Published by
NIGERIAN SOCIETY OF PHYSICAL SCIENCES
Available online @ https://journal.nsps.org.ng/index.php/jnsps

J. Nig. Soc. Phys. Sci. 5 (2023) 1464

Journal of the Nigerian Society of Physical Sciences

Numerical Analysis of Fractional-Order Dynamic Dengue Disease Epidemic in Sudan

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Abstract

The main idea of this work is numerical simulation and stability analysis for the fractional-order dynamics of the dengue disease outbreak in Sudan. This research uses a computer technique based on the Adams-Bashforth approach to numerically resolve a fractional-order dengue epidemic in Sudan. Analyses of numerical and dynamic stability show that the fractional-order dengue fever model is sensitive to initial conditions for those parameters. Therefore, the parameters' values are critical in establishing how many individuals will get better from their sickness and how many will become ill. The proposed method is effective in providing an illustration of the solution's dynamics over a very long horizon of time, which is crucial for making accurate predictions about the spread of dengue in Sudan. In addition, this method can be utilized to assess the efficacy of various intervention strategies and inform public health policies aimed at reducing the burden of dengue fever in Sudan. It can also assist in identifying areas most susceptible to dengue infestations and prioritizing disease control resources.

DOI:10.46481/jnsps.2023.1464

Keywords: A fractional, Adams-Bashforth, Prediction, simulation, Dengue.

Article History :
Received: 25 March 2023
Received in revised form: 06 May 2023
Accepted for publication: 10 May 2023
Published: 28 May 2023

Communicated by: B. J. Falaye

1. Introduction

Dengue fever is a problem in Sudan. In 2010, 2013, and 2017, there were several outbreaks that were recorded. There is no information on the serotypes of dengue virus that are present in Sudan. In this regard, further research on the dengue virus (DENV) is required. In addition to the chikungunya, rift valley fever, malaria, and cholera outbreaks that are still active, there is currently an outbreak of dengue fever. The public health sector's capability for epidemic control and response is constrained; long-running political and civil disputes have lowered the nation's ability to do so. Dengue has spread to seven states nationwide since the outbreak began on August 8th. A poor prognosis could result from the increased probability of co-infection with malaria and/or chikungunya, which complicates case management [1-8].

Fractional calculus and nonlinear equations have found applications in a vast variety of seemingly unrelated sectors of science and engineering over the last decade. Epidemics, acoustics, biology, electromagnetics, engineering, Dengue is a significant public health concern in tropical and subtropical regions.

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It is transmitted by mosquitoes of the species Aedes aegypti and Aedes albopictus. Four distinct serotypes can induce dengue illness. When a person infected with one serotype recovers, he or she develops complete immunity to that serotype but only partial and temporary immunity to the other [9-11]. In this paper, the fractional-order dengue epidemic model is investigated. Examining the stability of equilibrium locations Given are the numerical solutions for this model. We like to contend that fractional-order equations are more appropriate than integer-order equations for modeling memory-sensitive biological, economic, and social systems (generally complex adaptive systems). The Adams-Bashforth algorithm was used to solve and simulate the differential equation system.

The format is as follows: The fractional model is introduced in Section 1. Section 2 provides fundamental definitions; Section 3 is devoted to the formulation model. Section 4 focuses on the Caputo derivative of the model while Sections 5 and 6 include stability analysis and numerical analysis. Section 7 is the conclusion.

2. Preliminaries

Definition 2.1. *The Riemann-Liouville fractional integral operator of order $\alpha > 0$ for a function $y(\tau)$ is given by [12] :*

$$D^{\alpha}y(t) := \frac{1}{\Gamma(n-\alpha)}\int_0^t (t-\tau)^{n-\alpha-1}y^n(\tau)d\tau. = I^{n-\alpha}y^n(t), t > 0. \tag{1}$$

Definition 2.2. *For $y\epsilon H^1(0,t), t > 0, T > 0, \alpha\epsilon(0,1]$ Then the CF fractional operator [12] is given by.*

$${}^{CF}_{0}D^{\alpha}_{t}y(t) := \frac{B(\alpha)}{1-\alpha}\frac{d}{dt}\int_0^t y(\tau)\exp\left(-\alpha\frac{t-\tau}{1-\alpha}\right)d\tau.0 < \alpha < 1 \tag{2}$$

In this expression $B(\alpha)$ satisfies the condition $B(0) = B(1) = 1$.

Definition 2.3. *The fractional integral of order α of a function f is defined as [13]*

$$I^{\gamma}_{t}y(t) := \frac{2(1-\gamma)}{(2-\gamma)M(\gamma)}y(t) + \frac{2(1-\gamma)}{(2-\gamma)M(\gamma)}\int_0^t y(\tau)d\tau.t \geq 0, 0 < \alpha < 1 \tag{3}$$

Definition 2.4. *Caputo derivative of order $0 \leq n-1 < \alpha < n$ with the lower limit zero for a function $y(\tau)$ is given by* [14] *:*

$$I^{\alpha}y(t) := \frac{1}{\Gamma(\alpha)}\int_0^t (t-\tau)^{\alpha-1}y(\tau)d\tau.t > 0 \tag{4}$$

Definition 2.5. *The Mittag-Leffler function is a generalization of the exponential function. This function can be expressed as follows:*

$$E_{\alpha}(t) = \sum_{k=0}^{\infty}\frac{t^k}{\Gamma(\alpha k+1)} \tag{5}$$

Definition 2.6. *For $y\epsilon H^1(0,t), t > 0, T > 0, \alpha\epsilon(0,1]$ then the AB fractional operator [12]* y(t) *in the Riemann-Liouville is given by:*

$${}^{AB}_{0}D^{\alpha}_{t}y(t) := \frac{B(\alpha)}{1-\alpha}\frac{d}{dt}\int_0^t y(\tau)E_{\alpha}\left(\frac{\alpha}{1-\alpha}(t-\tau)^{\alpha}\right)d\tau.0 < \alpha < 1. \tag{6}$$

In this expression $B(\alpha)$ satisfies the condition $B(0) = B(1) = 1$.

Definition 2.7. *For $y\epsilon H^1(0,t), t > 0, T > 0$ Then the* AB *fractional operator [12]* y(t) *in the Caputo sense is given by:*

$${}^{AB}_{0}D^{\alpha}_{t}y(t) := \frac{B(\alpha)}{1-\alpha}\int_0^t \frac{dy(\tau)}{d\tau}E_{\alpha}\left(\frac{\alpha}{1-\alpha}(t-\tau)^{\alpha}\right)d\tau.0 < \alpha < 1 \tag{7}$$

In this expression $B(\alpha)$ satisfies the condition $B(0) = B(1) = 1$.

Definition 2.8. *Let $0 < \alpha < 1$ and the fractional CF derivative is expressed as:*

$${}^{CF}_{0}D^{\alpha}_{t}y(t) = h(t). \tag{8}$$

3. The Model Formulation

In this part, we get the mathematical formulation of the dengue fever infectivity model, which is based on a number of propositions, including the following: The total number of humans (N_h) and mosquitoes (N_m) is assumed to be constant, the birth and mortality rates are assumed to be equal, the births in mosquito and human populations in each class are assumed to be the same, each individual in the population is likely to have the same number of mosquito bites, and the infected mosquito is likely to bite each component of the data provided. The variables used in the dengue fever illness model are listed in Table 1. The preceding model can be interpreted mathematically as a host-vector interaction model, which is the following fractional differential model:

$$\begin{cases} \frac{dS_h}{dt} = \mu_h N_h - \left(B\beta_{mh}\frac{I_h}{N_h} + \mu_h\right)S_h, \\ \frac{dI_h}{dt} = B\beta_{mh}\frac{S_h I_h}{N_h} - (\gamma_h + \mu_h)I_h, \\ \frac{dR_h}{dt} = \gamma_h I_h - \mu_h R_h, \\ \frac{dS_m}{dt} = \mu_m N_m - \left(B\beta_{mh}\frac{I_h}{N_h} + \mu_m\right)S_m, \\ \frac{dI_m}{dt} = B\beta_{mh}\frac{I_h}{N_h}S_m - \mu_m I_m \end{cases} \tag{9}$$

we extend the model (9) employing the newly proposed Caputo-Fabrizio-Caputo; fractional derivatives with variable order $\alpha(t)$.

4. The Caputo- derivative to the fractional model

Introducing the notion of fractional derivative in the sense of Riemann-Liouville to reformulate the dynamics of the classical model (9) in terms of fractional derivatives, we apply the Caputo derivative to the dengue fever model (9). The fractional

Table 1. Explanation of the components of the infectivity model:

Variable	Description
$N_h(t)$	Total number of humans (constant ≈ 44 million)
$S_h(t)$	Susceptible humans
$I_h(t)$	Infected humans
$R_h(t)$	Recovery humans
$S_m(t)$	Susceptible female mosquitoes
$I_m(t)$	Infected female mosquitoes
Parameter	**Description**
$\mu(h)$	Human mortality rate for every person
$\mu(m)$	Corresponding value for the mosquitoes
$\gamma(h)$	Recovery rate of the humans
B	The biting rate
$\beta(m)$	The likelihood that human to mosquito transfer may occur
$\beta(h)$	The likelihood that mosquito to human transfer may occur

dengue fever is obtained by replacing the classical derivative by the operator ${}_0^C D_t^{\alpha(t)}$:

$$\begin{aligned} {}_0^C D_0^{\lambda} S_h &= \theta_1 - (\theta_2 + \theta_3) S_h, \\ {}_0^C D_0^{\lambda} I_h &= \theta_2 S_h - (\theta_4 + \theta_3) I_h, \\ {}_0 D_0^{\lambda} R_h &= \theta_4 I_h - \theta_3 R_h, \\ {}_0^C D_0^{\lambda} S_m &= \theta_6 - (\theta_2 + \theta_5) S_m, \\ {}_0^C D_0^{\lambda} I_m &= \theta_2 S_m - \theta_5 I_m, \end{aligned} \tag{10}$$

where

$$\begin{aligned} &\theta_1 = \mu_h N_h, \theta_2 = B\beta_{mh}\frac{I_h}{N_h} = B\beta_{hm}\frac{I_h}{N_h}, \\ &\theta_3 = \mu_h, \theta_4 = \gamma_h, \theta_5 = \mu_m, \theta_6 = \mu_m N_m, \end{aligned} \tag{11}$$

with the initial conditions:

$$S_h(0) = c_1, I_h(0) = c_2, R_h(0) = c_3, S_m(0) = c_4, I_m(0) = c_5. \tag{12}$$

5. Stability Analysis

Here, we discuss this epidemiological model stability. The equilibrium points for system (10) and the Jacobian matrix are given by:

$$\boldsymbol{J} = \begin{bmatrix} -B\beta_{mh}\frac{I_h}{N_h} - \mu_h & -B\beta_{mh}\frac{S_h}{N_h} & 0 & 0 & 0 \\ B\beta_{mh}\frac{I_m}{N_h} & -(\gamma_h + \mu_h) & 0 & 0 & B\beta_{mh}\frac{S_h}{N_h} \\ 0 & \gamma_h & -\mu_h & 0 & 0 \\ 0 & -B\beta_{mh}\frac{S_m}{N_h} & 0 & -\mu_m - B\beta_{hm}\frac{I_h}{N_h} & 0 \\ 0 & B\beta_{mh}\frac{S_m}{N_h} & 0 & B\beta_{hm}\frac{I_h}{N_h} & -\mu_m \end{bmatrix} \tag{13}$$

The disease-free equilibrium point is given as ($44909351, 0, 0, 168000, 0$), and the endemic equilibrium points $(-3533, -8499, -2833, -132, 30017)$. The Jacobian matrix at disease free equilibrium point is given as follows:

Table 2. The values of the initial value of model and the parameters are given by real data:

Variable	Description	values
$N_h(t)$	total number of humans	constant ≈ 44 million
$S_h(0)$	susceptible humans	3326
$I_h(0)$	infected humans	482
$R_h(0)$	recovery humans	0
$S_m(0)$	susceptible female mosquitoes	117600
$I_m(t)$	infected female mosquitoes	
Parameter	**Range of values**	**References**
N_h	44909351	Constant
N_m	168000	Estimated
μ_h	0.0000031	Estimated
μ_m	0.1	[16]
γ_h	2-10 days – [1/3]	[16]
B	0.7	[16]
β_{mh}	0.36	[16]
β_{hm}	0.36	[16]

$$J = \begin{bmatrix} -0.0000038 & 0.000000026 & 0 & 0 & 0 \\ 0.000000045 & -0.11 & 0 & 0 & 0.000000026 \\ 0 & 0.01 & -0.1 & 0 & 0 \\ 0 & -0.0000009 & 0 & -0.100000026 & 0 \\ 0 & 0.0000009 & 0 & 0.000000038 & -0.1 \end{bmatrix} \tag{14}$$

The eigenvalues corresponding to matrix J are:

$$\begin{aligned} \sigma_1 = -0.0000003, \sigma_2 = -0.0000003, \sigma_3 = 0.000003, \sigma_4 \\ = -0.01, \sigma_5 = -0.0000003. \end{aligned} \tag{15}$$

The system is stable because all the eigenvalues are negative. The system is unstable at the endemic equilibrium point because some eigenvalues are positive.

5.1. The Basic Reproduction Number:

The expected value of the secondary infections rate per time unit is denoted by R_0, and the basic reproduction number is a baseline metric in epidemiology. Based on the fractional model of equation (10), We have two infected classes $I_h(t), I_m(t)$.

$${}_0^{CF} D_0^{\lambda} I_h = \theta_2 S_h - (\theta_4 + \theta_3) I_h \tag{16}$$

$${}_0^{CF} D_0^{\lambda} I_m = \theta_2 S_m - \theta_5 I_m. \tag{17}$$

We assume that the infection risk rate is a constant $\beta(t)$ taking the maximum value $\beta(0) = \beta_0$ and the minimum value $\beta(t^*) = \beta^*$.

Let $x = (I_h, I_m)$.and rewrite the system of equation (7) for the susceptible and infected classes in the general from

$$\frac{dx}{dt} = f(x) - v(x), \tag{18}$$

where

$$f(x) = \begin{bmatrix} 0.252 & 0.036 \\ 0.252 & 1.262 \end{bmatrix}, v(x) = \begin{bmatrix} 0.00000026 & 0 \\ 0.000009 & 0 \end{bmatrix}. \quad (19)$$

Now the Jacobian of $f(x)$ and $v(x)$ of the disease-free equilibrium point is

$$F = \begin{bmatrix} 0.000000026 & 0 \\ 0.0000009 & 0 \end{bmatrix} \quad (20)$$

$$V = \begin{bmatrix} 160.66 & 0 \\ 0 & 0.1 \end{bmatrix}. \quad (21)$$

Therefore

$$V^{-1} = \begin{bmatrix} 0.006 & 0 \\ 0 & 0.1 \end{bmatrix}. \quad (22)$$

By using Eq. (11), we have

$$R_0 = \rho\left(FV^{-1}\right) = 10, \quad (23)$$

6. Numerical analysis:

We do a numerical simulation of the fractional model of dengue fever outbreaks in Sudan, epidemiological numerical analysis, and stability. By using real data in Sudan and evaluating various possibilities by increasing and/or decreasing the model parameters' values, we obtained a numerical simulation of the fractional dengue fever model. The Euler approach is employed to generate the numerical results for the model (10). We used the values of numerous parameters from different credible sources to compute numerical results.

6.1. Adams-Bashforth Applied on Fractional Order System

This section presents an explanation of the numerical procedure that will be used by us to get the phase pictures of the fractional-order system (10). The Adams-Bashforth approach described by Garrappa in his review paper [17] is the one that we use. The solution to the fractional differential system (10) can be described as follows:

$$\begin{aligned} \phi(t, x_1) &= \theta_1 - (\theta_2 + \theta_3) S_h, \\ \varphi(t, x_2) &= \theta_2 S_h - (\theta_4 + \theta_3) I_h, \\ \theta(t, x_3) &= \theta_4 I_h - \theta_3 R_h, \\ \beta(t, x_4) &= \theta_6 - (\theta_2 + \theta_5) S_m, \\ \rho(t, x_5) &= \theta_2 S_m - \theta_5 I_m, \end{aligned} \quad (24)$$

as well as point t_n; Eq. (6) may be recast in the following ways in accordance with a numerical strategy known as the Adams-Bashforth method:

$$x(t_n) = x(0) + h^n \left[\bar{\kappa}_n^{(a)} \phi(0) + \sum_{j=1}^{n-1} \kappa_{n-j}^{(a)} \phi\left(t_j, x_{1j}\right) + \kappa_0^{(a)} \phi\left(t_j, x_{1v}^p\right)\right]$$

$$y(t_n) = y(0) + h^a \left[\bar{\alpha}_n^{(a)} \varphi(0) + \sum_{j=1}^{N-1} \kappa_{n-j}^{(a)} \varphi\left(t_j, x_{1j}\right) + x_0^{(a)} \varphi\left(t_j, x_{1n}^p\right)\right]$$

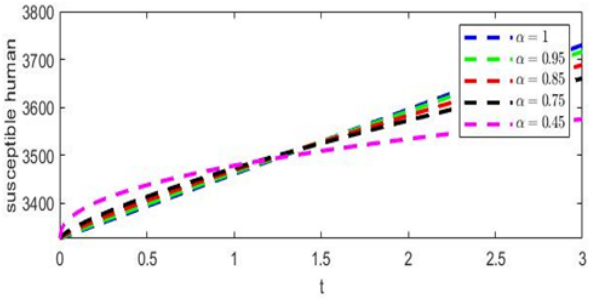

Figure 1. The size of susceptible human with time.

$$z(t_n) = z(0) + h^a \left[\bar{\kappa}_n^{(a)} \theta(0) + \sum_{j=1}^{n-1} x_{n-j}^{(a)} \theta\left(t_j, x_{1j}\right) + x_0^{(a)} \theta\left(t_j, x_{1n}^p\right)\right] \quad (25)$$

$$w(t_n) = z(0) + h^a \left[\bar{\kappa}_n^{(a)} \beta(0) + \sum_{j=1}^{n-1} x_{n-j}^{(a)} \beta\left(t_j, x_{1j}\right) + x_0^{(a)} \beta\left(t_j, x_{1n}^p\right)\right]$$

$$v(t_n) = z(0) + h^a \left[\bar{\kappa}_n^{(a)} \rho(0) + \sum_{j=1}^{n-1} x_{n-j}^{(a)} \rho\left(t_j, x_{1j}\right) + x_0^{(a)} \rho\left(t_j, x_{1n}^p\right)\right].$$

The discretization parameters are specified as follows (h is the step size):

$$\bar{\pi}_n^{(a)} = \frac{(n-1)^n - n^a(n - \alpha - 1)}{\Gamma(2 + \alpha)}. \quad (26)$$

When $n = 1, 2, \ldots$, we set the parameters as follows:

$$\begin{aligned} \kappa_0^{(a)} &= \frac{1}{\Gamma(2 + \alpha)^n} \\ \kappa_n^{(a)} &= \frac{(n-1)^{n+1} - 2n^{a+1} + (n+1)^{a+1}}{\Gamma(2 + \alpha)}. \end{aligned} \quad (27)$$

We get an approximation of the functions in our model:

$$\begin{aligned} \phi\left(t, x_{1j}\right) &= \theta_1 - (\theta_2 + \theta_3) S_{hj} \\ \phi\left(t, x_{2j}\right) &= \theta_2 S_{hj} - (\theta_4 + \theta_3) I_{hj} \\ \phi\left(t, x_{3j}\right) &= \theta_4 I_{hj} - \theta_3 R_{hj} \\ \phi(t, x_4 j) &= \theta_6 - (\theta_2 + \theta_5) S_{mj} \\ \phi\left(t, x_{5j}\right) &= \theta_2 S_m j - \theta_5 I_{mj}. \end{aligned} \quad (28)$$

The discretization technique that is going to be discussed in this part provides a lot of benefits. the procedure is reliable and guarantees convergence, and the Matlab implementation is both practical and simple.

7. Results and Discussion

We present numerical results assuming the initial values of the model are:

$$S_h(0) = 3326, I_h(0) = 482, R_h(0) = 0, S_m(0) = 117600, I_m(0) = 5600$$

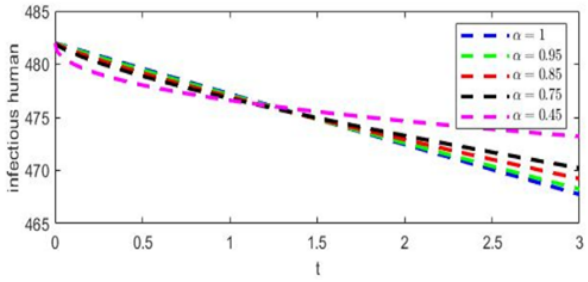

Figure 2. The size of infectious human with time.

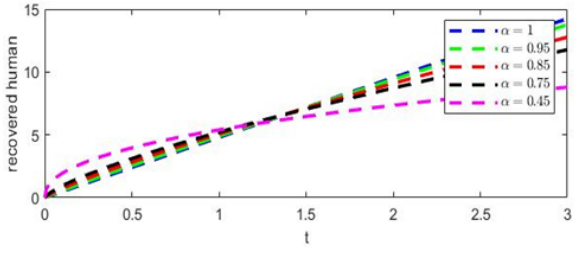

Figure 3. The size of recovered human with time.

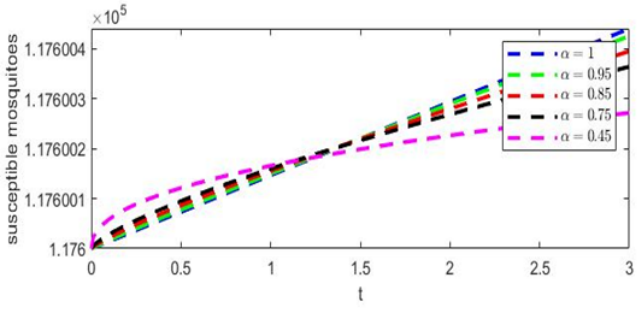

Figure 4. The size of mosquitoes with time.

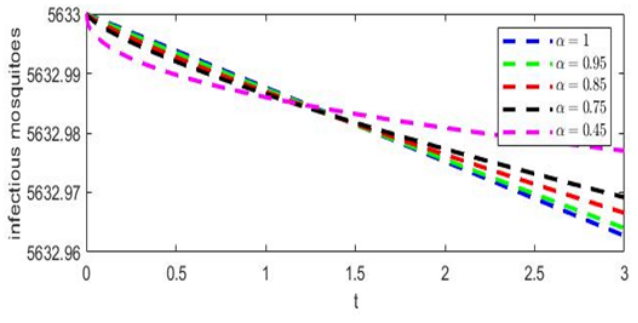

Figure 5. The size of infectious mosquitoes with time.

Figure 1 show the determine the property of a fractional order models. Figure 2 demonstrate the behavior of susceptible human with t. From Figure 2, it is clear that susceptible human group increases with t. Figure 3 shows the behavior of infectious human with t. From Figure 3, It is clear that infectious people group decreases with time. Figure 4 demonstrate the behavior of recovery human with t. From Figure 4, It is clear that recovery human group increases with t. Figure 5 demonstrate the behavior of susceptible mosquitoes with time. Figure 6 demonstrates the behavior of infectious mosquitoes with time. Based on the frequency of dengue fever in Sudan, the fundamental reproduction number indicates that one sick individual can spread the disease to up to ten additional people.

8. Conclusion

In order to numerically resolve a fractional-order outbreak of dengue disease in Sudan, a computational technique built on the Adams-Bashforth approach has been applied in this study. The illustrations in this paper demonstrate how parameter values and fractional derivatives both continually affect the result. From numerical and stability analysis, it is clear that the fractional-order dengue fever model depends on its parameters at a given time t. As a result, the parameter values are crucial in determining how many people recover from their illness and how many contract it. The suggested method works well to demonstrate the behavior of the solution over a lengthy time horizon, which is useful for precisely forecasting the dengue virus outbreak in Sudan. In the future, we want to solve several novel fractional models, such as those in [17,20], and compare them to other numerical approaches [21,25].

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