Dynamics and Analysis of Dengue Epidemics: A Fractional Order SIR Model with Next-Generation Matrix Methodology

Suleman Alfalqi
King Khalid University
Azmat Ullah Khan Niazi (azmatullah.khan@math.uol.edu.pk)
The University of Lahore
Easha Ramay
The University of Lahore
Bilal Ahmed
University of Science and technology of Fujairah UAE
Mohammed Alhagyan
Prince Sattam Bin Abdulaziz University

Research Article

Keywords: Dengue fever, Basic reproduction number, Fractional-order SIR model, Stability, Epidemiology, Mathematical modeling

Posted Date: December 15th, 2023

DOI: https://doi.org/10.21203/rs.3.rs-3744826/v1

Additional Declarations: No competing interests reported.

Dynamics and Analysis of Dengue Epidemics: A Fractional Order SIR Model with Next-Generation Matrix Methodology

Suleman Alfalqi [1], Azmat Ullah Khan Niazi[2,*], Easha Ramay[2], Bilal Ahmed[3], Mohammed Alhagyan[4]

[1] *Mathematics Department, Faculty of Sciences and Arts, King Khalid University, Muhayil Asir, Saudi Arabia.*

[2] *Department of Mathematics and Statistics, The University of Lahore, Sargodha, Pakistan*

[3] *College of Humanities and Sciences, University of Science and Technology of Fujairah, UAE*

[4] *Mathematics department, College of Humanities and Science in Al Aflaj, Prince Sattam Bin Abdulaziz University, Saudi Arabia, 11912,*

Email addresses: salfalqi@kku.edu.sa (S. Alfalqi)
azmatniazi35@gmail.com (A. U. K. Niazi)
easharamay19@gmail.com (E. Ramay)
bilalmaths7@yahoo.com (B. Ahmed)
m.alhagyan@psau.edu.sa (M. Alhagyan)

Abstract

One of the major infectious diseases in the world is dengue. Dengue fever, a mosquito-borne viral infection, continues to pose a significant public health threat in tropical and subtropical countries. In this article, we analyze the susceptible-infected-recuperated (SIR) model-based fractional order differential equation of the dengue epidemic system and we analyze of fractional model for the dengue transmission utilizing the new term Human hospitalized. The next-generation matrix methodology is used to obtain the threshold quantity value R_0, which is comparable to the essential reproduction value. In the case of constant controls, we evaluate the presence and consistency of the disease-free and infectious equilibrium simulation alternatives. The disease-free equilibrium (DFE) point and the endemic equilibrium point's local stability are discussed. We were able to determine that DFE is locally asymptotically stable when $R_0 < 1$ and unstable when $R_0 > 1$ by applying the linearization theorem. Numerical simulations are conducted to validate the proposed model against real-world dengue data. For various parameter values of the derivative α order, numerical simulations are provided. The proposed model is validated using published every year (390 millions) dengue cases are reported in world wide. The presented model, it is noted, offers a more accurate means of analyzing the dynamics of the disease dengue.

Keywords: Dengue fever; Basic reproduction number; Fractional-order SIR model; Stability; Epidemiology; Mathematical modeling
2010 MSC: 26A33, 34K37.

1 Introduction

A painful, life-threatening tropical disease spread by mosquitoes, dengue fever, also referred to as dengue, is brought on by the dengue virus. It is a virus that spreads through the bite of an Aedes mosquito

carrying any one of the four serotypes, which are represented by the letters DEN-I, DEN-II, DEN-III, and DEN-IV, in that order. The dengue virus has become more widespread in recent years, and the World Health Organization (WHO) reports that millions of cases are reported annually throughout the world. People who contract each of these mosquito versions imparts a permanent antibodies to it; another only causes an instantaneous cross-immunity serotype. Dengue fever symptoms often start to show up thirteen to fourteen days following the infectious bite. The symptoms can range from a low-grade fever to a high-grade fever that is so severe that it causes severe headaches, rashes, and pain in the muscles and joints. Dengue hemorrhagic fever (DHF) and the virus that causes den Shudder Disorder are two of the more severe types of the virus. These are destructive and mostly affect children. The only methods for stopping human-vector contact or treating the mosquito vector are those for preventing and controlling the dengue virus [1]. To provide an improved comprehension of the underlying process of disease transmission and guidance on regulating the spread of the disease, a reliable mathematical model is mandatory. Epidemiological models are usually developed over decades using conventional integer order derivatives [2]. Subsequently, though, this model will be unable to sufficiently explain the disease's natural evolution. A Fractional Order SIR (FO-SIR) epidemic model for dengue transmission incorporates fractional derivatives to describe the dynamics of the susceptible (S), infected (I), hospitalized (H), and recovered (R) compartments in a population. Fractional calculus generalizes the concept of derivatives and integrals to non-integer orders, providing a more flexible way to model complex systems with memory and long-range dependence. The generalized fractional order derivatives are used in this paper to derive a simulation of the dengue pandemic that has been postulated. Since fractional order calculus provides a method for describing the memory consequences and biological properties of different materials, it is now thought to be more appealing for modeling real-world problems than classical integer order calculus. According to recent entomological research, mosquitoes choose their host to feed on based on their prior knowledge of human location and defenses rather than feeding randomly on human blood [3]. As a result, an overview of the transmission does influence the subsequent state of dengue transmission. It is determined that the most effective method for modeling the transmission is to use fractional order differential equations. Using the fractional order derivative, a more accurate mathematical model of dengue transmission than those previously published in the literature is proposed and explored in this work [3],[5],[6],[10],[13],[27]. Furthermore, this research proposes to apply the Caputo definition of the SIR dengue model, which was fractionalized by Bailey [4], incorporating the dynamics of the mosquito population's aquatic phase. An analysis is conducted to determine the local stability of the endemic and disease-free equilibrium. To support the stability study conducted theoretically, we report the mathematical results of the proposed fractional ordering equipment.

The structure of this paper is as follows. The fundamental definitions of the fractional-order operators are reviewed in Section 2, along with a few of the most helpful mathematical properties that will be utilized in this paper. The stability of the disease-free and endemic equilibrium points is discussed in

Section 3. In order to validate the theoretical analysis conducted in Section 3, the numerical results and discussions are presented in Section 4. Section 5 concludes with some concluding observations.

2 Basic Mathematical properties

Leibniz was the first to propose the concept of fractional calculus in 1695. Researchers in math are acquainted with fractional calculus, especially in the pure branches, and have been for the past three centuries.Properties and evaluation of the fractional order SIR model involve studying the stability, existence, and uniqueness of solutions, Additionally, numerical simulations are used to demonstrate the methods by which the epidemic over time. This has only recently gained traction in a number of applied engineering and scientific domains because fractional order models can provide a more accurate understanding of the actual issue [10].

The term "fractional derivative" has been defined in the literature in a number of ways. The advantages of the Caputo derivative approach in applied problems are the reason for its use in this paper. For example, the Grunwald-Letnikov derivative, the Caputo derivative, and the Riemann-Liouville derivative are the definitions of the fractional derivative that are most frequently used. By avoiding solvability problems, the primary benefit of employing according to Caputo's method, the beginning conditions of the integer differential equation with a Caputo derivatives are also the beginning circumstances of a fractional order differential equation.

The definition of the Caputo fractional derivative is defined such as:

$$\mathfrak{D}^{\alpha}_{\mathfrak{C}} f(t) = J^{n-\alpha}[f^{n}(t)], = \frac{1}{\Gamma(n-\alpha)} \int_{0}^{t} (t-\omega)^{n-\alpha-1} f^{(n)}(\omega) d\omega \tag{1}$$

where n represents the integer larger than α. The definition of the Caputo fractional derivative's Laplace transform is

$$\mathfrak{L}[D^{\alpha}_{\mathfrak{C}} f(t)] = \lambda^{\alpha} F(\omega) - \sum_{k=0}^{n-1} f^{(k)}(0) \lambda^{\alpha-k-1}. \tag{2}$$

We consider the following infinite power series as the Mittag-Leffler function:

$$\mathbf{E}_{\alpha,\beta}(\mathbf{z}) = \sum_{k=0}^{\infty} \frac{\mathbf{z}^{k}}{\Gamma(\alpha k + \beta)}. \tag{3}$$

When the function is Laplace transformed, it's called

$$\mathfrak{L}[t^{\beta-1} \mathbf{E}_{\alpha,\beta}(\pm \alpha t^{\alpha})] = \frac{\omega^{\alpha-\beta}}{\omega^{\alpha} \mp \alpha}. \tag{4}$$

Let α,β>0 and $\mathbf{z} \in \mathfrak{C}$, and the equity defined by Theorem 4.2 in the Mittag-Leffler functions are accomplished in [10]

$$\mathbf{E}_{\alpha,\beta}(\mathbf{z}) = \mathbf{z}\mathbf{E}_{\alpha,\alpha+\beta}(\mathbf{z}) + \frac{1}{\Gamma(\beta)}. \tag{5}$$

3 Establishment of the system

We analyze the A_m, M_s, M_i, H_s, H_i, H_h, H_r Human-mosquito fractional model, which consists of two isolated populations, which comprises human populations and mosquito populations. Three human epidemiological states are contained in the syntax applied in a fractional order dengue model proposal:

$H_s(t)$ susceptible (people who are capable of contracting the virus)
$H_i(t)$ infected (people with a tendency for transmitting the virus to other people)
$H_h(t)$ hospitalized human (patients in hospitals who have become infected)
$H_r(t)$ recovered (the people who have been obtained immunity)
Suppose that the number of individuals of all people N_h remains constant, $N_h(t)$=$H_s(t)$+$H_i(t)$+$H_h(t)$+$H_r(t)$.
Only the susceptible and virus-infected mosquitoes are examined for the mosquitoes scenario, considering that due to its short lifespan, the infected mosquitoes do not go through the healing period. While,the mosquito population is categorized into two parts:
$A_m(t)$ aquatic phase (include the stages of yolks, larvae, and adults)
$M_s(t)$ susceptible (the bites of mosquito capable of catching the infection)
$M_i(t)$ infected (The virus can be spread to individuals by mosquito)
M=$M_s + M_i$, where the degree of the derivative of a fraction is denoted by $\alpha \in (0, 1]$. It is assumed that every parameter is not negative. For the suggested host-vector model, the configuration of fractionally ordered differential equations that are nonlinear varies as shown below:

$$\begin{cases} D^\alpha A_m = p\phi(1 - \frac{A_m}{C})M - (\psi_A + \mu_A), \\ D^\alpha M_s = \psi_A A_m - \frac{b^\alpha \beta_m}{H} M_s H_i - \mu_m M_s, \\ D^\alpha M_i = \frac{b^\alpha \beta_m}{H} M_s H_i - \mu_m M_i, \\ D^\alpha H_s = \mu_h(H - H_s) - \frac{b^\alpha \beta_h}{H} H_s M_i - \nu_h^\alpha H_s, \\ D^\alpha H_i = \frac{b^\alpha \beta_h}{H} H_s M_i - (\gamma_h + \mu_h + \nu_h) H_i, \\ D^\alpha H_h = \mu_h H_i - (\xi_h^\alpha + \gamma_h + \nu_h^\alpha) H_h, \\ D^\alpha H_r = \gamma_h H_i - \mu_h H_r. \end{cases} \tag{6}$$

The preliminary requirements are
$A_m \geq 0 \quad M_s(0) \geq 0 \quad M_i(0) \geq 0 \quad H_s(0) \geq 0 \quad H_i(0) \geq 0 \quad H_h(0) \geq 0 \quad H_r \geq 0 \quad \forall t \in R,$
While host-vector and vector-host infection with dengue have identical factors, it is assumed that α for both $0 < \alpha < 1$.
The table below lists the various parameters used in this fractional model along with their values and references:

Table 1: The dengue model's (6) variables are listed along with any conceivable ranges for them.

Parameters	Interpretation	Range of values	References
p	Proportion of eggs	0-1	[25]
Φ	The rate of laying eggs	0-11.2 per day	[25]
ψ_A	Rate of change from aquatic to grown-up life	0-0.19 per day	[25]
μ_A	Estimated frequency of aquatic deaths	0.01-0.47	[25]
$\frac{1}{\mu_m}$	Estimated mature mosquito longevity	11-56	Estimated
$\frac{1}{\mu_h}$	Human Beings longevity generally	73-75 years	[16]
b	The intensity of bites	0-1 per day	[11]
β_m	The possibility of human-to-vector the emission	0.375	[2]
β_h	Vector-to-human the emission	0.375	[2]
γ_h	Rate of healing within the host community	0.328833 per day	[7]
υ_h	natural death rate of human	0.0137	Assumed
ϵ_h	disease-related death rate of human	0.0001452	Estimated
Q	Mosquito carrying capacity	-	

Table provides a list of the parameters that were included in our model. In model 6, all of the Caputo interpretation extends to the derivatives of fractions. The model's parameters are obtained from a variety of sources. Because the Ministry of Health Malaysia data is lacking in information, the aquatic cycle-associated parameter values are obtained from [25], although the human and vector transmission probability rate was obtained from [2].

4 Model stability analysis

The stability of Disease-Free Equilibrium points can be analyzed using linear stability analysis or fractional stability analysis methods, such as the Caputo fractional derivative. Linear stability analysis typically involves computing the Jacobian matrix and evaluating its eigenvalues. The stability of the symbols of the actual elements of the eigenvalues determines the state of equilibrium points. We initiate by demonstrating the existence of the restricted and compassed set Ω that is appealing and entirely unaltered alongside referring to the model.

Theorem 4.1. *The closed set* $\Omega = (A_m, M_s, M_i, H_s, H_i, H_h, H_r) \in R_+^5 : \ 0 \leq H_s + H_i + H_h + H_r = \ k : 0 \leq M_s + M_i \leq V_1$ *and* $V_1 \geq \frac{\psi_A A_m}{\mu_m}; 0 \leq A_M \leq V_2$ *and* $V_2 \geq p\Phi M$ *is entirely invariant with respect to model.*

Proof. The most recent three calculations in (6) added as well as combining the calculation $D^\alpha M_s + D^\alpha M_i$. With regard to the vast majority of people and vectors, we obtain the following two fractional order differential equations:

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

and,

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

Equation (8) gets solved is $H(t) = K$.A constant's Caputo derivative is zero, therefore $H(0) = K$. Following the Laplace transform method, we are now solving an equation (8). Here is a solution that we have:

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

When we use the Laplace transform (4), we get

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

by implementing equivalence (5) and characteristics (4) of the Laplace transform, which can be defined as follows:

$$\begin{aligned}
\mathfrak{L}^{\alpha}(M(t))(\lambda^{\alpha} + \mu_m) &= \psi_A A_m + \lambda^{\alpha-1}M(0)\lambda^{\alpha} + \mu_m \\
\mathfrak{L}(M(t)) &= \frac{\psi_A A_m}{\lambda^{\alpha} + \mu_m} + \frac{\lambda^{\alpha-1}M(0)}{\lambda^{\alpha} + \mu_m} \\
&\leq \frac{\psi_A A_m}{\mu_m} + t^{\alpha-1}\mathbf{E}_{\alpha,\alpha}(-\mu_m t^{\alpha})M(0) \\
&\leq V_1 + Q_1 t^{\alpha-1}\mathbf{E}_{\alpha,\alpha}(-\mu_m t^{\alpha})
\end{aligned} \tag{10}$$

Where $V_1 \geq \frac{\psi_A A_m}{\mu_m}, Q_1$ is an arbitrary constant, $0 < \alpha \leq 1$ and $\mathbf{E}_{c,d}(\mathbf{z})$ is the Mittag-Leffler function has two variables, which are a and b[10, **?**]. Given that the Mittag-Leffler function is a complete function, subsequently $\mathbf{E}_{\alpha,\alpha}(-\mu_m t^{\alpha})$ is limiting to all individuals $t > 0$. Therefore, as $t \to \infty$ we have $M(t) \leq V_1$. We have the following for the fractional order differential equation of the vector's aquatic stage of growth:

$$D^{\alpha}A_m(t) = q\Phi M - \frac{q\Phi M}{Q}A_m - (\psi_A + \mu_A)A_m \tag{11}$$

$$\leq q\Phi M - (\psi_A + \mu_A)A_m \tag{12}$$

Applying the Laplace transform, we get

$$\lambda^{\alpha}\mathfrak{L}(A_m(t)) - \lambda^{\alpha-1}(A_m(0)) \leq q\Phi M - (\psi_A + \mu_A)A_m(t) \tag{13}$$

it is possibly expressed essentially by applying the equality (5) and characteristics (4), that can be defined

as follows:

$$\begin{aligned}
\mathfrak{L}(A_m(t))(\lambda^{\alpha} &+ (\psi_A+\mu_A)) \leq q\Phi M + \lambda^{\alpha-1}(A_m(0)) \\
\mathfrak{L}(A_m(t)) &\leq \frac{q\Phi M}{\lambda^{\alpha}+(\psi_A+\mu_A)} + \frac{\lambda^{\alpha-1}A_m(0)}{\lambda^{\alpha}+(\psi_A+\mu_A)} \\
&\leq \frac{q\Phi M}{\psi_A+\mu_A} + t^{\alpha-1}\mathbf{E}_{\alpha,\alpha}(-(\psi_A+\mu_A)t^{\alpha})A_m(0) \\
&\leq V_2 + Q_2 t^{\alpha-1}\mathbf{E}_{\alpha,\alpha}(-(\psi_A+\mu_A)t^{\alpha}) \qquad (14)
\end{aligned}$$

where $V_2 \geq \frac{q\Phi M}{\psi_A+\mu_A}$ are the in uncertainty integers. As a result, the proof identical to that of the vector model is observed. Since it is Ω entirely invariant, the closed set is desirable to the model (6). □

With regards to $N_h = H_s + H_i + H_h + H_r$.We have $H_r = N_h - H_s - H_i - H_h$. A System (6) can therefore be simplified which includes this:

$$\begin{aligned}
D^{\alpha}A_m &= q\phi(1-\frac{A_m}{Q})M - (\psi_A+\mu_A), \\
D^{\alpha}M_s &= \psi_A A_m - \frac{b^{\alpha}\beta_m}{H}M_s H_i - \mu_m M_s, \\
D^{\alpha}M_i &= \frac{b^{\alpha}\beta_m}{H}M_s H_i - \mu_m M_i, \\
D^{\alpha}H_s &= \mu_h(H-H_s) - \frac{b^{\alpha}\beta_h}{H}H_s M_i - \nu_h^{\alpha}H_s, \\
D^{\alpha}H_i &= \frac{b^{\alpha}\beta_h}{H}H_s M_i - (\gamma_h+\mu_h+\nu_h)H_i, \\
D^{\alpha}H_h &= \mu_h H_i - (\xi_h^{\alpha}+\gamma_h+\nu_h^{\alpha})H_h. \qquad (15)
\end{aligned}$$

In relation to system (15), the circumference $\Omega_1 = (A_m, M_s, M_i, H_s, H_i, H_h) \in R_+^4 | 0 \leq H_s + H_i + H_h \leq K; 0 \leq M_s + M$ and $V_1 \geq \frac{\psi_A A_m}{\mu_m}; 0 \leq A_m \leq V_2$ and $V_2 \geq q\Phi M$ is both repulsive and entirely invariant.

4.1 Equilibrium points

Theorem 4.2. *Assuming R_m to represent the bite of a mosquito population's offspring*
$R_m = \frac{q\Phi\psi_A}{\mu_m(\psi_A+\mu_A)}$
There are two disease-free equilibrium points in the system of equations (15) *at most:*
1. If $R_m \leq 0$,trivial equilibrium is a disease-free state of equilibrium(DEF), $E_0 = (0,0,0,H)$;
2. If $R_m > 0$, there exists a disease-free equilibrium (BRDEF) that is realistically based on biology, $E_1 = (\overline{A}_m, \overline{M}_s, 0, H, 0)$.

Proof. The equilibrium points are evaluated by letting

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

The model (15) has four equilibrium phases, which are obtained using the Mapie software. Two are referred to as "disease-free equilibrium(DFE)."

Trivial stability is the name given to the initial (DFE), since $A_m = 0$, Consequently, there are no mosquitoes, and no epidemics of disease:
$E_0 = (0, 0, 0, H, 0)$
The biologically realistic disease-free equilibrium (RDEF) is a better term for the second DFE, which is the situation when there is only one disease outbreak but interactions between humans and the vector. Because it is connected to natural phenomena, contrasting this equilibrium to the earlier one, it is more efficient,
$E_1 = (\overline{A}_m, \overline{M}_s, 0, H, 0)$,
where $\overline{A}_m$ and $\overline{M}_s$ are given by
$\overline{A}_m = Q(1 - \frac{1}{R_m})$ and $\overline{M}_s = \frac{\psi_A \overline{A}_m}{\mu_m}$
Consequently, we conclude with the following

$$E_1 = (\frac{Q(p\Phi\psi_A - \mu_A\mu_m - \mu_m\psi - A)}{p\Phi\psi_A}, \frac{Q(p\Phi\psi_A - \mu_A\mu_m - \mu_m\psi - A)}{p\Phi\psi_m}, 0, H, 0)$$

$$E_1 = (Q(1 - \frac{1}{R_m}), \frac{Q\psi_A}{\mu_m}(\frac{R_m - 1}{R_m}), 0, H, 0)$$

While $R_m = \frac{q\Phi\psi_A}{\mu_m(\psi_A + \mu_A)}$.This only has biological significance if $R_m > 1$ since this suggests that the mosquito population is growing. □

Theorem 4.3. *If $R_m > 0$ and $R_0 > 1$, The dominant equilibrium system-wide* (15) *is offered by* $E_2 = (A_m^*, M_s^*, M_i^*, H_s^*, H_i^*, H_h^*)$.

Proof. The positive epidemic equilibrium point is the definition of the 3rd equilibrium conclusion. In this situation, people and mosquitoes reside together, but the virus still affects two populations. Here, the dengue virus spreads quickly, and the viral infection becomes endemic. The third equilibrium point implies that there are multiple equilibrium points in the system, and you are interested in the behavior at the third one. This equilibrium is only of interest for when $R_m > 1$.

$$E_2 = (A_m^*, M_s^*, M_i^*, H_s^*, H_i^*)$$

where

$$\begin{aligned}
A_m^* &= \frac{Q(p\Phi\psi_A - \mu_A\mu_m - \mu_m\psi_A)}{p\Phi\psi_A} = Q(1 - \frac{1}{R_m}) \\
M_s^* &= \frac{(\gamma_h + \mu_h)H(-\mu_m(-p\Phi\mu_h + Q(\psi_A + \mu_A))b^{-\alpha} + Qp\Phi\psi_A\beta_h)}{p\Phi\beta_h((\gamma_h + \mu_h)\mu_m + \mu_h b^{\alpha}\beta_m)} \\
M_i^* &= \frac{H^3\mu - h\mu_m(\gamma_h + \mu_h)(p\Phi R_0^2 - 1)}{b^{\alpha}\beta_h(b^{2\alpha}\beta_h\beta_m + (\gamma_h + \mu_h)\mu_m H^2)} \\
H_s^* &= \frac{\mu_m H^2 p\Phi(\mu_m(\gamma_h + \mu_h)b^{-\alpha} + \mu_h\beta_m)}{\beta_m(Q\beta_h(p\Phi\psi_A - \mu_m(\psi_A + \mu_A))b^{\alpha} + Hp\Phi\mu_h\mu_m)} \\
H_i^* &= \frac{H^2\mu_h\mu_m^2(p\Phi\psi_A R_0^2 - 1)}{b^{\alpha}\beta_m\psi_A(Hp\Phi\mu_m\mu_h - Qb^{\alpha}\beta_h\mu_m(\psi_A + \mu_A) + p\Phi\psi_A Qb^{\alpha}\beta_h)}
\end{aligned} \tag{16}$$

Since some of the components of the fourth equilibrium are negative, indicating that it does not belong in the Ω set, it will not be taken into consideration. $\square$

4.2 Disease-free equilibrium and basic reproductive number

This model's basic reproduction number, or R_0, is computed using the next-generation matrix method and is a vital factor. In a population of people who are fully susceptible to dengue,R_0 represents the average number of people who will be infected by a single contagious individual in a population that is entirely susceptible to the disease. It is a key epidemiological parameter used to assess the potential for an infectious disease to spread within a population. In terms, if $R_0 < 1$, the transmission chains are unable to start an immense epidemic because they are not self-sustaining. Whereas, if $R_0 > 1$, Individuals who have contracted the disease will become more numerous with each subsequent era, and eventually the virus will propagate. We were able to obtain the appropriate R_0 of system (15) evaluating at the $BRDFE$ by employing the following kind of matrix methodology. It seems like R_0 is being defined in terms of the spectral radius of the matrix $K = FV^{-1}$. The specific details of the model would depend on the context and the specific definitions of the matrices F, V, and $BRDFE$, as well as the interpretation of the basic reproduction number R_0 in the context of the infection model.

$$F = \begin{pmatrix} 0 & \frac{b^{\alpha}\beta_m}{H}\overline{M}_s \\ b^{\alpha}\beta_h & 0 \end{pmatrix}, \qquad V^{-1} = \begin{pmatrix} -\frac{1}{\mu_m} & 0 \\ 0 & -\frac{1}{\gamma_i+\mu_h+\upsilon_h} \end{pmatrix}.$$

The transition and infection rates close to the equilibrium are represented by the letters F and V. Here, V^{-1} stands for the time that is spent in each state. FV^{-1} stands for the development of new infections during the pandemic. The basic number's associative has the largest eigenvalue in FV^{-1}.

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

The eignvalues of FV^{-1} is:

$$= \pm\sqrt{\frac{b^{2\alpha}\beta_m\beta_h\overline{M}_s}{(\gamma_i+\mu_h+\upsilon_h)\mu_m H}}$$

$$= \pm\sqrt{\frac{b^{2\alpha}\beta_m\beta_h}{(\gamma_i+\mu_h+\upsilon_h)\mu_m}\frac{\overline{M}_s}{H}}$$

In relation to this, one of the primary eigenvalue of FV^{-1} is

$$R_0 = \sqrt{\frac{b^{2\alpha}\beta_m\beta_h}{(\gamma_i+\mu_h+\upsilon_h)\mu_m}\frac{\overline{M}_s}{H}} \tag{17}$$

Here, $\overline{M}_s = \frac{\psi_A\overline{A}_m}{\mu_m}$.

The R_0 for the fractional system (15), it should be noted, is of dimension $[time]^{-\alpha}$. Thus, It doesn't

constitute an identical measure in the sense that is commonly applied when using an integer stability, an essential reproduction integer. As a requisite amount $R_0 \propto b^\alpha$ that depends on memory, R_0 is defined in (17).Consequently, the average monthly [3] bite rate per mosquito decreases as the value of b^α decreases in tandem with the decreasing value of α.

4.3 Local stability and global stability of E_0

Theorem 4.4. *The BRDFE, E_1 has asymptotic stability locally a case R_0 as well as become unstable when $R_0 > 1$.*

Proof. While each of the corresponding eigenvalues is positive, then the disorder-free equilibrium has asymptotic stability locally $\lambda_i, i = 1, 2, 3, 4, 5, 6$ accomplish the subsequent condition of the Jacobi matrix $J(E_1)$:
$|arg(\lambda_i)| > \frac{\alpha\pi}{2}$
The Jacobian matrix of (15) becomes

$$J(E_1) = \begin{pmatrix} -R_m(\sigma_A + \mu_A) & 0 & 0 & 0 & 0 & 0 \\ \sigma_A & -\mu_m & 0 & 0 & -\frac{b^\alpha \beta_m}{H}\overline{M}_s & 0 \\ 0 & 0 & -\mu_m & 0 & \frac{b^\alpha \beta_m}{H}\overline{M}_s & 0 \\ 0 & 0 & -b^\alpha \beta_h & -\mu_h - \upsilon_h^\alpha & 0 & 0 \\ 0 & 0 & b^\alpha \beta_h & 0 & -(\gamma_h + \mu_h + \upsilon_h) & 0 \\ 0 & 0 & 0 & 0 & \mu_h & (\epsilon_h^\alpha + \upsilon_h + \nu_h^\alpha) \end{pmatrix}.$$

The eigenvalues calculated are $\lambda_1 = -R_m(\psi_A + \mu_A), \lambda_2 = -\mu_m, \lambda_3 = -\mu_h - \upsilon_h^\alpha, \lambda_4 = (\epsilon_h^\alpha + \gamma_h + \upsilon_h^\alpha)$; the initial roots of the 2nd degree polynomial are other individuals

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

As a result, it was demonstrated that E_1 is unstable $R_0 > 1$ and locally asymptotically stable if $R_0 < 1$ and the condition $R_m > 1$ is satisfied. □

4.4 Local equilibrium stability of the epidemic method

Similar to local stability, linearize the system around the endemic equilibrium point and analyze a Jacobian matrix's eigenvalue. If all eigenvalues contain actual negative components, the endemic stability of equilibrium. We now analyze the positive endemic equilibrium's local stability. The Jacobian matrix determined for the system (15) at the endemic equilibrium E_2:

$$J = \begin{pmatrix} -\frac{q\Phi(M_s^* + M_i^*)}{Q} - (\psi_A + \mu_A) & 0 & 0 & 0 & 0 & 0 \\ \sigma_A & -\frac{b^\alpha \beta_m}{H} H_i^* - \mu_m & 0 & 0 & \frac{b^\alpha \beta_m}{H} M_s^* & 0 \\ 0 & -\frac{b^\alpha \beta_h}{H} H_i^* & -\mu_m & 0 & \frac{b^\alpha \beta_m}{H} M_s^* & 0 \\ 0 & 0 & -\frac{b^\alpha \beta_h}{H} H_s^* & -\mu_h - \frac{b^\alpha \beta_h}{H} M_i^* - \upsilon_h^\alpha & 0 & 0 \\ 0 & 0 & \frac{b^\alpha \beta_h}{H} M_s^* & \frac{b^\alpha \beta_m}{H} M_i^* & -(\gamma_h + \mu_h + \upsilon_h) & 0 \\ 0 & 0 & 0 & 0 & \mu_h & -(\epsilon_h^\alpha + \nu_h + \upsilon_h^\alpha) \end{pmatrix} \quad (18)$$

The following is the defining equation to obtain (18):

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

where

$a_1=\theta a+b_1+\frac{p}{Q}(M_s^*+M_i^*)$

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

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

$\theta=\psi_A+\mu_A$

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

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

5 Results and analysis

Numerous analysis and computational methods have been put advanced for resolving these kinds of problems. In order to find a solution for fractional order derivative, Diethelm and Freed [10] developed an alternative method called FracPECE, which is based on the conventional anticipate, assess, accurate, and analyze (PECE) sort methodology and has been significantly altered [30]. In this article, we implemented the PECE method—proposed through Diethelm and Freed in [10] to computationally find solutions fractional order derivatives via Matlab software **fde12.m**, developed by Garrappa R. Trapezoidal method [30]. The methodology combines the fractional $\mathbf{Adams-Bashforth-Moulton}$ techniques, a set of results integrating principles. An adequate simulation has been determined using α ranging from the range of **0.7** and **0.9** for the initial coefficient values.For the sake of simulation, the following parametric values were used: Q = 3H, H = 31,200,200, ϕ = 7.5, β_m= 0.375, β_h = 0.375, ψ_A = 0.079, m= 6, and υ_h = 0.0137, ϵ_h = 0.0001452, μ_h = 0.01351, γ_h = 0.328. Our team analyzed the system with several various amounts as α, particularly utilizing $\alpha\ \epsilon$ {i/100 : i = 1, 2,..., 100}. Figure 2 demonstrates the plots for various values of α related to the infected individuals. We noticed that when the α value approaches one, the conclusion corresponds to the structure of the conventional integer-valued equipment. Figures 3 and 4 make it obvious that the outcomes approximate periodically to the disease-free state of equilibrium or the constant state. Therefore, the outcome of the equilibrium's local stability evaluation corresponds with the computational findings obtained from the dynamics of the graphs in Figures 3 and 4. We observed neither dengue epidemic in this set of resolution lines figure 5 at α = 0.58, indicating that the solutions approximate the free-of-illness state of equilibrium rapidly. The characteristics of consistency of the system (15) are represented in Figure 6. Solutions of the system generally converge to the stable equilibrium or the disease-free equilibrium for a range of initial circumstances. As illustrated in Figure 6, the solution graph approaches the epidemic an equilibrium E_2 for a given initial value for α. The acceptable amount estimate R_0 in this instance is found to be higher than 1.

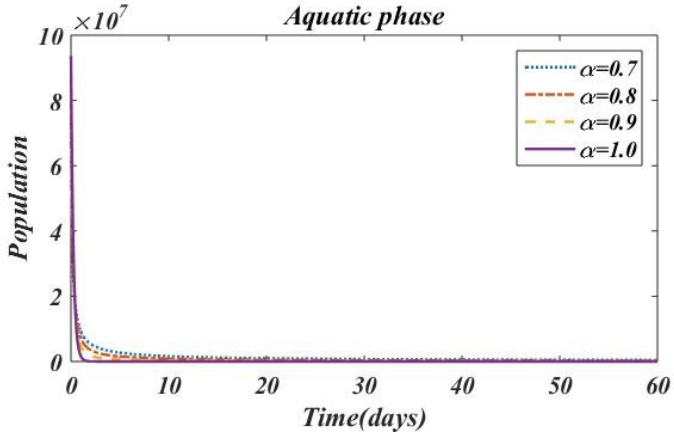

Figure 1: The dynamics of those $A_m(t)$ who are aquatic phase to dengue transmission.

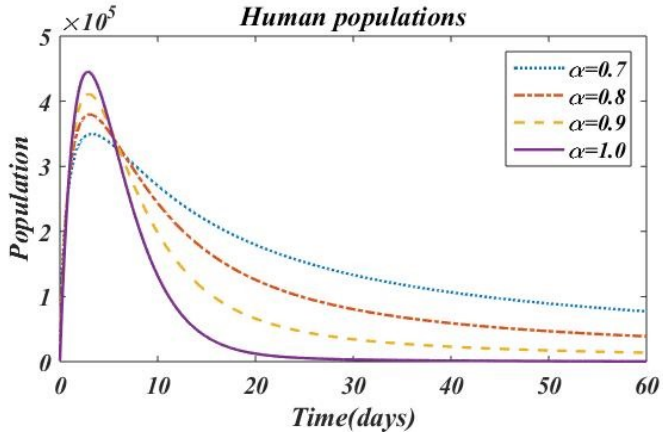

Figure 2: The solution of the fractional order model of an human population using various order α numbers.

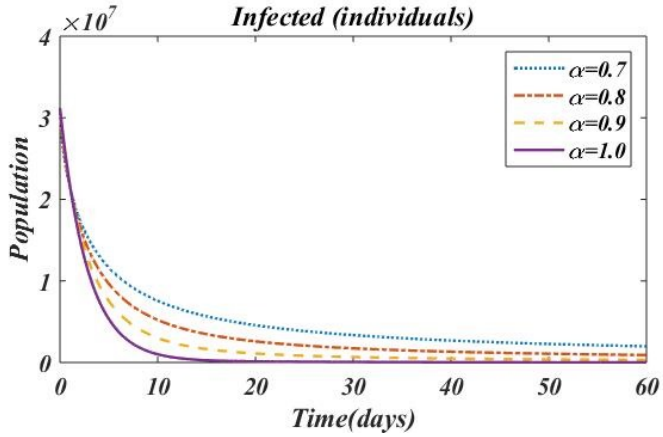

Figure 3: The plot revolves around the dynamics of those $I(t)$ who are infected individuals to dengue transmission with $\alpha = 0.7$.

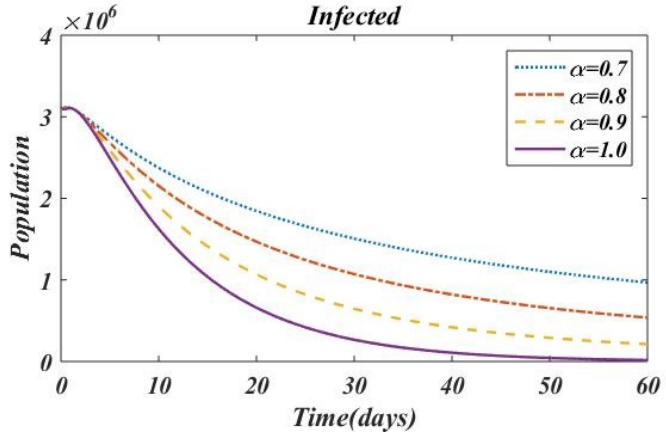

Figure 4: Plotting the dengue transmission infected $I(t)$ using solution to the fractional order model with α.

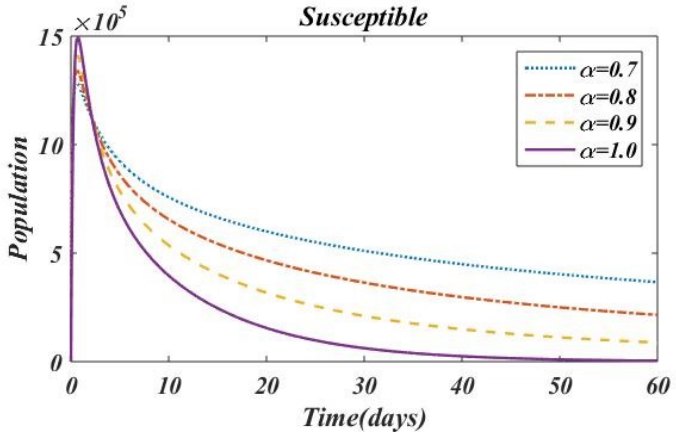

Figure 5: The dynamics of those $S(t)$ who are susceptible to dengue transmission with a solution of fractional order.

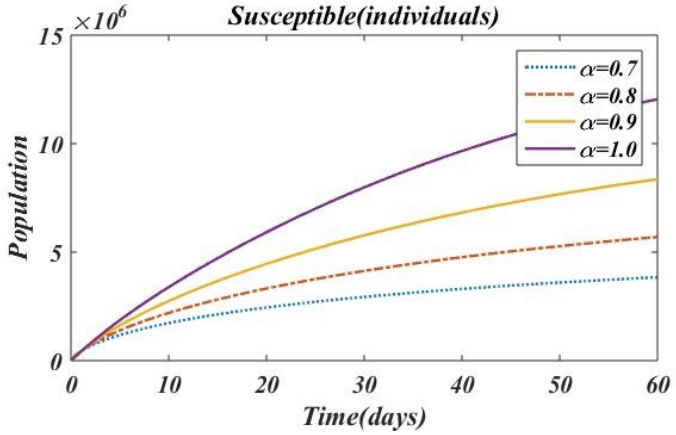

Figure 6: The solution of the fractional order model of susceptible individuals using various order $0 < \alpha < 1$.

6 Conclusion

In this study, we analyze a new fractional-order SIR epidemic model for dengue transmission. The objective of this work is to understand, analyze, and find the solution to the fractional epidemiological models. It has been demonstrated and determined theoretically that the equilibrium points are locally asymptotically stable. Locally and internationally, this concept is being implemented. We demonstrated that the DFE is secure locally and internationally if we take the basic reproduction to be $R_0 < 1$, and that the positive endemic equilibrium is stable locally asymptotically and globally asymptotically if $R_0 > 1$. Since the fractional order model's solution responds with the fixed point over an extended duration for a period than the integer order model's, despite the fact that both models' disease-free equilibrium points are the same, as previously discussed in [5]. According to Sardar et al [3], reducing human memory ($\alpha \to 0$) and increasing mosquito populations will reduce the intensity of dengue transmission. On the other hand, the dengue infections take longer to vanish as α gets closer to 0. Therefore, in order to determine the finest order α value for the suggested model using the specific real data set, a comprehensive investigation must be prevailed in conducted. Our control problem's explicit and physiological goal is to reduce the number of infected people and raise the number of people who are healthy in order to mask the damage caused by the dengue virus. Because most people are uneducated and unaware of viral infections and diseases associated with them, notably dengue virus, it indicates that the government should encourage sanitary measures in the general populace. In our research, we visually and quantitatively analyse the aquatic Phase, infected, hospitalized, and recovered people. Observed that b (biting rate), β_m, β_h are the most critical parameters that highly contribute to the control and subsequent spread of dengue infection. Numerical simulations are carried out and dynamics of the populations are shown to vary for different values of α. Therefore, in order to determine the significance of each parameter for the disease's transmission and how parameter values impact the selection of α, a thorough sensitivity analysis of each parameter must be conducted in a subsequent study. However, because the fractional order differential equation has memory, it is determined in this study shown that it provides an especially enticing and accurate dengue transmission model than the ordinary differential equation (ODE). We can propose that the biting rate of humans by mosquitoes and fractional order α can effectively regulate and significantly lower the disease incidence in society.

Acknowledgements

The authors extend their appreciation to the Deanship of Scientific Research at King Khalid University for funding this work through Larg Groups Project under grant number RGP. 2/ 554/ 44.

References

[1] Rodrigues, Helena Sofia, M. Teresa T. Monteiro, Delfim FM Torres, and Alan Zinober. "Dengue disease, basic reproduction number and control." International Journal of Computer Mathematics 89, no. 3 (2012): 334-346.Esteva, Lourdes, and Cristobal Vargas. "Analysis of a dengue disease transmission model." Mathematical biosciences 150, no. 2 (1998): 131-151.

[2] Esteva, Lourdes, and Cristobal Vargas. "Analysis of a dengue disease transmission model." Mathematical biosciences 150, no. 2 (1998): 131-151.Al-Sulami, Hamed, Moustafa El-Shahed, Juan J. Nieto, and Wafa Shammakh. "On fractional order dengue epidemic model." Mathematical Problems in Engineering 2014 (2014): 1-6.

[3] Sardar, Tridip, Sourav Rana, and Joydev Chattopadhyay. "A mathematical model of dengue transmission with memory." Communications in Nonlinear Science and Numerical Simulation 22, no. 1-3 (2015): 511-525.

[4] Bailey, Norman TJ. The mathematical theory of infectious diseases and its applications. Charles Griffin Company Ltd, 5a Crendon Street, High Wycombe, Bucks HP13 6LE., 1975

[5] Al-Sulami, Hamed, Moustafa El-Shahed, Juan J. Nieto, and Wafa Shammakh. "On fractional order dengue epidemic model." Mathematical Problems in Engineering 2014 (2014): 1-6.

[6] Derouich, Mohammed, and Abdesslam Boutayeb. "Dengue fever: Mathematical modelling and computer simulation." Applied Mathematics and Computation 177, no. 2 (2006): 528-544. childhood vaccination. Recommendations of the Immunization Practices Advisory Committee (ACIP). Morb. Mort. Wkly. Rep., Recomm. Rep. 40(RR-13), 1–25 (1991)

[7] Syafruddin, Side, and M. S. M. Noorani. "SEIR model for transmission of dengue fever in Selangor Malaysia." In International journal of modern physics conference series, vol. 9, pp. 380-389. 2012.

[8] Pooseh, Shakoor, Helena Sofia Rodrigues, and Delfim FM Torres. "Fractional derivatives in dengue epidemics." In AIP Conference Proceedings, vol. 1389, no. 1, pp. 739-742. American Institute of Physics, 2011.

[9] Kilicman, Adem. "Basic epidemic model of Dengue transmission using the fractional order differential equations." Malaysian Journal of Science 38, no. Sp 1 (2019): 1-18.

[10] Diethelm, Kai. "A fractional calculus based model for the simulation of an outbreak of dengue fever." Nonlinear Dynamics 71 (2013): 613-619.

[11] Ang, Keng Cheng, and Fung Yin Pang. "Modelling the spread of dengue in Singapore." (2002).

[12] Hamdan, Nur 'Izzati, and Adem Kilicman. "Analysis of the fractional order dengue transmission model: a case study in Malaysia." Advances in Difference Equations 2019 (2019): 1-13.

[13] Sardar, Tridip, Sourav Rana, and Joydev Chattopadhyay. "A mathematical model of dengue transmission with memory." Communications in Nonlinear Science and Numerical Simulation 22, no. 1-3 (2015): 511-525.

[14] Srivastava, H. M., Rashid Jan, Asif Jan, Wejdan Deebani, and Meshal Shutaywi. "Fractional-calculus analysis of the transmission dynamics of the dengue infection." Chaos: An Interdisciplinary Journal of Nonlinear Science 31, no. 5 (2021).

[15] Nisar, Kottakkaran Sooppy, Aqeel Ahmad, Mustafa Inc, Muhammad Farman, Hadi Rezazadeh, Lanre Akinyemi, and Muhammad Mannan Akram. "Analysis of dengue transmission using fractional order scheme." (2022).

[16] Packierisamy, P. Raviwharmman. "The cost of Dengue Vector Control Programme in Malaysia." PhD diss., University of Malaya (Malaysia), 2017.

[17] Akter, Saima, and Zhen Jin. "Simulations and fractional modeling of dengue transmission in Bangladesh." Mathematical Biosciences and Engineering 20, no. 6 (2023): 9891-9922.

[18] Qureshi, Sania, and Abdon Atangana. "Mathematical analysis of dengue fever outbreak by novel fractional operators with field data." Physica A: Statistical Mechanics and its Applications 526 (2019): 121127.

[19] Pinho, Suani Tavares Rubim de, Claudia P. Ferreira, Lourdes Esteva, Florisneide Rodrigues Barreto, V. C. Morato e Silva, and M. G. L. Teixeira. "Modelling the dynamics of dengue real epidemics." Philosophical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences 368, no. 1933 (2010): 5679-5693.

[20] Ullah, Zakir. "Analytical Solution of the Mathematical Model of Dengue Fever by the Laplace Adomian Decomposition Method."

[21] Khan, T., Zaman, G., Algahtani, O.: Transmission dynamic and vaccination of hepatitis B epidemic model. Wulfenia 22, 230–241 (2015)

[22] Shah, Kamal, Fahd Jarad, and Thabet Abdeljawad. "On a nonlinear fractional order model of dengue fever disease under Caputo-Fabrizio derivative." Alexandria Engineering Journal 59, no. 4 (2020): 2305-2313.

[23] Defterli, Özlem. "Modeling the impact of temperature on fractional order dengue model with vertical transmission." (2020).

[24] Garrappa, Roberto. "Trapezoidal methods for fractional differential equations: Theoretical and computational aspects." Mathematics and Computers in Simulation 110 (2015): 96-112.

[25] Pinho, Suani Tavares Rubim de, Claudia P. Ferreira, Lourdes Esteva, Florisneide Rodrigues Barreto, V. C. Morato e Silva, and M. G. L. Teixeira. "Modelling the dynamics of dengue real epidemics." Philosophical Transactions of the Royal Society A: Mathematical, Physical and Engineering Sciences 368, no. 1933 (2010): 5679-5693.

[26] Matignon, Denis. "Stability results for fractional differential equations with applications to control processing." In Computational engineering in systems applications, vol. 2, no. 1, pp. 963-968. 1996.

[27] Pooseh, Shakoor, Helena Sofia Rodrigues, and Delfim FM Torres. "Fractional derivatives in dengue epidemics." In AIP Conference Proceedings, vol. 1389, no. 1, pp. 739-742. American Institute of Physics, 2011.

[28] Shah, Kamal, Fahd Jarad, and Thabet Abdeljawad. "On a nonlinear fractional order model of dengue fever disease under Caputo-Fabrizio derivative." Alexandria Engineering Journal 59, no. 4 (2020): 2305-2313.

[29] Srivastava, H. M., Rashid Jan, Asif Jan, Wejdan Deebani, and Meshal Shutaywi. "Fractional-calculus analysis of the transmission dynamics of the dengue infection." Chaos: An Interdisciplinary Journal of Nonlinear Science 31, no. 5 (2021).

[30] Garrappa, Roberto. "Trapezoidal methods for fractional differential equations: Theoretical and computational aspects." Mathematics and Computers in Simulation 110 (2015): 96-112.