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A fractional order SIR epidemic model for dengue transmission

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ABSTRACT

In the present work, we study the fractional order differential equation of the dengue epidemic system based on the susceptible-infected-recuperated (SIR) model. The threshold quantity value R_0 similar to the basic reproduction number is obtained using the next-generation matrix approach. The local stability of the disease-free equilibrium (DFE) point and endemic equilibrium point is presented. Using the linearization theorem, we achieved that DFE is locally asymptotically stable when $R_0 < 1$ and is unstable when $R_0 > 1$. When $R_0 > 1$, the endemic equilibrium is locally asymptotically stable. Numerical simulations are given for different parameter setting of the order of derivative α. The proposed model is validated using published weekly dengue cases in Malaysia which were recorded in 2016. It is observed that the proposed model provides a more realistic way to understand the dynamic of dengue disease.

1. Introduction

Dengue fever or commonly known as dengue is a painful, debilitating mosquito-borne tropical disease caused by the dengue virus. It is a viral disease transmitted by the bite of an *Aedes* mosquito infected with any of the four serotypes denoted by DEN-I, DEN-II, DEN-III, and DEN-IV, respectively. In recent decades, the spread of the dengue virus has increased rapidly and according to the World Health Organization (WHO), there are millions of dengue cases reported every year worldwide. A human that get infected by any of these dengue serotype produces permanent immunity to it, but only a temporary cross-immunity to the other serotypes [25].

Symptoms of dengue fever normally appear within 3 to 14 days after the infective bite. The symptoms can vary from a mild fever to incapacitating high fever, with a severe headache, rashes, muscle and joint pain. The more serious forms of dengue include dengue hemorrhagic fever (DHF) and dengue shock syndrome. These affecting mainly children and can cause death. There is no specific vaccine available for dengue. Preventing and controlling the dengue virus depends solely on the control of the mosquito vector or interruption of human-vector contact [20,25].

A reliable mathematical model is essential to give a deeper understanding of the mechanism of disease transmission and on how to control the spread of the disease. Generally, over decades, epidemiological models are formulated using classical integer order derivatives [11]. However, at some point, this model cannot fully explain the natural behaviour of the disease.

In this paper, the proposed dengue epidemic model is derived using the generalized fractional order derivatives. In the recent years, fractional order calculus is found to be more appealing in modelling for a real world problem in comparison to a classical integer order as it provides a tool for the description of memory effects and genetic properties of various materials. Recent entomological studies revealed that mosquito did not feed randomly on human blood, but they use their prior experience on human location and human defensiveness to select the host to feed on [21]. Thus, in dengue transmission, a future state does depend on the history of the transmission. Hence, fractional order differential equation is found to be the best approach to model the transmission.

The purpose of this study is to propose and study a more accurate mathematical model of dengue transmission using the fractional order derivative than those previously presented in the literature [1,5,7,19,21,22]. Further, this study aims to use the fractionalization the SIR dengue model that was established by Bailey [3] using Caputo definition including the dynamics of the aquatic phase of the mosquito population. The local stability of the disease-free and endemic equilibrium is performed. Numerical results of the proposed fractional order system are presented to verify the theoretical study of the stability.

This paper is organized as follows. In Section 2, we recall some basic definitions of the fractional-order operators, and we present some of the most useful mathematical properties that will be used

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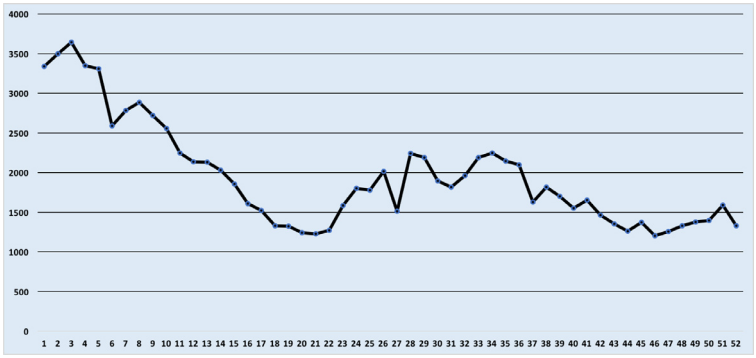


Fig. 1. Number of dengue cases reported in Malaysia in 2016 (weeks).

throughout the paper. In Section 3, the disease-free and endemic equilibrium points are obtained and its stability is discussed. The numerical results and discussions are presented in Section 4 to verify the theoretical analysis done in Section 3. Finally, conclusions are given in Section 5.

2. Basic mathematical properties

The idea of fractional calculus was first triggered by Leibniz in 1695. For the past three centuries, fractional calculus is renowned among the mathematicians mainly in the pure branch. Only in the last few years, this is drawn to several applied fields of engineering and sciences, since fractional order model can give a more realistic interpretation of the real problem [9].

There are several different definitions of fractional derivative in the literature. In this paper, the Caputo derivative approach has been used due to its advantages in applied problems. The main advantage of using Caputo's approach is that the initial conditions for fractional order differential equation with Caputo derivative is the same as that of integer differential equation, avoiding solvability issues.

The definition of the Caputo fractional derivative is defined as follows

$$D_C^{\alpha} f(t) = J^{n-\alpha}[f^{(n)}(t)] = \frac{1}{\Gamma(n-\alpha)} \int_0^t (t-s)^{n-\alpha-1} f^{(n)}(s) ds, \quad (1)$$

where n is the first integer which is greater than α.

The Laplace transform of the Caputo fractional derivative is given by

$$\mathscr{L}[D_C^{\alpha} f(t)] = \lambda^{\alpha} F(s) - \sum_{k=0}^{n-1} f^{(k)}(0) \lambda^{\alpha-k-1}. \quad (2)$$

The Mittag–Leffler function is defined by the following infinite power series:

$$E_{\alpha,\beta}(z) = \sum_{k=0}^{\infty} \frac{z^k}{\Gamma(\alpha k + \beta)} \quad (3)$$

The Laplace transform of the function is

$$\mathscr{L}[t^{\beta-1} E_{\alpha,\beta}(\pm \alpha t^{\alpha})] = \frac{s^{\alpha-\beta}}{s^{\alpha} \mp \alpha} \quad (4)$$

Let α, $\beta > 0$ and $z \in \mathbb{C}$, and the Mittag–Leffler functions satisfy the equality given by Theorem 4.2 in [6]

$$E_{\alpha,\beta}(z) = z E_{\alpha,\alpha+\beta}(z) + \frac{1}{\Gamma(\beta)}. \quad (5)$$

3. Formulation of the model

The important aspect in the model that considered by many researchers to interpret the dynamical behaviour of the infectious disease is the susceptible-infected-recuperated model (SIR) introduced by Kermack and McKendrick in 1927 [15]. Bailey in [3], developed a simple vector-host transmission model provides the basis for dengue models by addressing a single serotype, based on an SIR model for the host population. Whereas the SI model for the vector population, since once infected, the vector-mosquito was assumed to remain infectious until death. In this study, we fractional the dengue model established by Bailey, by including not only the adult stages of the female mosquitoes but also the aquatic stages of them.

The notation used in the proposed fractional order dengue model includes three epidemiological states of humans:

$H_s(t)$ susceptible (individuals who can contract the virus)
$H_i(t)$ infected (individuals who capable to transmitting the virus to others)
$H_r(t)$ recovered/resistant (individuals who have required immunity)

We assumed that the total human population $N_h = H$ is constant, so $H = H_s + H_i + H_r$. For the female mosquito model, we will only consider the susceptible and infected mosquito, since the mosquito does not enter the recovery phase after infected due to the shortened lifespan.

$A_m(t)$ aquatic phase (includes the egg, larva, and pupa stages)
$M_s(t)$ susceptible (mosquitoes that are able to contract the virus)
$M_i(t)$ infected (mosquitoes capable to transmit the virus to human)

Here, $M = M_s + M_i$. Further, we also assumed the following in formulating our model:

- There is no immigration of infected individuals into the human population.
- The coefficient of transmission of the disease is fixed and do not vary seasonally.
- Both human and mosquito are assumed to be born susceptible, no natural protection.
- Birth and death in both human and mosquito do not possess memory.
- Host-vector and vector-host dengue transmission follow a similar dynamic, so α for both is assumed to be the same between $0 < \alpha < 1$.

Based on the above assumptions, we can now write down the system of differential equations to representing the dynamics of a single strain mosquito-borne infection following Diethelm [7] and

Table 1
Description of the dengue model (6) parameters and their possible feasible ranges.

Parameter	Biological meaning	Range of values	References
q	Proportion of eggs	0–1	[14]
ϕ	Oviposition rate	0–11.2 per day	[14]
σ_A	Transition rate from aquatic to adult	0–0.19 per day	[14]
μ_A	Average aquatic mortality rate	0.01–0.47 per day	[14]
$1/\mu_m$	Average lifespan of adult mosquito	11–56 days	[23]
$1/\mu_h$	Average lifespan of human	73–75 years	[16]
b	The biting rate	0–1 per day	[2]
β_m	Transmission probability from human to vector	0.375	[11]
β_h	Transmission probability from vector to human	0.375	[11]
γ_h	Recovery rate in the host population	0.328833 per day	[23]
C	Mosquito carrying capacity	–	

Sardar et.al [22] as:

$$
\begin{aligned}
D^\alpha A_m &= q\phi(1 - A_m/C)M - (\sigma_A + \mu_A)A_m \\
D^\alpha M_s &= \sigma_A A_m - \frac{b^\alpha \beta_m}{H} M_s H_i - \mu_m M_s \\
D^\alpha M_i &= \frac{b^\alpha \beta_m}{H} M_s H_i - \mu_m M_i \\
D^\alpha H_s &= \mu_h(H - H_s) - \frac{b^\alpha \beta_h}{H} H_s M_i \\
D^\alpha H_i &= \frac{b^\alpha \beta_h}{H} H_s M_i - (\gamma_h + \mu_h)H_i \\
D^\alpha H_r &= \gamma_h H_i - \mu_h H_r
\end{aligned} \tag{6}
$$

where, $\alpha \in (0, 1]$ is the order of the fractional derivative. All model parameters are assumed to be positive. The following Table 1 lists out the parameters which were used in our model. The fractional derivatives used in the model (6) are all in the Caputo sense.

Parameters used in the model are determined from various sources. The values for the aquatic phase related parameter are taken from [14] and the transmission probability rate for human and the vector is taken from [11] due to lack of information in the Ministry of Health Malaysia (KKM) data. According to Halstead [13], the population of Southeast Asia and tropical America are similar and all four dengue viruses of Asian origin are endemic in both regions. Hence, these parameter estimations are considered reliable in this study. Some of the values are taken from KKM from 2016 database and from the case study in Selangor, Malaysia in [23]. Besides, the model also used parameter values from Singapore for the biting rate of the mosquito per day [2]. Since Malaysia and Singapore share the same climate, then the value of the parameter estimates for mosquito infection rates is acceptable.

4. Stability analysis of the model

We begin by showing that there exists a closed and bounded set Ω, which is positively invariant and attracting with respect to the system (6).

Theorem 4.1. *The closed set* $\Omega = \{(A_m, M_s, M_i, H_s, H_i, H_r) \in \mathbb{R}^5_+ : 0 \le H_s + H_i + H_r = K; 0 \le M_s + M_i \le V_1$ *and* $V_1 \ge \frac{\sigma_A A_m}{\mu_m}; 0 \le A_m \le V_2$ *and* $V_2 \ge q\phi M\}$ *is positively invariant with respect to model (6).*

Proof. (Following Sardar et al. [22]) Adding the last three equations of (6) and adding equation $D^\alpha M_s + D^\alpha M_i$, we get two fractional order differential equations with respect to the total human and vector population as follows:

$$D^\alpha H(t) = 0, \tag{7}$$

and

$$D^\alpha M(t) = \sigma_A A_m - \mu_m M. \tag{8}$$

Solution to the Eq. (7) is $H(t) = K$, since the Caputo derivative of a constant is zero and $H(0) = K$.

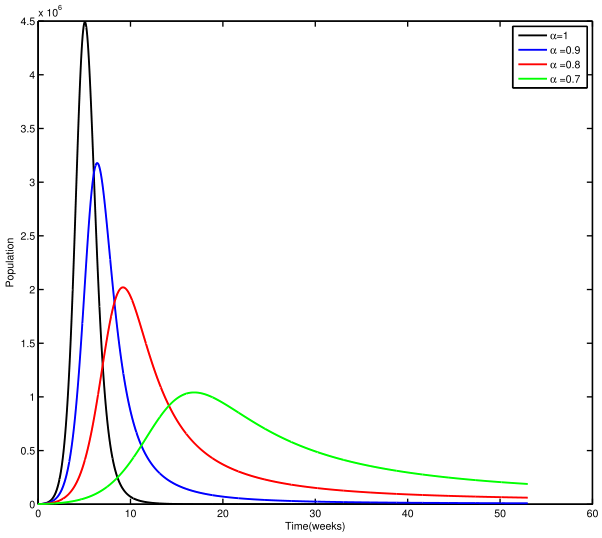


Fig. 2. Solution to the fractional order model of the infected human with different value of order α.

Now, we solve Eq. (8) by using the Laplace transform method [18], we have the following solution:

$$D^\alpha M(t) = \sigma_A A_m - \mu_m M(t)$$

Applying the Laplace transform (2), we have

$$\lambda^\alpha \mathscr{L}(M(t)) - \lambda^{\alpha-1}(M(0)) = \sigma_A A_m - \mu_m \mathscr{L}(M(t)), \tag{9}$$

that can be written as below using the Laplace transform properties (4) and equality (5),

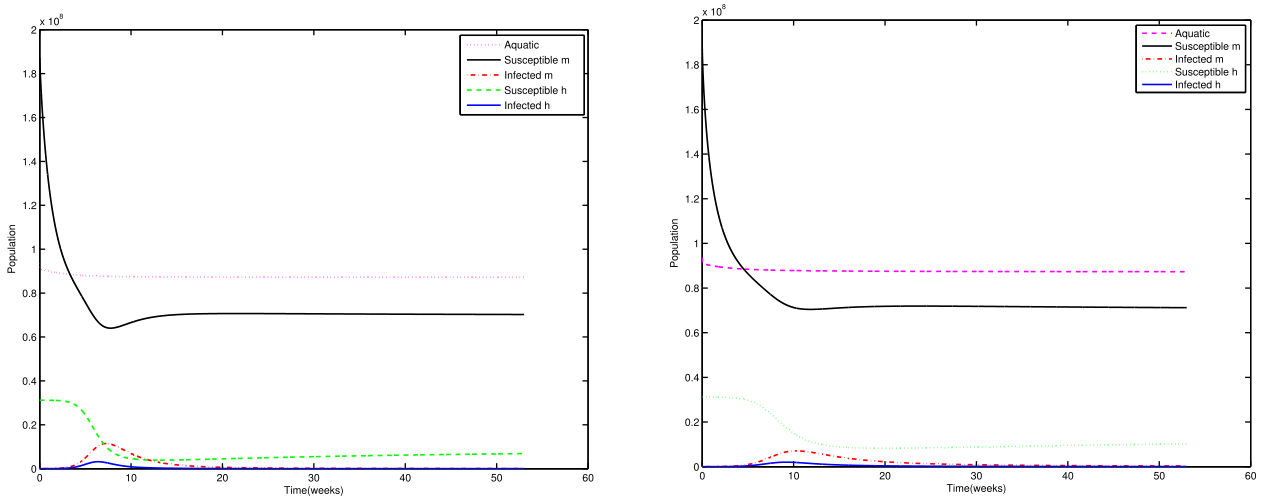
$$
\begin{aligned}
\mathscr{L}(M(t))(\lambda^\alpha + \mu_m) &= \sigma_A A_m + \lambda^{\alpha-1} M(0)\lambda^\alpha + \mu_m \\
\mathscr{L}(M(t)) &= \frac{\sigma_A A_m}{\lambda^\alpha + \mu_m} + \frac{\lambda^{\alpha-1} M(0)}{\lambda^\alpha + \mu_m} \\
&\le \frac{\sigma_A A_m}{\mu_m} + t^{\alpha-1} E_{\alpha,\alpha}(-\mu_m t^\alpha) M(0) \\
&\le V_1 + C_1 t^{\alpha-1} E_{\alpha,\alpha}(-\mu_m t^\alpha)
\end{aligned} \tag{10}
$$

where $V_1 \ge \frac{\sigma_A A_m}{\mu_m}$, C_1 is an arbitrary constant, $0 < \alpha \le 1$ and $E_{a,\,b}(z)$ is the two parameter Mittag–Leffler function with parameter a and b [6,18]. Since Mittag–Leffler function is an entire function, thus $E_{\alpha,\alpha}(-\mu_m t^\alpha)$ is bounded for all $t > 0$. Therefore, as $t \to \infty$ we have $M(t) \le V_1$.

For the fractional order differential equation of aquatic phase of the vector we have

$$D^\alpha A_m(t) = q\phi M - \frac{q\phi M}{C} A_m - (\sigma_A + \mu_A)A_m \tag{11}$$

$$\le q\phi M - (\sigma_A + \mu_A)A_m. \tag{12}$$



(a) $\alpha = 0.9$ (b) $\alpha = 0.8$

Fig. 3. Solution to the fractional order model.

Applying Laplace transform, we have

$$\lambda^{\alpha}\mathscr{L}(A_m(t)) - \lambda^{\alpha-1}(A_m(0)) \le q\phi M - (\sigma_A + \mu_A)\mathscr{L}(A_m(t)), \quad (13)$$

that can be written as below using the Laplace transform properties (4) and equality (5),

$$\begin{aligned}\mathscr{L}(A_m(t))(\lambda^{\alpha} + (\sigma_A + \mu_A)) &\le q\phi M + \lambda^{\alpha-1}A_m(0)\\ \mathscr{L}(A_m(t)) &\le \frac{q\phi M}{\lambda^{\alpha} + (\sigma_A + \mu_A)} + \frac{\lambda^{\alpha-1}A_m(0)}{\lambda^{\alpha} + (\sigma_A + \mu_A)}\\ &\le \frac{q\phi M}{\sigma_A + \mu_A} + t^{\alpha-1}E_{\alpha,\alpha}(-(\sigma_A + \mu_A)t^{\alpha})A_m(0)\\ &\le V_2 + C_2 t^{\alpha-1}E_{\alpha,\alpha}(-(\sigma_A + \mu_A)t^{\alpha}) \qquad (14)\end{aligned}$$

where $V_2 \ge \frac{q\phi M}{\sigma_A+\mu_A}$ and C_2 are the arbitrary constant. Hence, it follows the same argument as in the vector model. Thus, closed set Ω is positively invariant and attracting to the system (6). □

With the relation of $N_h = H = H_s + H_i + H_r$, we have $H_r = H - H_s - H_i$. Thus, system (6) can be reduced as follows:

$$\begin{aligned}D^{\alpha}A_m &= q\phi(1 - A_m/C)M - (\sigma_A + \mu_A)A_m\\ D^{\alpha}M_s &= \sigma_A A_m - \frac{b^{\alpha}\beta_m}{H}M_s H_i - \mu_m M_s\\ D^{\alpha}M_i &= \frac{b^{\alpha}\beta_m}{H}M_s H_i - \mu_m M_i\\ D^{\alpha}H_s &= \mu_h(H - H_s) - \frac{b^{\alpha}\beta_h}{H}H_s M_i\\ D^{\alpha}H_i &= \frac{b^{\alpha}\beta_h}{H}H_s M_i - (\gamma_h + \mu_h)H_i \qquad (15)\end{aligned}$$

For the system (15), the region $\Omega_1 = \{(A_m, M_s, M_i, H_s, H_i) \in \mathbb{R}^4_+ | 0 \le H_s + H_i \le K; 0 \le M_s + M_i \le V_1$ and $V_1 \ge \frac{\sigma_A A_m}{\mu_m}; 0 \le A_m \le V_2$ and $V_2 \ge q\phi M\}$ is positively invariant and attracting.

4.1. Equilibrium points

Theorem 4.2. *Consider R_m to be the basic offspring of the mosquito population*

$$R_m = \frac{q\phi\sigma_A}{\mu_m(\sigma_A + \mu_A)}.$$

The system of equation (15) has at most two disease-free equilibrium points:

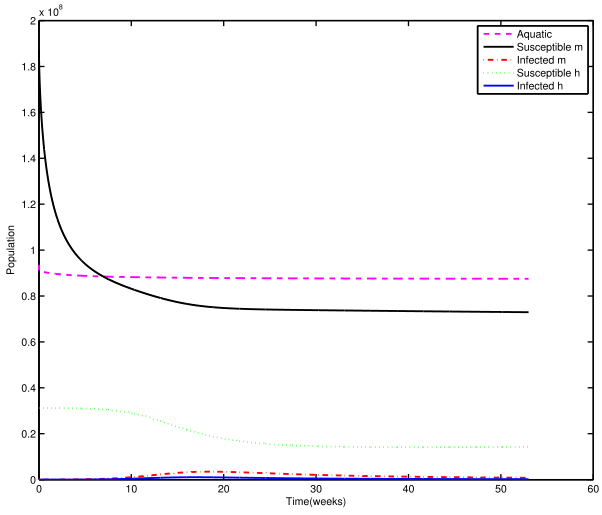


Fig. 4. Solution to the fractional order model with $\alpha = 0.7$.

- *if $R_m \le 0$, there is a disease-free equilibrium (DFE), knows as trivial equilibrium, $E_0 = (0, 0, 0, H, 0,)$;*
- *if $R_m > 0$, there is a biologically realistic disease-free equilibrium (BRDFE), $E_1 = (\bar{A_m}, \bar{M_s}, 0, H, 0)$.*

Proof. To evaluate the equilibrium points, we let

$$D^{\alpha}A_m = 0, \quad D^{\alpha}M_s = 0, \quad D^{\alpha}M_i = 0, \quad D^{\alpha}H_s = 0, \quad D^{\alpha}H_i = 0$$

By using Maple software, we obtain four equilibrium points for system (15). Two of them are known as *disease-free equilibrium* (DFE).

The first DFE is called *trivial equilibrium*, since $A_m = 0$, so the mosquitoes do not exist, hence no disease occurs:

$$E_0 = (0, 0, 0, H, 0,).$$

The second DFE is better called as the *biologically realistic disease-free equilibrium* (BRDFE), is the case when human and vector interact, but only one outbreak of the disease. Thus, the disease will die out over time without any action taken on the mosquito population. This equilibrium is more realistic than the previous one

as it is related to the natural phenomena,

$E_1 = (\bar{A_m}, \bar{M_s}, 0, H, 0)$,

where $\bar{A_m}$ and $\bar{M_s}$ are given by

$$\bar{A_m} = C(1 - \frac{1}{R_m}) \qquad \text{and} \qquad \bar{M_s} = \frac{\sigma_A \bar{A_m}}{\mu_m}.$$

Thus we obtained the following:

$$E_1 = \left(\frac{C(q\phi\sigma_A - \mu_A\mu_m - \mu_m\sigma_A)}{q\phi\sigma_A}, \frac{C(q\phi\sigma_A - \mu_A\mu_m - \mu_m\sigma_A)}{q\phi\mu_m}, 0, H, 0\right)$$

$$E_1 = \left(C(1 - \frac{1}{R_m}), \frac{C\sigma_A}{\mu_m}(\frac{R_m - 1}{R_m}), 0, H, 0\right)$$

where $R_m = \frac{q\phi\sigma_A}{\mu_m(\sigma_A + \mu_A)}$. This is biologically interesting only if $R_m > 1$ as this implies a positive population of mosquitoes. □

Theorem 4.3. *If $R_m > 0$ and $R_0 > 1$, the system (15) has an endemic equilibrium given by $E_2 = (A_m^*, M_s^*, M_i^*, H_s^*, H_i^*)$.*

Proof. The third equilibrium point is known as the positive endemic equilibrium point. In this condition, humans and mosquitoes interact and live together, but the disease persists in two populations. This is where the dengue virus rapidly spread and the disease becomes endemic. This equilibrium is only of interest for when $R_m > 1$.

$$E_2 = (A_m^*, M_s^*, M_i^*, H_s^*, H_i^*), \quad \text{where}$$

$$A_m^* = \frac{C(q\phi\sigma_A - \mu_A\mu_m - \mu_m\sigma_A)}{q\phi\sigma_A} = C(1 - \frac{1}{R_m})$$

$$M_s^* = \frac{(\gamma_h + \mu_h)H(-\mu_m(-q\phi\mu_h + C(\sigma_A + \mu_A))b^{-\alpha} + Cq\phi\sigma_A\beta_h)}{q\phi\beta_h((\gamma_h + \mu_h)\mu_m + \mu_h b^\alpha\beta_m)}$$

$$M_i^* = \frac{H^3\mu_h\mu_m(\gamma_h + \mu_h)(q\phi R_0^2 - 1)}{b^\alpha\beta_h(b^{2\alpha}\beta_h\beta_m + (\gamma_h + \mu_h)\mu_m H^2)}$$

$$H_s^* = \frac{\mu_m H^2 q\phi(\mu_m(\gamma_h + \mu_h)b^{-\alpha} + \mu_h\beta_m)}{\beta_m(C\beta_h(q\phi\sigma_A - \mu_m(\sigma_A + \mu_A))b^\alpha + Hq\phi\mu_h\mu_m)}$$

$$H_i^* = \frac{H^2\mu_h\mu_m^2(q\phi\sigma_A R_0^2 - 1)}{b^\alpha\beta_m\sigma_A(Hq\phi\mu_m\mu_h - Cb^\alpha\beta_h\mu_m(\sigma_A + \mu_A) + q\phi\sigma_A Cb^\alpha\beta_h)} \tag{16}$$

The fourth equilibrium will not be considered, since some of its components are negative, which implies that it does not belong to the Ω set. □

4.2. The basic reproduction number

Generally, the basic reproduction number, R_0 of the epidemic is defined as the expected number of secondary infections generated by a single, typical infection in a completely susceptible population. In the sense of vector-borne disease, this can be interpreted as the number of persons who would be infected from a single person initially infected by a mosquito. Theoretically, if $R_0 < 1$, the transmission chains are not self-sustaining and are unable to generate a major epidemic. Whereas, if $R_0 > 1$, the number of infected individuals will increase with each generation and the disease will blowout.

By using the next generation matrix approach, we obtained the following R_0 of system (15) evaluating at the BRDFE. In this case, R_0 is equal to the spectral radius of $K = FV^{-1}$ of BRDFE, where F is the non-negative matrix of the infection terms, and V is the non-singular M-matrix of the transition terms.

$$F = \begin{pmatrix} 0 & \frac{b^\alpha\beta_m}{H}\bar{M_s} \\ b^\alpha\beta_h & 0 \end{pmatrix}$$

and

$$V^{-1} = \begin{pmatrix} -\frac{1}{\mu_m} & 0 \\ 0 & -\frac{1}{\gamma_i + \mu_h} \end{pmatrix}$$

therefore,

$$FV^{-1} = \begin{pmatrix} 0 & \frac{-b^\alpha\beta_m\bar{M_s}}{H(\gamma_i + \mu_h)} \\ \frac{-b^\alpha\beta_h}{\mu_m} & 0 \end{pmatrix}.$$

The eigenvalues of FV_{-1} is:

$$= \pm\sqrt{\frac{b^{2\alpha}\beta_m\beta_h\bar{M_s}}{H(\gamma_i + \mu_h)\mu_m}}$$

$$= \pm\sqrt{\frac{b^{2\alpha}\beta_m\beta_h}{(\gamma_i + \mu_h)\mu_m}\frac{\bar{M_s}}{H}}$$

Therefore, the dominant eigenvalue of FV^{-1} is

$$R_0 = \sqrt{\frac{b^{2\alpha}\beta_m\beta_h}{(\gamma_i + \mu_h)\mu_m}\frac{\bar{M_s}}{H}} \tag{17}$$

where $\bar{M_s} = \frac{\sigma_A\bar{A_m}}{\mu_m}$.

Note that the R_0 calculated for fractional system (6) is of dimension $[\text{time}]^{-\alpha}$, hence it is not a dimensionless quantity as generally defined for the basic reproduction number in the integer order setting. The threshold quantity R_0 defined in (17) is a memory dependent threshold quantity as $R_0 \propto b^\alpha$. Therefore, as the value of α is getting smaller, the value of b^α is decreasing, thus, less effective the average bite rate per mosquito per month [21].

4.3. The local stability of the BRDFE

Theorem 4.4. *The BRDFE, E_1 is locally asymptotically stable if $R_0 < 1$ and is unstable if $R_0 > 1$.*

Proof. The disease-free equilibrium is locally asymptotically stable if all the eigenvalues, $\lambda_i, i = 1, 2, 3, 4, 5$ of the jacobin matrix $J(E_1)$ satisfy the following condition:

$$|\arg(\lambda_i)| > \frac{\alpha\pi}{2}.$$

The Jacobian matrix of the system evaluated at the equilibrium point, E_1:

$$J(E_1) = \begin{pmatrix} -R_m(\sigma_A + \mu_A) & 0 & 0 & 0 & 0 \\ \sigma_A & -\mu_m & 0 & 0 & \frac{b^\alpha\beta_m}{H}\bar{M_s} \\ 0 & 0 & -\mu_m & 0 & \frac{b^\alpha\beta_m}{H}\bar{M_s} \\ 0 & 0 & -b^\alpha\beta_h & -\mu_h & 0 \\ 0 & 0 & b^\alpha\beta_h & 0 & -(\gamma_h + \mu_h) \end{pmatrix}$$

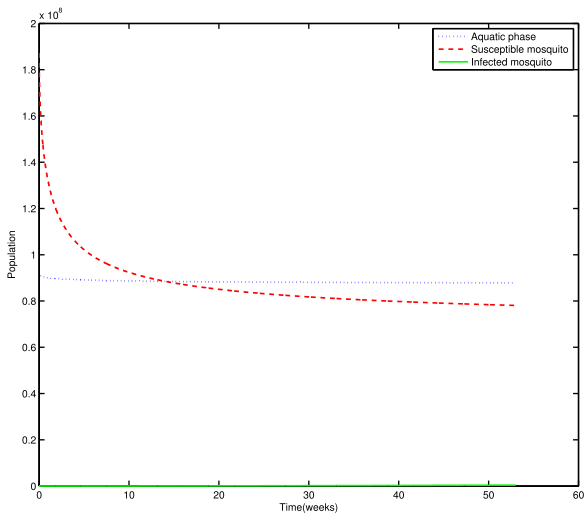
The calculated eigenvalues are $\lambda_1 = -R_m(\sigma_A + \mu_A), \lambda_2 = -\mu_m, \lambda_3 = -\mu_h$; the other two roots are determined by the quadratic equation

$$\lambda^2 + (\mu_m + \gamma_h + \mu_h)\lambda + \mu_m(\gamma_h + \mu_h)(1 - R_0) = 0.$$

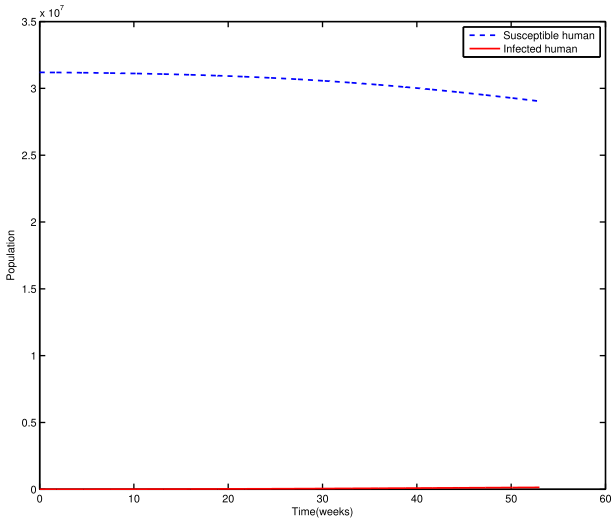
Hence, proved that E_1 is locally asymptotically stable if $R_0 < 1$ and is unstable if $R_0 > 1$ and the condition $R_m > 1$ is satisfied [17]. □

4.4. The local stability of the endemic equilibrium

Now, we move on to the local stability of the positive endemic equilibrium (16). The Jacobian matrix evaluated at the endemic equilibrium, E_2 for the system (15):



(a) Vector compartmental model



(b) Host compartmental model

Fig. 5. Solution to the fractional order model with $\alpha = 0.58$.

$$J = \begin{pmatrix} -\frac{q\phi(M_s^*+M_i^*)}{C} - (\sigma_A + \mu_A) & 0 & 0 & 0 & 0 \\ \sigma_A & -\frac{b^\alpha \beta_m}{H} H_i^* - \mu_m & 0 & 0 & \frac{b^\alpha \beta_m}{H} M_s^* \\ 0 & \frac{b^\alpha \beta_h}{H} H_i^* & -\mu_m & 0 & \frac{b^\alpha \beta_m}{H} M_s^* \\ 0 & 0 & -\frac{b^\alpha \beta_h}{H} H_s^* & -\mu_h - \frac{b^\alpha \beta_h}{H} M_i^* & 0 \\ 0 & 0 & \frac{b^\alpha \beta_h}{H} H_s^* & \frac{b^\alpha \beta_h}{H} M_i^* & -(\gamma_h + \mu_h) \end{pmatrix}. \tag{18}$$

The characteristic equation of (18) is as follows:

$$(\lambda + \mu_m)(\lambda + (\gamma_h + \mu_h))(\lambda^3 + a_1\lambda^2 + a_2\lambda^3 + a_3) = 0 \tag{19}$$

where

$$a_1 = \theta + b_1 + \frac{q}{C}(M_s^* + M_i^*)$$

$$a_2 = \frac{b_1 q}{C}(M_s^* + M_i^*) + \theta b_1 + b_2$$

$$a_3 = \frac{a_2 q}{C}(M_s^* + M_i^*) + \theta b_2$$

$$\theta = \sigma_A + \mu_A$$

$$b_1 = \mu_h + \frac{b^\alpha \beta_h}{H} M_i^* + \frac{b^\alpha \beta_m}{H} H_i^* + \mu_m$$

$$b_2 = \mu_h \mu_m + \frac{\mu_h b^\alpha \beta_m}{H} H_i^* + \frac{b^{2\alpha} \beta_m \beta_h}{H^2} M_i^* H_i^* + \frac{\mu_m b^\alpha \beta_h}{H} M_i^*$$

If $p(x) = x^3 + a_1x^2 + a_2x + a_3$. Let $D(p)$ be the discriminant of a polynomial $p(x)$; then

$$D(p) = -\begin{pmatrix} 1 & a_1 & a_2 & a_3 & 0 \\ 0 & 1 & a_1 & a_2 & a_3 \\ 3 & 2a_1 & a_2 & 0 & 0 \\ 0 & 3 & a_1 & a_2 & 0 \\ 0 & 0 & 3 & 2a_1 & a_2 \end{pmatrix}$$

$$= 18a_1a_2a_3 + (a_1a_2)^2 - 4a_3a_1^3 - 4a_2^3 - 27a_3^2.$$

Following [1,9,17] we have the following proposition.

Proposition 4.1. *One assumes that E_2 exists in R_+^3.*

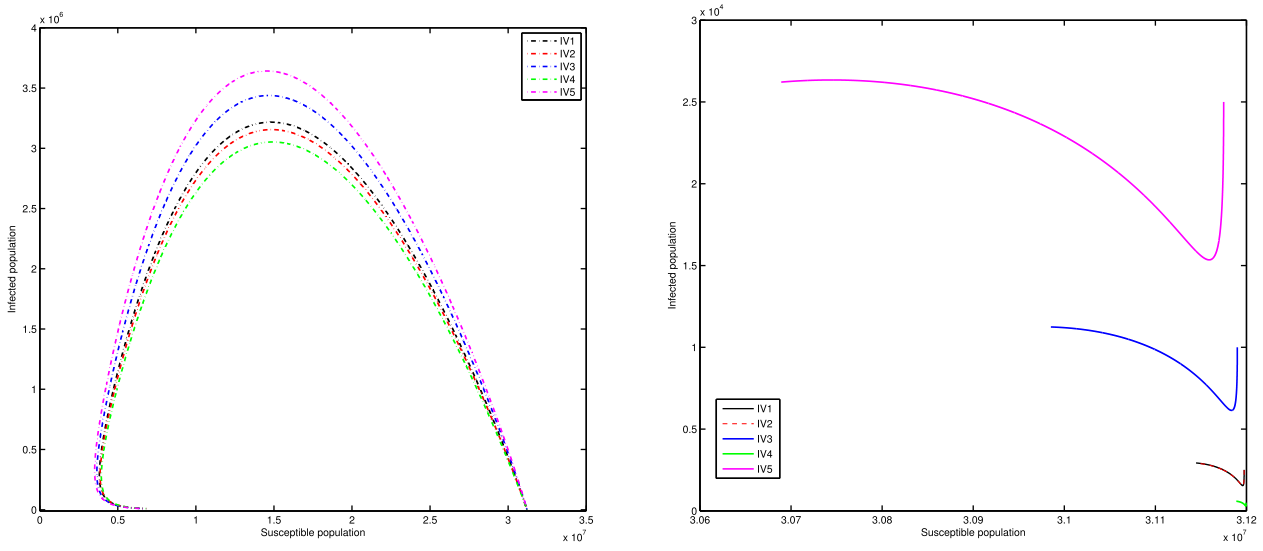
1. *If $R_0 > 1$, then E_2 is locally asymptotically stable.*
2. *If the discriminant of $p(x)$, $D(p)$, is positive and Routh–Hurwitz are satisfied, that is, $D(p) > 0$, $a_1 > 0$, $a_3 > 0$, and $a_1a_2 > a_3$, then E_2 is locally asymptotically stable.*
3. *If $D(p) < 0, a_1 > 0, a_2 > 0, a_1a_2 = a_3$, and $\alpha \in [0, 1)$, then E_2 is locally asymptotically stable.*
4. *If $D(p) < 0$, $a_1 < 0$, $a_2 < 0$, and $\alpha > 2/3$, then E_2 is unstable.*
5. *The necessary condition for the equilibrium point E_2, to be locally asymptotically stable, is $a_3 > 0$.*

5. Results and discussions

There are several analytical and numerical methods have been proposed to solve such systems. Diethelm and Freed [8] proposed a new algorithm called *FracPECE*, that based on the classical predict, evaluate, correct, evaluate (PECE) type approach, appropriately modified to be able to solve for fractional order derivative [12]. In this paper, we used Matlab code **fde12.m** established by Garrappa [12] that numerically to solve fractional order derivatives using PECE method proposed by Diethelm and Freed in [8]. This method is a combination of some product integration rules, known as fractional Adams–Bashforth–Moulton methods. The simulations were carried out using the parameter values taken from [10,11,14,24] and dengue cases reported in Malaysia for the year 2016.

The numerical simulation is done using the parameters value $\phi = 7.5, b = 0.7$, $\beta_m = 0.375$, $\beta_h = 0.375, \mu_A = 1/4$, $\mu_m = 1/11$, $\mu_h = 1/74$, $\gamma_h = 1/3$, $\sigma_A = 0.08$, $H = 31{,}200{,}000$, $C = 3H$, $k = 3$, $m = 6$, with the initial conditions set to be $H_s(0) = H - 2511$, $H_i(0) = 2511$, $H_r(0) = 0$, $A_m(0) = kH$, $M_s(0) = mH, M_i(0) = 0$. As the real epidemic data in Malaysia is collected for a period of a year, we decided to simulate using a period of time that is 52 weeks long. The step size has been chosen to be 10^{-3} weeks. Control computations with much smaller step size is not necessary since it does not lead to a significantly different or better result.

In this study, the choice of the order of the differential operator based on the idea of Diethelm 2013 in [7]. We solved the system for various different values of α, specifically we have used



(a) For $\alpha = 0.9$ (b) For $\alpha = 0.5$

Fig. 6. Phase portrait of the dynamics of susceptible population and the infective population (S–I) plane.

$\alpha \in \{i/100 : i = 1, 2, \ldots, 100\}$. From these values, we found that a good approximation was obtained with α is between 0.7 to 0.9 for the base parameter values.

Fig. 2 shows the curves related to the infected human population for different value of α. We observed that as the α value getting close to one, the solution follows the pattern of the classical integer order system. The peak of the plot is reduced as the α value decreased. This tells us that the disease needs a longer time to be eradicated. This feature is important from an epidemiological point of view since its interpretation shows a longer period of the disease in which this situation can affect the health system.

The data in Fig. 2 can be compared with the data obtained from KKM for dengue cases in Malaysia in 2016, as shown in Fig. 1. According to Fig. 1, the number of dengue cases will reach the maximum peak within the next two months, meanwhile, Fig. 2 shows that the number of infected individuals reaches the maximum level differently according to the value of α. For $\alpha = 1$ in which reflects the traditional derivative, and we observed that the outbreak occurs in a short period of time and the number of infected people reduced to close to zero for the next 10 months. This tells us that the classical derivative solution gives a shorter period of infectiousness which implies that an epidemic is of smaller magnitude and lasts only for a short period of time. However, in the fractional order derivative, the outbreak appeared later and takes more time to reduce the number of infected people based on the α value. If we compared these two results with the actual data reported in Fig. 1, the solution obtained from the fractional order differential equation is more relevant and portray the real transmission of the dengue disease in Malaysia in terms of the widespread of the disease over a longer period of time.

From the Figs. 3 and 4, it is clear that the solutions converge, in time, towards the steady state that is the disease-free equilibrium. Hence, the result of the local stability analysis of the equilibrium matches the numerical outcomes represented by the curves behaviour in Figs. 3 and 4. Thus, Theorem 4.4 is verified. In Fig. 5, for $\alpha = 0.58$ the curves show that the solutions approach the disease-free steady state in a very short period of time and we observed no dengue outbreak in this solution curves. This contradicts with the real phenomena of dengue outbreak in Malaysia. Thus, we can conclude that by setting the order α to be less than the selected α range mentioned earlier will result in a poor approximation.

Fig. 6 exemplify the invariance properties of the system (15). Generally, for varying initial conditions, solutions of the system either converges to the disease-free equilibrium or endemic equilibrium. It can be observed from Fig. 6(a), that for the chosen initial value, the solution curve tends to the endemic equilibrium point E_2, for different value of α chosen. In this case, the threshold quantity value R_0 is determined to be greater than 1. Hence, we can conclude that the system (15) is globally stable about the endemic equilibrium point E_2 for the set of parameters chosen when $R_0 > 1$. In Fig. 6(b), when $R_0 < 1$, the trajectory shows an unstable behaviour where the solution curves do not converge to the endemic equilibrium.

6. Conclusion

In this work, a model of dengue transmission with a fractional order derivative is introduced as the generalization of an integer order model. Some of the theoretical and epidemiological findings of the study are as follows:

- The dynamic behaviour of the fractional order system (15) such as the threshold quantity similar to the reproduction number R_0 is derived and it has shown that the disease can be eradicated if the R_0 is less than unity, in this case, is one.
- The model (15) has a locally asymptotically stable disease-free equilibrium whenever the associated $R_0 < 1$, and locally asymptotically stable endemic equilibrium whenever $R_0 > 1$.
- The positive endemic equilibrium of the model (15) is shown to be globally asymptotically stable when $R_0 > 1$ numerically.

As discussed in [1,4], we note that even though the disease-free equilibrium point of integer order model and fractional order model are the same, the solution of fractional order model tends to the fixed point over a longer period of time. The results obtained from this study are in agreement with Sardar et.al [22], where increasing the mosquito and human memory ($\alpha \to 0$) will reduce the intensity of the dengue transmission. However, as α approaches 0, the dengue disease needs longer time to be eliminated. Hence, a

thorough investigation needs to be done, to ensure the best value of order α is chosen for the proposed model with the particular real data set.

The obtained results might not be the best approximation of the model yet. This is due to the factor of parameter estimation. The parameter used might not be appropriate although the determination of these parameters meet the requirements of the SIR model [23]. Hence, a complete sensitivity analysis of the parameter needs to be done in the future study to see how important each parameter to the transmission of the disease and how does the parameter values affect the choice of α. However, in this study, the idea of using the fractional order differential equation is found to be more appealing and realistic in modelling the dengue transmission compared with the ordinary differential equation as it possesses memory.

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References

[1] Al-Sulami H, El-Shahed M, Nieto JJ, Shammakh W. On fractional order dengue epidemic model. Math Probl Eng 2014:1–6.
[2] Ang KC, Li Z. Modelling the spread of dengue in Singapore. In: Conference proceedings for the international congress on modeling and simulation 1999, 2. New Zealand: Hamilton; 2014. p. 555–60.
[3] Bailey NTJ. The mathematical theory of infectious diseases and its applications. London: Griffin; 1975.
[4] Demirci E, Unal A, Özalp N. A fractional order SEIR model with density dependent death rate. Hacettepe J Math Stat 2011;40(2):287–95.
[5] Derouich M, Boutayeb A. Dengue fever: mathematical modelling and computer simulation. Appl Math Comput 2006;177:528–44.
[6] Diethelm K. The analysis of fractional differential equations: an application-oriented exposition using operators of caputo type. Springer; 2004.
[7] Diethelm K. A fractional calculus based model for the simulation of an outbreak of dengue fever. Nonlinear Dyn 2013;71(4):613–19.
[8] Diethelm K, Freed AD. The fracPECE subroutine for the numerical solution of differential equations of fractional order. Forschung Wiss Rechnen 1998:57–71.
[9] Diethelm K, Ford NJ. Analysis of fractional differential equations. J Math Anal Appl 2002;260(2):229–48.
[10] Esteva L, Yang HM. Assessing the effects of temperature and dengue virus load on dengue transmission. J Biol Syst 2015;23(4):527–54.
[11] Esteva L, Vargas C. Analysis of dengue transmission model. Math Biosci 1998;15(2):131–51.
[12] Garrappa R. Trapezoidal methods for fractional differential equations: theoretical and computational aspects. Math Comput Simul 2015;11:96–112.
[13] Halstead SB. Dengue in Americas and Southeast Asia: do they differ? Rev Panam Salud Publ 2006;6:407–15.
[14] Pinho STR, Ferreira CP, Esteva L, Barreto FR, Morato E, Silva VC, Teixeira MGL. Modelling the dynamics of dengue real epidemics. Philos TransR Soc 2006;368:5679–93.
[15] Kermack WO, McKendrick AG. A contribution to the mathematical theory of epidemics. Proc R Soc A Math Phys Eng Sci 1927;115:700–21.
[16] KKM. The current situation of dengue fever in Malaysia epid week. 2016Director of infection control, 2016 Newspaper Fact1–52.
[17] Matignon D. Stability results for fractional differential equations with applications to control processing. Proc Comput EngSyst Appl 1996;2:963–8.
[18] Podlubny I. Fractional differential equations. San Diego, California: Academic Press; 1999.
[19] Pooseh S, Rodrigues H, Torres D. Fractional derivatives in dengue epidemics. In: Simos T, Psihoyios G, Tsitouras C, Anastassi Z, editors. Numerical analysis and applied mathematics ICNAAM. Melville: American Institute of physics; 2011. p. 739–42.
[20] Rodrigues HS, Monteiro MTT, Torres DFM, Zinober A. Dengue disease, basic reproduction number and control. Int J Comput Math 2011:1–20.
[21] Sardar T, Rana S, Chattopadhyay J. A mathematical model of dengue transmission with memory. Commun Nonlinear Sci Numer Simul 2014;22:511–25.
[22] Sardar T, Rana S, Bhattacharya S, Al-Khaled K, Chattopadhyay J. A generic model for a single strain mosquito-transmitted disease with memory on the host and the vector. Math Biosci 2015. doi:10.1016/j.mbs.2015.01.009.
[23] Syafruddin S, Noorani MSM. SEIR model for transmission of dengue fever in Selangor Malaysia. Int J Modern Phys Conf Ser 2012;9:380–9.
[24] Yang HM, Ferreira CP. Assessing the effects of vector control on dengue transmission. Appl Math Comput 2008;198:401–13.
[25] World Health Organisation (WHO). Dengue. http://www.who.int/denguecontrol/disease/en, December 2017.