the principal vector of dengue virus transmission. Another interesting fact is the shift of patients' phenomena where dengue fever previously attacks children of primary school age, but now everybody is vulnerable to the fever [8].

II. SEIR MODEL

SEIR model is one of a mathematical model to analyse the simulation of the spreading of one serotype of dengue virus between host and vector. The model is based on the Susceptible, Exposed, Infected, Removed (SEIR) of infectious disease epidemiology, which was adopted [5]. SEIR model obtained two vectors, human population (N_h) and Population vector (N_v). Human population (N_h) are divided into four groups, such as people that have the potential to get infected by dengue virus (S_h), people who shows exposed of virus infection (E_h), people who infected (I_h) and people who have recovered (R_h). Population vector or mosquitoes (N_v) are divided into three groups of mosquitoes that potentially infected by dengue virus (S_v), mosquitoes are exposed to infection (E_v) and mosquitoes that were infected with dengue virus (I_v).

In this study, it is assumed that there is numbers of people in the populations that have already infected by the virus while others have not. It is also assumed that the transmission of the virus continues in the population but number of mosquitoes as the vector is constant. People and mosquitoes are categorized in one group at a time. People in the group S_h have a probability of being infected with dengue virus at a rate $\frac{\beta_h b I_v}{N_h}$, where $\beta_h b$ is sufficient rate of correlation from human to the vector and count in to the spreading probability from an infected individual to mosquitoes that potentially infected (β_h). In addition, the percentage of infected mosquitoes is (p), average bite of mosquitoes that potentially infected is (b) and the proportional rate for people exposed to dengue virus infection is (φ_h). Once humans infected by dengue virus, they will be given help treatment. Hence, the model assumes that every human being treated will have life time immunity so there will be no re-infection cases. Person's healing rate from a virus infection stipulated from a given treatment or the duration of infection in the body is proportional to the individual (γ_h).

Changes for the group S_v show that each has a probability of mosquitoes infected with dengue virus at a rate $\left(\frac{\beta_v b I_h}{N_h}\right)$, where $\beta_v b = \gamma_v$ is sufficient rate of correlation from vectors to humans and count in to the probability of transmission from infected mosquitoes to the potentially infected human (β_v). In addition, average bite of an infected mosquitoes is (b), the proportional rates of mosquitoes exposed to the virus infection is (δ_v). Both group of people and mosquitoes will be reduced due to natural death, symbolized with (μ_h) and (μ_v) respectively. For the people who have infected, there is a death caused by dengue itself with the content (α_h). Changes that occur in every group of people and mosquitoes can be defined as the following mathematical model.

Human Population

$$\frac{dS_h}{dt} = \mu_h N_h - \left(\frac{\beta_h b I_v}{N_h} + p + \mu_h\right) S_h \quad (1)$$

$$\frac{dE_h}{dt} = \left(\frac{\beta_h b I_v}{N_h} + p\right) S_h - (\mu_h + \varphi_h) E_h \quad (2)$$

$$\frac{dI_h}{dt} = \varphi_h E_h - (\mu_h + \gamma_h + \alpha_h) I_h \quad (3)$$

$$\frac{dR_h}{dt} = \gamma_h I_h - \mu_h R_h \quad (4)$$

Vector Population

$$\frac{dS_v}{dt} = A - \left(\frac{\beta_v b I_h}{N_h} + \mu_v\right) S_v \quad (5)$$

$$\frac{dE_v}{dt} = \frac{\beta_v b I_h}{N_h} S_v - (\mu_v + \delta_v) E_v \quad (6)$$

$$\frac{dI_v}{dt} = \delta_v E_v - \mu_v I_v \quad (7)$$

with condition;

$$N_h = S_h + E_h + I_h + R_h \Rightarrow R_h = N_h - S_h - E_h - I_h \quad (8)$$

$$N_v = \frac{A}{\mu_v} = S_v + E_v + I_v \Rightarrow S_v = \frac{A}{\mu_v} - E_v - I_v \quad (9)$$

Thus, the model for the human and mosquito populations can be simplified as follows;

$$\frac{dS_h}{dt} = \mu_h N_h - \left(\frac{\beta_h b I_v}{N_h} + p + \mu_h\right) S_h \quad (10)$$

$$\frac{dE_h}{dt} = \left(\frac{\beta_h b I_v}{N_h} + p\right) S_h - (\mu_h + \varphi_h) E_h \quad (11)$$

$$\frac{dI_h}{dt} = \varphi_h E_h - (\mu_h + \gamma_h + \alpha_h) I_h \quad (12)$$

$$\frac{dE_v}{dt} = \frac{\beta_v b I_h}{N_h} S_v - (\mu_v + \delta_v) E_v \quad (13)$$

$$\frac{dI_v}{dt} = \delta_v E_v - \mu_v I_v \quad (14)$$

The model can be simplified by assuming the following fractions,

$$x = \frac{S_h}{N_h}, u = \frac{E_h}{N_h}, y = \frac{I_h}{N_h}, w = \frac{E_v}{N_v} \text{ and } z = \frac{I_v}{N_v} = \frac{I_v}{A/\mu_v} \quad (15)$$

Thus, the model for the human and mosquito populations can be simplified as follows;

$$\begin{aligned} \frac{dx}{dt} &= \mu_h(1-x) - px - \alpha xz \\ \frac{du}{dt} &= (\alpha z + p)x - (\mu_h + \varphi_h)u \\ \frac{dy}{dt} &= \varphi_h u - (\mu_h + \gamma_h + \alpha_h)y \\ \frac{dw}{dt} &= \gamma_v(1-z-w)y - (\mu_v + \delta_v)w \\ \frac{dz}{dt} &= \delta_v w - \mu_v z \end{aligned} \quad (16)$$

$$\text{with value } \alpha = \frac{\beta_h b A}{N_h \mu_v}$$

III. RESULT AND DISCUSSION

A. Equilibrium Point for SEIR Model

Critical point will occur while the value of

$\frac{dx}{dt} = \frac{du}{dt} = \frac{dy}{dt} = \frac{dw}{dt} = \frac{dz}{dt} = 0$. Simplify model in eq (16) as follows:

$$\begin{aligned} 0 &= a - (b + cz)x \\ 0 &= (d + cz)x - eu \\ 0 &= fu - gy \\ 0 &= h(1 - z - w)y - jw \\ 0 &= kw - lz \end{aligned}$$

with $a = \mu_h$, $b = a + p$, $c = \alpha$, $d = p$, $e = a + \varphi_h$, $f = \varphi_h$, $g = a + \gamma_h + \alpha_h$, $h = \gamma_v$, $j = \mu_v + \delta_v$, $k = \delta_v$ and $l = \mu_v$.

By using MAPLE, we obtained equilibrium point are:

$$\begin{aligned} x_1(t) &= m(\sqrt{q} - n), w_1(t) = \frac{1}{k}m(\sqrt{q} - n), \\ x_2(t) &= \frac{a}{b - am(\sqrt{q} - n)}, u_1(t) = -\frac{g[m(\sqrt{q} - n)]}{f[m(\sqrt{q} - n)](k + l) - fkn} \text{ and} \\ y_1(t) &= -\frac{[m(\sqrt{q} - n)]}{am(\sqrt{q} - n)(k + l) - kn} \text{, also} \end{aligned}$$

$$x_2(t) = -m(\sqrt{q} + n), w_2(t) = -\frac{1}{k}m(\sqrt{q} + n),$$

$$x_2(t) = \frac{a}{b - am(\sqrt{q} + n)}, u_2(t) = \frac{g[m(\sqrt{q} + n)]}{-f[m(\sqrt{q} + n)](k + l) - fkn} \text{ and}$$

$$y_2(t) = \frac{[m(\sqrt{q} + n)]}{-am(\sqrt{q} + n)(k + l) - kn}$$

With $m = \frac{1}{2[a(fkh + afkh + lgv)]}$,

$$\begin{aligned} n &= afdkh + afdlh - afckh + lgvb \text{ and} \\ q &= (afdkh)^2 + 2kl(afdlh)^2 + 2dc(afckh)^2 + \\ & 2afkdhlgv + (afdlh)^2 + 2dlck(afh)^2 + 2afdhlgvbi^2 + \\ & (afckh)^2 - 2afckhlgv + (lgv)^2 + 4afdkhlgv \end{aligned}$$

B. Eigen Values of The Model

Eigen values of the SEIR model obtained if only if $|J - \lambda I| = 0$, where J is the Jacobian matrix as a linearization matrix of equation (16) for the endemic equilibrium point, λ is the eigenvalue and I is the identity matrix, thus eigen values for the equilibrium x_1, u_1, y_1, w_1 and z_1 as follows:

$$\begin{vmatrix} -(b+cm\sqrt{q}-n)-\lambda & 0 & 0 & 0 & -\frac{ca}{cm\sqrt{q}-n+b} \\ cm\sqrt{q}-n+d & -e-\lambda & 0 & 0 & \frac{ca}{cm\sqrt{q}-n+b} \\ 0 & f & -g-\lambda & 0 & 0 \\ 0 & 0 & h-\frac{hkm\sqrt{q}-n(k+1)}{k} & \frac{hljm\sqrt{q}-n}{-kh+hm\sqrt{q}-n(k+l)}-j-\lambda & \frac{hljm\sqrt{q}-n}{-kh+hm\sqrt{q}-n(k+l)} \\ 0 & 0 & 0 & -\frac{hljm\sqrt{q}-n}{-l-\lambda} & 0 \end{vmatrix} = 0$$

$$\text{then } \begin{aligned} & (-b - bc\sqrt{q} + bn - \lambda)(-e - \lambda)(-g - \lambda) \\ & \left[\left(\frac{hljm\sqrt{q}-n}{-kh+hm\sqrt{q}-n(k+l)} - f - \lambda \right)(-l - \lambda) - \frac{hljm\sqrt{q}-n}{-kh+hm\sqrt{q}-n(k+l)} \right] = 0 \end{aligned}$$

So that, eigen value equation of the model is:

$$K_1 + K_2\lambda + K_3\lambda^2 + K_4\lambda^3 + K_5\lambda^4 - \lambda^5 = 0$$

With: $K_1 = C_1C_2C_3(C_4C_5 - C_6)$

$$K_2 = -\frac{(C_1C_2C_3(C_4 + C_5) + (C_1C_2 + C_1C_3 + C_2C_3)(C_4C_5 - C_6))}{(C_1 + C_2 + C_3)(C_4C_5 - C_6)}$$

$$K_3 = \frac{C_1C_2C_3 + (C_1 + C_2)(C_1C_3 + C_2C_3) + (C_1 + C_2 + C_3)(C_4C_5 - C_6)}{(C_1 + C_2 + C_3)(C_4C_5 - C_6)}$$

$$K_4 = -\frac{(C_1C_2 + C_1C_3 + C_2C_3) + (C_1 + C_2 + C_3)(C_4 + C_5)(C_4C_5 - C_6)}{(C_1 + C_2 + C_3)(C_4C_5 - C_6)}$$

$$K_5 = C_1 + C_2 + C_3 + C_4 + C_5$$

and

$$\begin{aligned} C_1 &= -b - bc\sqrt{q} + bn \\ C_2 &= -e \\ C_3 &= -g \\ C_4 &= \frac{hljm\sqrt{q}-n}{-kh+hm\sqrt{q}-n(k+l)} - j \\ C_5 &= -l \\ C_6 &= \frac{hljm\sqrt{q}-n}{-kh+hm\sqrt{q}-n(k+l)} \end{aligned}$$

Conclusion of the eigen value equation is: If $K_i > 0$ or $K_i < 0, \forall K_i, i=1, 2, \dots, 5$ then:

- ❖ The SEIR model always gives the most valuable eigen value of Real and others Complex-value. ($\lambda_1 = a, \lambda_{2,3} = b \pm ci$ and $\lambda_{4,5} = b \pm ci$) with $a, b, c, d, e \in R$.
- ❖ Stability analysis of the system is focus asymptotically stable and focus unstable.

If the model using parameters have been determined using the values published in previous studies as shown on table 1.

TABLE 1.
PARAMETER VALUES

Name of Parameter	Notation	Value
Infected rate of host to recover	$\frac{1}{F_R}$	0.3288330
Effective contact rate, human to vector	$b\beta_v$	0.3750000
Effective contact rate, vector to human	$b\beta_h$	0.7500000
Possibility to death caused by dengue itself	α_R	0.0000002
Percentage of mosquitoes are infected	p	0.0900000
Rate for people exposed to dengue infected	φ_R	0.1667000
Rate of exposed mosquitoes to the virus infection	δ_V	0.1428000
Human life span	$\frac{1}{M_H}$	0.0000460
Vector life span	$\frac{1}{M_V}$	0.0323000

The equilibrium point is determined using a set of SEIR model with parameters in South Sulawesi has been set. Then, to determine the critical point, equation (16) is set equal to zero, as shown below,

$$0.000046(1-x) - 0.09xz - 0.2925xz - 0 \quad (17)$$

$$0.2925xz + 0.09xz - (0.1667 + 0.000046)u = 0 \quad (18)$$

$$0.1667u - (0.328833 + 0.000046 + 0.0000002)y = 0 \quad (19)$$

$$0.375(1-x-w)y - (0.1428 + 0.0323)w = 0 \quad (20)$$

$$0.1428w - 0.0323z = 0 \quad (21)$$

By using the software MAPLE obtained equilibrium points as follows:

$$(x, u, y, w, z) = (274.626866, -0.08537, -0.037234, -0.069632, -0.307849) \text{ and } (0.000509, 0.000276, 0.00014, 0.000299, 0.001321).$$

The equilibrium points (274.626866, -0.08537, -0.037234, -0.069632, -0.307849) is not suitable to be studied because only the value of S_R is positive while other value is negative and it is illogical.

Eigen values λ for Eq. (16) are the equilibrium point (274.626866, -0.08537, -0.037234, -0.069632, -0.307849) is obtained eigen values: $\lambda = -0.172238 + 0.99089i, \lambda = -0.172238 - 0.99089i, \lambda = -1.175266, \lambda = 0.830726$ and $\lambda = -0.000046$ and the equilibrium point (0.000509, 0.000276, 0.00014, 0.000299, 0.001321) is obtained eigen values: $\lambda = -0.171385 + 0.01045i, \lambda = -0.171385 - 0.01045i, \lambda = -0.329126, \lambda = -0.089131$ and $\lambda = -0.032483$.

Refer to the equilibrium points (0.000509, 0.000276, 0.000140, 0.000299, 0.001321) are the focus equilibrium points which are asymptotically stable. It shows that if the number of people who have the potential to be infected at rate 0.0005090, the number of people who are exposed at rate 0.0002760, the number of people who are infected at rate

0.0001400 of the human population. The dengue fever is asymptotically stable and focused. Our model shows that dengue fever is not alarming in this area.

C. Numerical Result of SEIR Model

Simulation carried out using ODESOLVE, MATLAB. Stability analysis was carried out for the epidemic and values of the threshold were obtained. Illustration of the dynamics of each epidemic is given in figure 1 and figure 2.

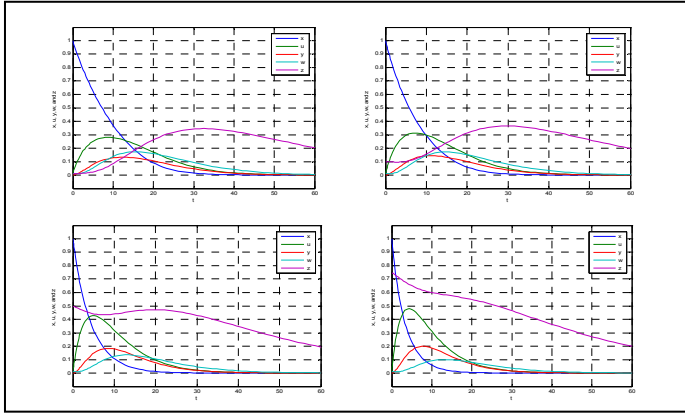


Fig. 1. Illustration of the dynamics system with $R_0 \leq 1$ (Convergence)

Figure 1 shows the typical behaviour of the solutions indicating the rate of Susceptible, Exposed, Infectious and Removed approaches asymptotically, the trivial state of the system (the ideal state) to the case where all the population is will remain healthy.

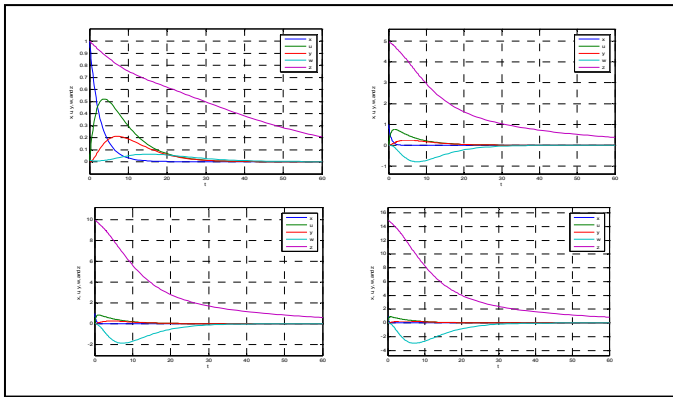


Fig. 2. Illustration of the dynamics system with $R_0 > 1$ (Oscillation)

Figure 2 illustrates an oscillatory behaviour near the neighbourhood of the endemic equilibrium point. This behaviour can be justified by the fact that if $R_0 > 1$ and if the initial value I_h satisfy the solution.

Result of SEIR model simulation with parameters by using MATLAB as follow:

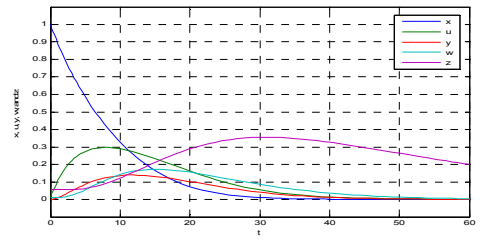


Fig 3: Transmission of dengue fever with initial condition

$$S_h(0) = \frac{7675406}{7675893}, E_h(0) = \frac{76759}{7675893}, I_h(0) = \frac{487}{7675893}$$

$$E_v(0) = 0.01 \text{ and } I_v(0) = 0.056 \text{ with parameter}$$

$$\mu_h = 0.000046, \rho = 0.09, C_{vh} = 0.75, \phi_h = 0.1667$$

$$C_{hv} = 0.375, \delta_v = 0.1428$$

$$\sigma_h = 0.0000002, \gamma_h = 0.328833 \text{ and}$$

$$\mu_v = 0.0323.$$

According to Figure 3, number of dengue fever cases (virus-infected people) shows that the total of infected people rapidly took over for the 12th month to reach the highest level (15%) of the human population. The number of people infected will be reduced close to zero for the next 35th month. In addition, the number of people exposed will reach a peak at the 9th month and will fall close to zero for the next 35th month. This is happen because the parameters used in appropriate, except that the determination of these parameters meet the conditions for SEIR model of the cure rate should be lower than average infection rates. Meanwhile, the number of infected mosquitoes in Figure 3 takes about for the next 30th month to achieve the highest total for almost 40% of the population of mosquitoes. In addition, the number of infected mosquito takes more than 60 months to approach zero point. This indication means that the mosquito population takes more time off.

Simulation using SEIR model for dengue fever cases also found that the total of cases had not reached a serious level. Cases of dengue fever were as high as 15% of the total population of 7.675893 people.

D. Breeding Rates, R_0

Searching for the re-breeding rates R_0 is important because it shows how many infections will occur to individuals as a result of an infection. If an infection can infect others for more than one, so the value $R_0 > 1$ and dengue fever become epidemic. Determination of the reproduction rate has been introduced by [6]. The basis for determining value R_0 is use to prevail the infection rate to individuals who have the potential to be infected ($\frac{\beta I_h}{N_h}$) and rates for individuals who have recovered (γ_h).

The formula of threshold parameter value R_0 for Selangor can be rewritten in mathematical form as follows:

$$R_0 = \frac{(C_{hv} I_v) / N_h}{\gamma_h} S(0)$$

The reproductive rates depend on the number of infected mosquitoes (I_v). Determination of value R_0 is accomplished by replacing I_v to some of the different values shown in table 1. The difference between these values I_v is very significant.

TABLE 2
DETERMINATION OF THE REPRODUCTIVE VALUE
OF INFECTED MOSQUITOES

I_v value	R_0 value
0.1	0.11403
0.5	0.5702
1	1.1403
5	5.7015
10	11.403

Table 2 shows, if the density of infected mosquitoes less than one, $I_v < 1$ then the value $R_0 < 1$. If the density of mosquitoes infected more than one, ($I_v > 1$), then the value $R_0 > 1$. Corollary, the spreading of dengue virus causes more than one person infected.

IV. CONCLUSIONS

Result of the SEIR model indicates that infection to human is based on the data. This is because dengue virus infection occur when there is a continuous correlation between human and mosquito. Furthermore, the SEIR model is a potential for the studies and can be applied to the real data in the country. Latent period in SEIR model gives a good positively effect to the result.

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