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Global analysis and numerical simulations of Caputo fractional order derivatives of epidemiological model with coupled incidence

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Abstract. We aim to study a nonlinear epidemic model coupling direct and indirect transmission of infectious disease by using Caputo's fractional derivatives. This non-local operator takes into account the history of the dynamic system and grants it a memory effect. After rigorous mathematical study, we calculate the basic reproduction number $\mathcal{R}_0$ and determine the equilibrium points. We demonstrate the uniqueness of the equilibrium point according to the $\mathcal{R}_0$ value. We further demonstrate that the local and global dynamics of the system are related to the basic reproduction. Our model generalizes various disease models, including those for HIV, Zika virus, H1N1, and many others. Using the Adam-Bashforth-Moulton method and Python version 3.7, we present numerical simulations depending on the fractional order to support the theoretical demonstration.

1 Introduction

The mathematical modeling of phenomena is essential in the field of applied science. In physics, chemistry, biology, and many other fields, mathematical models are the pillars of a rigorous scientific study, enabling predictions about observed phenomena. Infectious diseases are increasingly becoming a major focus of mathematical modeling. HIV, Zika virus, avian influenza, H1N1, Malaria, Dengue [38, 40], Ebola virus disease,
schistosomiasis, COVID-19 [14, 39] are among many other infectious diseases that are regularly the subject of mathematical studies [18, 19, 26]. A. Guiro et al. [10] analysed a mathematical model of the spread of the coronavirus disease 2019 (COVID-19) in Burkina Faso. B. Ivorra et al. [14] worked on a mathematical modeling of the spread of the coronavirus disease 2019 (COVID-19), taking into account the undetected infections (the case of China). In the modelling of schistosomiasis, A. Guiro et al. [11] worked on stability analysis of a model with delays. In recent years, fractional order calculus has been found to be more appealing in modeling [2, 12] for real-world problems in comparison to classical integer order calculus, as it provides a tool for the description of memory effects and genetic properties of various materials.
In 2023, Shah et al [28] studied a fractional order dynamical system of viral infection disease under piecewise derivative. In their work, they stated on a fractional order dynamics in the Caputo sense of the deadly disease Nipah virus (NiV). In 2024, Eiman et al [9] proposed a two-strain model of Covid-19 transmission governed by conformable fractional order derivatives. In the same year, Shah et al [29] proposed a fractal-fractional hybrid model with reinfection. The mentioned model was considered to deduce the qualitative theory and numerical aspects. Also, in

the paper [30], Shah et al using piecewise modified ABC fractional order derivative proposed a model on rotavirus infectious disease. In their model, they considered susceptible, vaccinated, infected, and recovered (SVIR) classes. Some qualitative conclusions have been established for the complicated pediatric disease epidemic model of rotavirus, which travels through a population at an inconsistent rate. The model has been fitted with piecewise equations of non-singular kernel-type derivatives in the modified Atangana-Balaneu-Caputo (mABC) sense.
Entomological studies revealed that mosquitoes don't feed randomly on human blood, but they use their prior experience on human location and human defensiveness to select the host to feed [3]. Thus, in some transmissions of diseases like dengue, Zika virus, and HIV, a future state does depend on the history of the transmission. Hence, the fractional order differential equation is found to be the best approach to model the transmission.

In this paper, we propose an epidemic model coupling both direct and indirect transmission mechanisms of infectious diseases using fractional order differential equations. We subdivide all the elements involved in the transmission into three compartments x, y and z. Our model has potential applications in the study of various diseases. For example, it generalizes the HIV model where x, y and z correspond to uninfected cells, infected cells and virus, respectively. In the study of Zika virus, we let x, y, z be the uninfected individuals, infected individuals, and infected mosquitoes, respectively. When we apply our model to analyze the epidemic waves of H1N1 and seasonal influenza, x and y still denote uninfected and infected individuals, respectively, while z stands for the contaminated environment such as classrooms, buses, theaters, or other public places. We could also use our model to study the cross transmission of avian influenza among migratory birds and domestic poultry, where x, y, z denote the uninfected migratory birds, infected migratory birds, and infected domestic poultry, respectively.

Our paper is organized as follows. In Section 2, we present some important definitions about the fractional derivatives. In Section 3, we present the system of fractional order differential equations after briefly presenting the work of Shu Hongying et al. [32]. In Section 4, we make sure that our mathematical model is well defined. Indeed, we exhibit the mathematical properties of the model, calculate the equilibrium points and the basic reproduction number. We then study in Section 5 the stability of the equilibrium points. We numerically simulate the model with some real data and some estimated data using Python version 3.7 in Section 6.2 and we conclude in Section 7.

2 Preliminaries on fractional derivative

The idea of fractional calculus was first triggered by Leibniz in 1695. For the past three centuries, fractional calculus has been renowned among mathematicians, mainly in the pure branch. Only in the last few years, this has been drawn to several applied fields of engineering and sciences, since fractional order model can give a more realistic interpretation of the real problem [8, 25, 27]. There are several different definitions of fractional derivative in the literature [8]. 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 a fractional order differential equation with Caputo derivative are the same as those of an integer differential equation, avoiding solvability issues.

Definition 2.1. ([41]) A gamma function $\Gamma :]0; +\infty[\to \mathbb{R}$ is defined by

$$\Gamma(\alpha) = \int_0^{\infty} x^{\alpha-1} e^{-x} dx.$$

Definition 2.2. ([22]) The Riemann-Liouville's fractional integral of order α for a function f is defined by

$$I^{\alpha} f(t) = \frac{1}{\Gamma(\alpha)} \int_0^t \frac{f(s)}{(t-s)^{1-\alpha}} ds, \quad \alpha > 0, \quad t > 0.$$

Definition 2.3. ([22]) The Caputo fractional derivative of order α for a function f is defined by

$${}^{C}_{t_0} D^{\alpha}_{t} f(t) = I^{n-\alpha} \left[f^{n}(t) \right] = \frac{1}{\Gamma(n-\alpha)} \int_{t_0}^{t} \frac{f^{(n)}(s)}{(t-s)^{\alpha-n+1}} ds \quad \text{if} \quad n-1 < \alpha < n.$$

Definition 2.4. ([22]) The Laplace transform for the Caputo fractional derivative of the function f is

$$\mathcal{L}[{}_{t_0}^{C}D_t^{\alpha} f(t)] = s^{\alpha}F(s) - \sum_{k=0}^{n-1} s^{n-k-1} f^{(k)}(0), \quad n \in \mathbb{N}, \quad n-1 < \alpha < n \tag{2.1}$$

Definition 2.5. ([7]) The Mittag-Leffler is defined by

$$E_{\alpha,\beta}(z) = \sum_{k=0}^{\infty} \frac{z^k}{\Gamma(\alpha k + \beta)} \qquad \alpha, \beta > 0 \tag{2.2}$$

$$E_{\alpha}(z) = E_{\alpha,1}(z) = \sum_{k=0}^{\infty} \frac{z^k}{\Gamma(\alpha k + 1)} \qquad \alpha > 0 \tag{2.3}$$

$$E_1(z) = \sum_{k=0}^{\infty} \frac{z^k}{\Gamma(k+1)} = \sum_{k=0}^{\infty} \frac{z^k}{k!} = e^z \tag{2.4}$$

and the Laplace transform for the Mittag-Leffler function is

$$\mathcal{L}[1 - E_{\alpha}(\mp dt^{\alpha})] = \frac{d}{s^{\alpha} \pm d}$$

and

$$\mathcal{L}[E_{\alpha}(\mp dt^{\alpha})] = \frac{s^{\alpha-1}}{s^{\alpha} \pm d}.$$

Theorem 2.6. *([7, 8]) Consider the two-parameter $\alpha, \beta > 0$ for Mittag-Leffler function $E_{\alpha,\beta}(z)$. The power series defining $E_{\alpha,\beta}(z)$ is convergent for all $z \in \mathbb{C}$. In order words, $E_{\alpha,\beta}(z)$ is an entire function.*

3 Mathematical model

The model we propose is a Caputo fractional order derivative model of the problem developed by Shu Hongying and Wang Xiang-Sheng [32] :

$$\begin{cases} \dot{x}(t) &= b - \beta_1 \dfrac{x(t)y(t)}{x(t)+y(t)} - \beta_2 x(t)z(t) - \mu x(t), \\ \dot{y}(t) &= \beta_1 \dfrac{x(t)y(t)}{x(t)+y(t)} + \beta_2 x(t)z(t) - \gamma y(t), \\ \dot{z}(t) &= py(t) - \delta z(t) \end{cases} \tag{3.1}$$

with the initial conditions $x(t_0) = x_0 > 0, y(t_0) = y_0 > 0, z(t_0) = z_0 > 0$.
The variables x, y denote the susceptible and infected population sizes respectively and the constants μ, γ are their death rates. b is a constant birth rate. The disease could transmit directly via a standard incidence function $\beta_1 \dfrac{xy}{x+y}$ and indirectly via a mass-action infection term $\beta_2 xz$, where z accounts for the vector of the indirect transmission. It assume in the third equation that the growth of disease vector is proportional to the number of infected individuals, and its decay rate is a constant δ. The units of parameters β_1, μ, p, δ are the same as the reciprocal of time unit, but the unit for b is the unit of β_1 multiplied by the population size/density unit, while the unit of β_2 is the unit of β_1 divided by the population size/density unit.

Thus, our model take into account both direct and indirect transmission of the disease. It generalizes various disease models on HIV, Zika virus, avian influenza and H1N1.

Our aim is to propose a fractional approach to the model (3.1) using Caputo's derivatives of fractional order with directly standard incidence function $\beta_1 \frac{x(t)y(t)}{x(t)+y(t)}$ and indirectly standard incidence function $\beta_2 \frac{x(t)z(t)}{x(t)+y(t)}$.
We assumed in the formulation of our model :

- the humans are assumed to be born susceptible, no natural protection;
- β_1 is the transmission rate of humans directly infected by the disease;
- β_2 is the transmission rate of humans indirectly infected by the disease;
- μ and η are respectively the natural death rate and the death rate due to the disease in the population ; p is the growth rate of the disease vectors. This number is proportional to the number of infected individuals y;
  δ is the decay rate of the vectors.

It is eminent that memory is strongly involved in the dynamics of mosquitoes-borne infections. Memory there in host population is related with individual awareness, which lowers the rate of interaction between hosts and vectors, whereas vectors use prior experience on host position, blood choice, color, and human defense policy to choose a host being to feed [4, 36]. In recent decades, many physical problems have been modeled using the fractional calculus. The main reasons given for using fractional derivative models are that many systems show memory, history, or non-local effects, which can be difficult to model using integer order derivatives.

Globally, fractional order derivative provides a memory effect and the biological elements of our system have it. By following Boulaaras et al. [2] and Hamdan et al. [12], we proposed fractional order model as follows:

$$\begin{cases} {}^{C}_{t_0}D^{\alpha}_{t}x(t) &= b - \beta_1^{\alpha}\dfrac{x(t)y(t)}{x(t)+y(t)} - \beta_2^{\alpha}\dfrac{x(t)z(t)}{x(t)+y(t)} - \mu^{\alpha}x(t), \\ {}^{C}_{t_0}D^{\alpha}_{t}y(t) &= \beta_1^{\alpha}\dfrac{x(t)y(t)}{x(t)+y(t)} + \beta_2^{\alpha}\dfrac{x(t)z(t)}{x(t)+y(t)} - (\eta^{\alpha}+\mu^{\alpha})y(t), \\ {}^{C}_{t_0}D^{\alpha}_{t}z(t) &= p^{\alpha}y(t) - \delta^{\alpha}z(t) \end{cases} \tag{3.2}$$

with the initial conditions $x(t_0) = x_0 > 0, y(t_0) = y_0 > 0, z(t_0) = z_0 > 0, \alpha \in (0;1]$.
The fractional derivatives used in the model (3.2) are all in the Caputo sense and α is the order of the fractional derivative.

4 Properties of the mathematical model

In this section, we have discussed about the existence, uniqueness, non-negativity and boundedness of the solutions of the fractional order system (3.2).

4.1 Existence and uniqueness

To prove the existence and uniqueness of system (3.2) solutions, we need the following lemma.

Lemma 4.1. *([21]) Consider the system*

$$ {}^{C}_{t_0}D^{\alpha}_{t}\theta(t) = f(t,\theta), \quad t \geqslant t_0 \tag{4.1}$$

with initial condition $\theta(t_0) = \theta_0$, *where* $\alpha \in (0, 1]$, $f : [t_0, \infty) \times \Omega \to \mathbb{R}^n, \Omega \in \mathbb{R}^n$.
If $f(t, \theta)$ *satisfies the locally lipschitz condition with respect to* θ, *then there exists an unique solution of the system* (4.1) *on* Ω.

Proposition 4.2. *Let be* Γ *the following set :*
$\Gamma = \{\theta(t) = (x(t), y(t), z(t)) \in \mathbb{R}^3 \ / \ x(t) + y(t) \neq 0 \ \forall \ t \in \mathbb{R}^+\}$. *For each initial condition* $\theta(t_0) = \theta_0 = (x_0, y_0, z_0) \in \Gamma$, *there exists an unique solution* θ *of system* (3.2) *which is defined for all* $t \geqslant t_0$.

Proof.
Let $\theta = (x, y, z)$ and $\Gamma = \{\theta(t) = (x(t), y(t), z(t)) \in \mathbb{R}^3 \ / \ x(t) + y(t) \neq 0 \ \forall \ t \in \mathbb{R}^+\}$.
The initial conditions problem with respect to system (3.2) reads as follows

$$\begin{cases} {}^{C}_{t_0}D^{\alpha}_{t}\theta(t) = \mathcal{G}(\theta(t)), \\ \theta(t_0) = \theta_0, \end{cases} \tag{3.1}$$

where the function $\mathcal{G}$ is the right hand side of system (3.2). Since $\mathcal{G}$ is $\mathcal{C}^{\infty}$, then it is also $\mathcal{C}^1$. It follows that $\mathcal{G}$ is locally Lipschitzian . Therefore, the existence and the uniqueness of the Cauchy problem (3.1) maximal solution is ensured by Cauchy-Lipschitz's theorem [21] with the initial condition $(t_0, \theta_0) \in \mathbb{R}^+ \times \Gamma$.

4.2 Non-negativity and boundedness

To prove the non-negativity of solutions, we state the following lemma.

Lemma 4.3. *([23]) Let* $f \in \mathcal{C}[a, b]$ *and* ${}^{C}_{t_0}D^{\alpha}_{t} f(t) \in \mathcal{C}[a, b]$ *for* $0 < \alpha \leqslant 1$. *Therefore :*

1) If ${}^{C}_{t_0}D^{\alpha}_{t} f(t) \geqslant 0, \forall t \in (a, b)$, *then* $f(t)$ *is no decreasing.*

2) If ${}^{C}_{t_0}D^{\alpha}_{t} f(t) \leqslant 0, \forall t \in (a, b)$, *then* $f(t)$ *is no increasing.*

Lemma 4.4. *The system* (3.2) *is invariant in* $\mathbb{R}^3_+$.

Proof. We have :

$$\begin{aligned} {}^{C}_{t_0}D^{\alpha}_{t} x\big|_{x=0} &= b \geqslant 0, \\ {}^{C}_{t_0}D^{\alpha}_{t} y\big|_{y=0} &= \beta_2^{\alpha} z(t) \geqslant 0, \\ {}^{C}_{t_0}D^{\alpha}_{t} z\big|_{z=0} &= p^{\alpha} y(t) \geqslant 0. \end{aligned}$$

Then it follows that according to the lemma 4.3, $\mathbb{R}^3_+$ is an invariant set for model (3.2).

Proposition 4.5. *The solutions* θ *of the system* (3.2) *are bounded and belong to the region* $\Omega = \left\{\theta = (x, y, z) \in \mathbb{R}^3_+ / 0 \leqslant x, y, z \leqslant \dfrac{bp^{\alpha}}{\delta^{\alpha}\mu^{\alpha}}\right\}$.

Proof. In the model (3.2), by adding the first two lines, we obtain :

$${}^{C}_{t_0}D^{\alpha}_{t}(x + y)(t) = b - \mu^{\alpha}x - (\eta^{\alpha} + \mu^{\alpha})y. \tag{4.2}$$

From Eq.(4.2), we get

$${}^{C}_{t_0}D^{\alpha}_{t}(x + y)(t) + \mu^{\alpha}(x + y)(t) \leqslant b. \tag{4.3}$$

Taking Laplace transform [7, 17] on both side, we have :

$$s^{\alpha}\mathcal{L}[(x + y)(t)] - s^{\alpha-1}(x + y)(0) + \mu^{\alpha}\mathcal{L}[(x + y)(t)] \leqslant b.$$

Namely,

$$\mathcal{L}[(x+y)(t)](s^\alpha+\mu^\alpha) \leqslant b + s^{\alpha-1}(x+y)(0),$$

then

$$\begin{aligned}\mathcal{L}[(x+y)(t)] &\leqslant \frac{b}{s^\alpha+\mu^\alpha} + (x+y)(0)\frac{s^{\alpha-1}}{s^\alpha+\mu^\alpha} \\ &\leqslant \frac{\mu^\alpha b}{\mu^\alpha(s^\alpha+\mu^\alpha)} + (x+y)(0)\frac{s^{\alpha-1}}{s^\alpha+\mu^\alpha}.\end{aligned}$$

Applying Laplace inverse on both sides, we get :

$$(x+y)(t) \leqslant \frac{b}{\mu^\alpha}\mathcal{L}^{-1}\left[\frac{\mu^\alpha}{s^\alpha+\mu^\alpha}\right] + (x+y)(0)\mathcal{L}^{-1}\left[\frac{s^{\alpha-1}}{s^\alpha+\mu^\alpha}\right].$$

Using the definition of Mittag-Leffler function (2.5), we can write

$$\begin{aligned}(x+y)(t) &\leqslant \frac{b}{\mu^\alpha}\left(1 - E_\alpha(-\mu^\alpha t^\alpha)\right) + (x+y)(0)E_\alpha(-\mu^\alpha t^\alpha) \\ &\leqslant \frac{b}{\mu^\alpha} - \left(\frac{b}{\mu^\alpha} - (x+y)(0)\right)E_\alpha(-\mu^\alpha t^\alpha) \\ &\leqslant \frac{b}{\mu^\alpha} - \xi E_\alpha(-\mu^\alpha t^\alpha).\end{aligned}$$

Consequently,

$$(x+y)(t) \leqslant \frac{b}{\mu^\alpha},$$

with $\xi = \left(\frac{b}{\mu^\alpha} - (x+y)(0)\right)$. According to Theorem (2.6), the quantity $E_{\alpha,1}(-\mu^\alpha t^\alpha)$ is bounded for all $t \geqslant 0$. This implies that $(x+y)$ is bounded. The components x, y are therefore bounded :

$$0 \leqslant x, y \leqslant \frac{b}{\mu^\alpha}$$

.

Using the third line of the system (3.2) and the boundedness of the component y, we have

$$\begin{aligned}{}^{C}_{t_0}D^\alpha_t z(t) + \delta^\alpha z(t) &= p^\alpha y(t) \\ &\leqslant \frac{p^\alpha b}{\mu^\alpha}.\end{aligned}$$

By the same method (Laplace transform [7, 17]), we get :

$$z(t) \leqslant \frac{p^\alpha b}{\delta^\alpha \mu^\alpha}.$$

It follows that

$$0 \leqslant x(t), y(t), z(t) \leqslant \frac{p^\alpha b}{\delta^\alpha \mu^\alpha}.$$

We can conclude now that all solutions $\theta = (x, y, z)$ of the model (3.2) belong to the set Ω. That means Ω is an attractive set of (3.2) and constitutes our domain biologically feasible.

5 Equilibria and stability analysis

Definition 5.1. Consider the Caputo fractional dynamic system ([21])

$$ {}^{C}_{t_0}D^{\alpha}_{t}\theta(t) = f(t,\theta) \tag{5.1}$$

with initial condition $\theta(t_0)$, where $\alpha \in (0,1)$, $f : [t_0,\infty] \times \Omega \to \mathbb{R}^n$ is piecewise continuous in t and locally Lipschitz in θ on $[t_0,\infty] \times \Omega$, and $\Omega \subset \mathbb{R}^n$ is a domain that contains the origin $\theta = 0$. The constant θ_e is an equilibrium point of Caputo fractional dynamic system (5.1) if and only if $f(t,\theta_e) = 0$.

Remark 5.2. (see [21]) When $\alpha \in (0,1)$, it follows that the Caputo fractional dynamic system (5.1) has the same equilibrium points as the integer-order system $\dot{\theta}(t) = f(t,\theta)$.

5.1 Equilibrium points

In this sub-section, we determine the equilibrium points of (3.2) and established its dynamic behavior. Let us consider $K = (x,y,z)$ an equilibrium point of model (3.2). On the point K it follows that

$$ b - \beta_1^{\alpha}\frac{x(t)y(t)}{x(t)+y(t)} - \beta_2^{\alpha}\frac{x(t)z(t)}{x(t)+y(t)} - \mu^{\alpha}x(t) = 0, \tag{5.2}$$

$$ \beta_1^{\alpha}\frac{x(t)y(t)}{x(t)+y(t)} + \beta_2^{\alpha}\frac{x(t)z(t)}{x(t)+y(t)} - (\eta^{\alpha}+\mu^{\alpha})y(t) = 0, \tag{5.3}$$

$$ p^{\alpha}y(t) - \delta^{\alpha}z(t) = 0. \tag{5.4}$$

From equations (5.2)-(5.4), we get

$$ y = \frac{b-\mu^{\alpha}x}{\eta^{\alpha}+\mu^{\alpha}}, \qquad z = \frac{(b-\mu^{\alpha}x)p^{\alpha}}{(\eta^{\alpha}+\mu^{\alpha})\delta^{\alpha}}. \tag{5.5}$$

Let θ^0 and θ^* be respectively the disease free equilibrium (DFE) point and the endemic equilibrium point of model (3.2). At the disease free equilibrium point, there is any infectious person ($y = 0$). By substituting y, z by 0 in (5.2) and (5.4), we get θ^0 given by:

$$ \theta^0 = (\frac{b}{\mu^{\alpha}}, 0, 0). \tag{5.6}$$

At endemic equilibrium point $\theta^*(y \neq 0)$, we have

$$ \theta^* = (x^*, y^*, z^*) \tag{5.7}$$

where

$$ y = \frac{b-\mu^{\alpha}x^*}{\eta^{\alpha}+\mu^{\alpha}}, \qquad z = \frac{(b-\mu^{\alpha}x^*)p^{\alpha}}{(\eta^{\alpha}+\mu^{\alpha})\delta^{\alpha}}. \tag{5.8}$$

5.2 Basic reproduction number $\mathcal{R}_0$

The basic reproduction number $\mathcal{R}_0$ is an important threshold parameter that governs the spread of a disease in a population. It helps to describe the stability of the disease-free equilibrium (DFE) of the model corresponding to the peak and final size of an epidemic. It is defined as the expected number of secondary cases of infection that will occur when a single infectious individual is introduced into a completely susceptible population. The basic reproduction number $\mathcal{R}_0$ is obtained using the next generation operator method described in [33].

Proposition 5.3. *The basic reproduction number $\mathcal{R}_0$ of model (3.2) is given by :*

$$\mathcal{R}_0 = \frac{\beta_1^\alpha}{\eta^\alpha+\mu^\alpha} + \frac{\beta_2^\alpha p^\alpha}{(\eta^\alpha+\mu^\alpha)\delta^\alpha}. \tag{5.9}$$

Proof. We use the next-generation matrix method ([33]) to calculate the reproduction number $\mathcal{R}_0$ of model (3.2). Let $\mathcal{F}$ and $\mathcal{V}$, the transmission and flow matrix between the infectious compartments I_{R_H}, I_{D_H} and I_V :

$$\mathcal{F} = \begin{pmatrix} \mathcal{F}_1 \\ \mathcal{F}_2 \end{pmatrix} \quad , \quad \mathcal{F} = \begin{pmatrix} \beta_1^\alpha \dfrac{x(t)y(t)}{x(t)+y(t)} + \beta_2^\alpha \dfrac{x(t)z(t)}{x(t)+y(t)} \\ 0 \end{pmatrix}$$

and

$$\mathcal{V} = \begin{pmatrix} \mathcal{V}_1 \\ \mathcal{V}_2 \end{pmatrix} \quad , \quad \mathcal{V} = \begin{pmatrix} -(\eta^\alpha+\mu^\alpha)y(t) \\ p^\alpha y(t) - \delta^\alpha z(t) \end{pmatrix}.$$

On the disease free equilibrium $\theta^0 = (\dfrac{b}{\mu^\alpha}, 0, 0)$, we obtain:

$$F = \mathcal{D}\mathcal{F} = \begin{pmatrix} \beta_1^\alpha & \beta_2^\alpha \\ 0 & 0 \end{pmatrix}$$

and

$$V = \mathcal{D}\mathcal{V} = \begin{pmatrix} -(\eta^\alpha+\mu^\alpha) & 0 \\ p^\alpha & -\delta^\alpha \end{pmatrix}.$$

Then, we get

$$V^{-1} = \begin{pmatrix} -\dfrac{1}{\eta^\alpha+\mu^\alpha} & 0 \\ \dfrac{-p^\alpha}{\delta^\alpha(\eta^\alpha+\mu^\alpha)} & -\dfrac{1}{\delta^\alpha} \end{pmatrix},$$

and

$$-FV^{-1} = \begin{pmatrix} \dfrac{\beta_1^\alpha}{\eta^\alpha+\mu^\alpha} + \dfrac{\beta_2^\alpha p^\alpha}{(\eta^\alpha+\mu^\alpha)\delta^\alpha} & \dfrac{\beta_2^\alpha}{\delta^\alpha} \\ 0 & 0 \end{pmatrix}$$

The basic reproduction number $\mathcal{R}_0$ ([33]) is defined as the dominant eigenvalue of the matrix $-FV^{-1}$. Therefore

$$\mathcal{R}_0 = \frac{\beta_1^\alpha}{\eta^\alpha+\mu^\alpha} + \frac{\beta_2^\alpha p^\alpha}{(\eta^\alpha+\mu^\alpha)\delta^\alpha}$$

$$= \frac{\delta^\alpha\beta_1^\alpha + \beta_2^\alpha p^\alpha}{(\eta^\alpha+\mu^\alpha)\delta^\alpha}.$$

Remark 5.4. .

If $\beta_1 = 0$ (namely, there is no direct transmission), the system (3.2) reduces to the classical HIV model [24], where x, y, z represent the densities of target cells, infected cells and the virus, respectively. It well know that the global dynamics of this reduced system is fully determined by the basic reproduction number ([6, 33])

$$\mathcal{R}_0^i = \frac{\beta_2^\alpha p^\alpha}{(\eta^\alpha + \mu^\alpha)\delta^\alpha} \tag{5.10}$$

Here, the superscript i means indirect disease transmission.

On the other hand, if the indirect transmission is ignored (that means $\beta_2 = 0$), then the third equation of (3.2) can be withdrawn and the remaining system (first and second equation of (3.2) with $\beta_2 = 0$) is the same as the Kermack-McKendrick epidemic model [16] with standard incidence function, while the infected class is assumed to be removed from the social activity after being recovered/quarantined (see [37]). The basic reproduction number for the reduced direct-transmission-only model is given by ([6, 33])

$$\mathcal{R}_0^d = \frac{\beta_1^\alpha}{\eta^\alpha + \mu^\alpha} \tag{5.11}$$

where the superscript d corresponds to the direct disease transmission.

Then, we can define the basic reproduction number of this coupled system as the sum of $\mathcal{R}_0^i$ and $\mathcal{R}_0^d$:

$$\mathcal{R}_0 = \mathcal{R}_0^i + \mathcal{R}_0^d. \tag{5.12}$$

Theorem 5.5.

i) If $\mathcal{R}_0 < 1$, then the system (3.2) has an unique disease free equilibrium point θ^0.

ii) If $\mathcal{R}_0 > 1$, then the system (3.2) has an unique endemic equilibrium point θ^*.

Proof.

Using the last two equations of (3.2) around point the equilibrium point $K = (x, y, z)$, we have:

$$\beta_1^\alpha \frac{xy}{x+y} + \beta_2^\alpha \frac{xz}{x+y} = (\eta^\alpha + \mu^\alpha)y; \tag{5.13}$$

$$z = \frac{p^\alpha}{\delta^\alpha} y. \tag{5.14}$$

Using (5.14) and replacing x with $\frac{b}{\mu^\alpha} - \frac{\eta^\alpha + \mu^\alpha}{\mu^\alpha} y$, we get :

$$\beta_1^\alpha \frac{\mu^\alpha}{b - \eta^\alpha y}\left(\frac{b}{\mu^\alpha} - \frac{\eta^\alpha + \mu^\alpha}{\mu^\alpha} y\right)\frac{\delta^\alpha}{p^\alpha} z + \beta_2^\alpha \frac{\mu^\alpha}{b - \eta^\alpha y}\left(\frac{b}{\mu^\alpha} - \frac{\eta^\alpha + \mu^\alpha}{\mu^\alpha} y\right) z = (\eta^\alpha + \mu^\alpha)\frac{\delta^\alpha}{p^\alpha} z.$$

Let

$$\Psi(y) = \beta_1^\alpha \frac{\mu^\alpha}{b - \eta^\alpha y}\left(\frac{b}{\mu^\alpha} - \frac{\eta^\alpha + \mu^\alpha}{\mu^\alpha} y\right)\frac{\delta^\alpha}{p} + \beta_2^\alpha \frac{\mu^\alpha}{b - \eta^\alpha y}\left(\frac{b}{\mu^\alpha} - \frac{\eta^\alpha + \mu^\alpha}{\mu^\alpha} y\right) - \frac{(\eta^\alpha + \mu^\alpha)\delta^\alpha}{p^\alpha}.$$

It follows that

$$\begin{aligned}
\lim_{y \to 0} \Psi(y) &= \beta_1^\alpha \frac{\delta^\alpha}{p^\alpha} + \beta_2^\alpha - \frac{(\eta^\alpha + \mu^\alpha)\delta^\alpha}{p^\alpha} \\
&= \frac{(\eta^\alpha + \mu^\alpha)\delta^\alpha}{p^\alpha}\left(\frac{\beta_1^\alpha}{\eta^\alpha + \mu^\alpha} + \frac{\beta_2^\alpha p^\alpha}{(\eta^\alpha + \mu^\alpha)\delta^\alpha} - 1\right) \\
&= \frac{p^\alpha}{(\eta^\alpha + \mu^\alpha)\delta^\alpha}\left(\mathcal{R}_0 - 1\right).
\end{aligned}$$

For $(\bar{x}, \bar{y}, \bar{z}) = (x, \frac{b}{\eta^\alpha + \mu^\alpha}, z)$, we have $\Psi(\bar{y}) = -\frac{(\eta^\alpha + \mu^\alpha)\delta^\alpha}{p^\alpha} < 0$.
When $\mathcal{R}_0 < 1$, we have $\lim_{y\to 0}\Psi(y) < 0$. That means there isn't any $y^* > 0$ such that $\Psi(y^*) = 0$.
The system (3.2) has therefore an unique disease-free equilibrium θ^0 when $\mathcal{R}_0 < 1$.
We have $\lim_{y\to 0}\Psi(y) > 0$ when $\mathcal{R}_0 > 1$. That implies there exists $y^* > 0$ such that $\Psi(y^*) = 0$.
That means the system (3.2) has therefore an unique endemic equilibrium θ^* when $\mathcal{R}_0 > 1$.

In the following subsections, we explore the behavior of the fractional dengue model (3.2) depending on the value of $\mathcal{R}_0$.

5.3 Stability analysis of the disease free equilibrium (DFE) point θ^0

Theorem 5.6.
When $\mathcal{R}_0 < 1$, the disease free equilibrium $\theta^0 = (\frac{b}{\mu^\alpha}, 0, 0)$ of the system (3.2) is locally asymptotically stable.

For the proof of the Theorem, we state the following lemma.

Lemma 5.7. *(Theorem 7.20, page 158 of [8])*
Consider the fractional-order system

$$ {}_{t_0}^{C}D_t^\alpha \theta(t) = f(t, \theta(t)) \qquad t_0 > 0 \tag{5.15}$$

with initial condition $\theta(t_0) = \theta_0$, where $\alpha \in (0, 1]$, $f \in \mathbb{R}^n$. The system is locally asymptotically stable around a point Θ if and only if all the eigenvalues λ_i of Jacobian Matrix $J(\Theta)$ satisfy $\left|arg(\lambda_i)\right| > \frac{\alpha\pi}{2}$.

Proof of Theorem 5.6. The Jacobian matrix of the system (3.2) evaluated at the disease free equilibrium point θ^0 is :

$$J(\theta^0) = \begin{pmatrix} -\mu^\alpha & -\beta_1^\alpha & -\beta_2^\alpha \\ 0 & -(\eta^\alpha + \mu^\alpha) & \beta_2^\alpha \\ 0 & p^\alpha & -\delta^\alpha \end{pmatrix}$$

and the characteristic polynomial is

$$\left|J(\theta^0) - \lambda I\right| = \begin{vmatrix} -\lambda - \mu^\alpha & -\beta_1^\alpha & -\beta_2^\alpha \\ 0 & -\lambda - (\eta^\alpha + \mu^\alpha) & \beta_2^\alpha \\ 0 & p^\alpha & -\lambda - \delta^\alpha \end{vmatrix}$$

$$= (-\lambda - \mu^\alpha)\Big((\lambda + \eta^\alpha + \mu^\alpha)(\lambda + \delta^\alpha) - \beta_2^\alpha p^\alpha\Big)$$

$$\left|J(\theta^0) - \lambda I\right| = (-\lambda - \mu^\alpha)\Big(\lambda^2 + (\eta^\alpha + \mu^\alpha + \delta^\alpha)\lambda + (\eta^\alpha + \mu^\alpha)\delta^\alpha - p^\alpha\beta_2^\alpha\Big).$$

The eigenvalues are such that

$$\begin{aligned}
\lambda_1 &= -\mu^\alpha < 0,\\
\lambda_2+\lambda_3 &= -(\eta^\alpha+\mu^\alpha+\delta^\alpha) < 0,\\
\lambda_2\lambda_3 &= (\eta^\alpha+\mu^\alpha)\delta^\alpha - p^\alpha\beta_2^\alpha,\\
&= (\eta^\alpha+\mu^\alpha)\delta^\alpha\left(1-\frac{p^\alpha\beta_2^\alpha}{(\eta^\alpha+\mu^\alpha)\delta^\alpha}\right) > 0,\\
\lambda_2\lambda_3 &= \mu^\alpha\delta^\alpha\left(1-\mathcal{R}_0^i\right) > 0 \quad \text{since} \quad \mathcal{R}_0^i < 1,\\
&\text{because of } \mathcal{R}_0 < 1.
\end{aligned}$$

From (5.16), (5.16) and (5.16), the eigenvalues λ_1, λ_2 and λ_3 are all negative. All the eigenvalues λ we have

$$|arg(\lambda)| = \pi > \frac{\alpha\pi}{2}$$

where

$$\alpha \in \big(0,1\big].$$

From the Lemma 5.7, we conclude that the disease free equilibrium point θ^0 is locally asymptotically stable when $\mathcal{R}_0 < 1$.

Theorem 5.8. *The disease free equilibrium θ^0 of the system (3.2) is globally asymptotically stable, when $\mathcal{R}_0 < 1$.*

Proof. To demonstrate this theorem, we use the Varga Lemma in [34] and the standard comparison theorem in [20]. Let us consider the infected classes y and z. By the equations corresponding to these states, we have the following system :

$$\begin{cases}
{}_{t_0}^{C}D_t^\alpha y(t) &= \beta_1^\alpha\dfrac{x(t)y(t)}{x(t)+y(t)} + \beta_2^\alpha\dfrac{x(t)z(t)}{x(t)+y(t)} - (\eta^\alpha+\mu^\alpha)y(t),\\
{}_{t_0}^{C}D_t^\alpha z(t) &= p^\alpha y(t) - \delta^\alpha z(t).
\end{cases} \tag{5.16}$$

Since $0 < \dfrac{x}{x+y} \leqslant 1$, we have :

$$\begin{cases}
{}_{t_0}^{C}D_t^\alpha y(t) &\leqslant \beta_1^\alpha y(t) + \beta_2^\alpha z(t) - (\eta^\alpha+\mu^\alpha)y(t),\\
{}_{t_0}^{C}D_t^\alpha z(t) &\leqslant p^\alpha y(t) - \delta^\alpha z(t)
\end{cases} \tag{5.17}$$

or

$$\begin{pmatrix} y \\ z \end{pmatrix} \leqslant \begin{pmatrix} \beta_1^\alpha y(t) + \beta_2^\alpha\dfrac{b}{\mu^\alpha}z(t) - (\eta^\alpha+\mu^\alpha)y(t) \\ p^\alpha y(t) - \delta^\alpha z(t) \end{pmatrix}. \tag{5.18}$$

That means :

$$\begin{pmatrix} y \\ z \end{pmatrix} \leqslant \begin{pmatrix} \beta_1^\alpha - (\eta^\alpha+\mu^\alpha) & \beta_2^\alpha \\ p^\alpha & -\delta^\alpha \end{pmatrix}\begin{pmatrix} y \\ z \end{pmatrix} \tag{5.19}$$

$$\begin{pmatrix} y \\ z \end{pmatrix} \leqslant (F+V)\begin{pmatrix} y \\ z \end{pmatrix}. \tag{5.20}$$

We consider the equation

$$\begin{pmatrix} \bar{y} \\ \bar{z} \end{pmatrix} = (F+V)\begin{pmatrix} \bar{y} \\ \bar{z} \end{pmatrix}. \tag{5.21}$$

We remark that $F \geqslant 0$ and V is an asymptotic stable Metzler inversible matrix.
Since $\mathcal{R}_0 = \rho(-FV^{-1}) < 1$, using the Varga's Lemma in [34] we get $M = F + V$ is asymptotically stable. That means the system (5.21) is asymptotically stable at origin $(0,0)$. In others words

$$(\bar{y}(t), \bar{z}(t)) \to (0,0) \quad when \quad t \to +\infty.$$

By Lakshmikantham standard comparison theorem in [20], $(y,z) \to (0,0)$ as $t \to +\infty$. We substitute y, z into the system (3.2) by 0 and we get $x \to x^0$ when $t \to +\infty$. It follows that when $\mathcal{R}_0 < 1$,

$$(x(t), y(t), z(t)) \to (\frac{b}{\mu^\alpha}, 0, 0) \quad as \quad t \to +\infty.$$

θ^0 is therefore globally asymptotically stable if $\mathcal{R}_0 < 1$.

5.4 Analysis stability of the endemic equilibrium (EE) point θ^*

We establish the global dynamics of the endemic equilibrium point θ^*.

Lemma 5.9. *(see [35])*
Let $u \in \mathbb{R}_+$ be a derivable function. Then, for any time instant $t \geqslant t_0$

$${}^{C}_{t_0}D^{\alpha}_{t}\left(u(t) - u^* - u^* \ln \frac{u(t)}{u^*}\right) \leqslant \left(1 - \frac{u^*}{u(t)}\right) {}^{C}_{t_0}D^{\alpha}_{t} u(t), u^* \in \mathbb{R}^+, \alpha \in (0,1).$$

Theorem 5.10. *(see [1, 5])*
Let $x = 0$ be an equilibrium of fractional order system

$${}^{C}_{t_0}D^{\alpha}_{t} x(t) = f(t,x), \quad x(t_0) = x_0,$$

let $\Omega \subseteq \mathbb{R}^n$ be a domain containing $x = 0$.
Let $V(t,x) : [t_0, \infty] \times \Omega \to \mathbb{R}$ be continuously differentiable function such that

$$W_1(x) \leq V(t,x) \leq W_2(x)$$

and

$${}^{C}_{t_0}D^{\alpha}_{t} V(t,x) \leq -W_3(x), \quad for\ t \geq 0,\ x \in \Omega,$$

where $W_1(x)$, $W_2(x)$ and $W_3(x)$ be continuous positive definite functions on Ω and V is a Lyapunov candidate function, then $x = 0$ is globally asymptotically stable.

Lemma 5.11. *Let consider the following function g define by :*

$g(I) = I - I^* - I^* \ln\left(\frac{I}{I^*}\right)$ $I, I^* \in \mathbb{R}^+$.

We have that : $g(I) \geqslant 0$.
Indeed, by limited development we get :

$$\begin{aligned} g(I) &= g(I^*) + g'(I^*)(I - I^*) + \frac{1}{2}g''(\xi)(I - I^*)^2 \\ &= \frac{1}{2}\frac{I^*}{I^2}(I - I^*)^2 \\ g(I) &\geqslant \frac{1}{2}\frac{I^*}{\left(\frac{b}{\mu}\right)^2}(I - I^*)^2 \end{aligned}$$

where ξ is a point between I and I^*.

Theorem 5.12.
If $p \leqslant \eta, sgn(x^* - x) = sgn(y^* - y) = sgn(z^* - z)$ and $\mathcal{R}_0 \geqslant 1$ then the endemic equilibrium θ^* of the system (3.2) is globally asymptotically stable.

Proof. At the endemic equilibrium point θ^*, by summing the three equation of the system (3.2) we get :

$$b = \mu^\alpha x^* - (\eta^\alpha + \mu^\alpha - p^\alpha)y^* - \delta^\alpha z^*.$$

Consider the Lyapunov function candidate :

$$V(\theta(t)) \quad = \quad (x+y+z) - (x^*+y^*+z^*) - (x^*+y^*+z^*)\ln\left(\frac{x+y+z}{x^*+y^*+z^*}\right).$$

- $V(\theta^*(t)) = 0$.
- $V(\theta(t)) > 0,\ \forall\ \theta \neq \theta^*$.
- Let us differentiate $V(\theta(t))$ with respect to the state $\theta(t)$ with the derivative order $\alpha \in (0,1)$. Using the lemma 5.9, we get :

$$\begin{aligned}
{}^C_{t_0}D^\alpha_t V(\theta(t)) &\leqslant \left(1 - \frac{x^*+y^*+z^*}{x+y+z}\right) {}^C_{t_0}D^\alpha_t (x+y+z) \\
&\leqslant \frac{1}{x+y+z}\Big((x+y+z) - (x^*+y^*+z^*)\Big) {}^C_{t_0}D^\alpha_t (x+y+z) \\
&\leqslant \frac{1}{x+y+z}\Big((x-x^*) + (y-y^*) + (z-z^*)\Big) \\
&\quad \times (b - \mu^\alpha x - (\eta^\alpha + \mu^\alpha - p^\alpha)y - \delta^\alpha z) \\
&\leqslant \frac{1}{x+y+z}\Big((x-x^*) + (y-y^*) + (z-z^*)\Big) \\
&\quad \times \Big((\mu^\alpha x + (\eta^\alpha + \mu^\alpha - p^\alpha)y + \delta^\alpha z) - (\mu^\alpha x^* + (\eta^\alpha + \mu^\alpha - p^\alpha)y^* + \delta^\alpha z^*)\Big) \\
&\leqslant \frac{1}{x+y+z}\Big((x-x^*) + (y-y^*) + (z-z^*)\Big)\Big(\mu^\alpha(x^*-x) \\
&\quad + (\eta^\alpha + \mu^\alpha - p^\alpha)(y^*-y) + \delta^\alpha(z^*-z)\Big) \\
&\leqslant \frac{1}{x+y+z}\Big(\Big(\mu^\alpha(x^*-x)(x-x^*) + (\eta^\alpha + \mu^\alpha - p^\alpha)(y^*-y)(x-x^*) \\
&\quad + \delta^\alpha(z^*-z)(x-x^*)\Big) + \Big(\mu^\alpha(x^*-x)(y-y^*) + (\eta^\alpha + \mu^\alpha - p^\alpha)(y^*-y) \\
&\quad \times (y-y^*) + \delta^\alpha(z^*-z)(y-y^*)\Big) + \Big(\mu^\alpha(x^*-x)(z-z^*) + (\eta^\alpha + \mu^\alpha - p^\alpha) \\
&\quad \times (y^*-y)(z-z^*) + \delta^\alpha(z^*-z)(z-z^*)\Big)\Big)
\end{aligned}$$

$$
\begin{aligned}
&\leqslant -\frac{1}{x+y+z}\Bigg(\Big(\mu^\alpha(x^*-x)^2+(\eta^\alpha+\mu^\alpha-p^\alpha)(y^*-y)(x^*-x)\\
&+\delta^\alpha(z^*-z)(x^*-x)\Big)+\Big(\mu^\alpha(x^*-x)(y^*-y)+(\eta^\alpha+\mu^\alpha-p^\alpha)(y^*-y)^2\\
&+\delta^\alpha(z^*-z)(y^*-y)\Big)\Big(\mu^\alpha(x^*-x)(z^*-z)+(\eta^\alpha+\mu^\alpha-p^\alpha)(y^*-y)\\
&\times(z^*-z)+\delta^\alpha(z^*-z)^2\Big)\Bigg)\\
{}^{C}_{t_0}D^\alpha_t V(\theta(t)) &\leqslant -\frac{1}{x+y+z}\Bigg(\Big(\mu^\alpha(x^*-x)^2+(\eta^\alpha+\mu^\alpha-p^\alpha)(y^*-y)^2+\delta^\alpha(z^*-z)^2\Big)\\
&+\Big((2\mu^\alpha+\eta^\alpha-p^\alpha)(x^*-x)(y^*-y)+(\delta^\alpha+\mu^\alpha)(x^*-x)(z^*-z)\\
&+(\delta^\alpha+\eta^\alpha+\mu^\alpha-p^\alpha)(z^*-z)(y^*-y)\Big)\Bigg)
\end{aligned}
$$

Since $p \leqslant \eta$ and $sgn(x^*-x)=sgn(y^*-y)=sgn(z^*-z)$, we get

$$
{}^{C}_{t_0}D^\alpha_t V(\theta(t)) \leqslant 0.
$$

By the same operations, we get for $\alpha = 1$,

$$
\begin{aligned}
\dot{V}(\theta(t)) &= -\frac{1}{x+y+z}\Bigg(\Big(\mu^\alpha(x^*-x)^2+(\eta^\alpha+\mu^\alpha-p^\alpha)(y^*-y)^2+\delta^\alpha(z^*-z)^2\Big)\\
&+\Big((2\mu^\alpha+\eta^\alpha-p^\alpha)(x^*-x)(y^*-y)+(\delta^\alpha+\mu^\alpha)(x^*-x)(z^*-z)\\
&+(\delta^\alpha+\eta^\alpha+\mu^\alpha-p^\alpha)(z^*-z)(y^*-y)\Big)\Bigg),\\
\dot{V}(\theta(t)) &= 0 \text{ if and only if } x=x^*, y=y^* \text{ and } z=z^*.
\end{aligned}
$$

It follows that $\big\{\theta(t)=(x(t),y(t),z(t))\in\mathbb{R}^3_+ \ / \ \dot{V}(\theta(t))=0\big\}=\{\theta^*\}$.
Then, by the theorem (5.10)([1, 5]) and the Lasalle Invariance Principle (Lemma 4.6 in [13]), the endemic equilibrium point θ^* is globally asymptotically stable.

6 Algorithm and numerical simulations

6.1 The algorithm

For numerical simulations, we discretize our model using the Adam-Bashforth-Moulton (ABM) method. Let $[t_0, T]$ be the simulation range that we subdivide by n discretization points. $h = (T-t_0)/n$ is the discretization step, $t_i = T+ih, i \in \{1,2,...,n-1\}$ the discretization points and $\alpha \in (0;1]$. By applying the ABM method on the model, we obtained the predictor values and the corresponding corrector values as follows :

$$x_{n+1} = x(0) + \frac{h^\alpha}{\Gamma(\alpha+2)}\left(b - \beta_1^\alpha \frac{x_{n+1}^p y_{n+1}^p}{x_{n+1}^p + y_{n+1}^p} - \beta_2^\alpha \frac{x_{n+1}^p z_{n+1}^p}{x_{n+1}^p + y_{n+1}^p} - \mu^\alpha x_{n+1}^p\right)$$
$$+ \frac{h^\alpha}{\Gamma(\alpha+2)} \sum_{j=0}^{n} a_{j,n+1}\left(b - \beta_1^\alpha \frac{x_j y_j}{x_j + y_j} - \beta_2^\alpha \frac{x_j z_j}{x_j + y_j} - \mu^\alpha x_j\right),$$

$$y_{n+1} = y(0) + \frac{h^\alpha}{\Gamma(\alpha+2)}\left(\beta_1^\alpha \frac{x_{n+1}^p y_{n+1}^p}{x_{n+1}^p + y_{n+1}^p} + \beta_2^\alpha \frac{x_{n+1}^p z_{n+1}^p}{x_{n+1}^p + y_{n+1}^p} - (\eta^\alpha + \mu^\alpha) y_{n+1}^p\right)$$
$$+ \frac{h^\alpha}{\Gamma(\alpha+2)} \sum_{j=0}^{n} a_{j,n+1}\left(\beta_1^\alpha \frac{x_j y_j}{x_j + y_j} + \beta_2^\alpha \frac{x_j z_j}{x_j + y_j} - (\eta^\alpha + \mu^\alpha) y_j\right),$$

$$z_{n+1} = z(0) + \frac{h^\alpha}{\Gamma(\alpha+2)}\left(p y_{n+1}^p - \delta z_{n+1}^p\right) + \frac{h^\alpha}{\Gamma(\alpha+2)} \sum_{j=0}^{n} a_{j,n+1}\left(p y_j - \delta z_j\right),$$

$$x_{n+1}^p = x(0) + \frac{1}{\Gamma(\alpha)} \sum_{j=0}^{n} b_{j,n+1}\left(b - \beta_1^\alpha \frac{x_j y_j}{x_j + y_j} - \beta_2^\alpha \frac{x_j z_j}{x_j + y_j} - \mu^\alpha x_j\right),$$

$$y_{n+1}^p = y(0) + \frac{1}{\Gamma(\alpha)} \sum_{j=0}^{n} b_{j,n+1}\left(\beta_1^\alpha \frac{x_j y_j}{x_j + y_j} + \beta_2^\alpha \frac{x_j z_j}{x_j + y_j} - (\eta^\alpha + \mu^\alpha) y_j\right),$$

$$z_{n+1}^p = z(0) + \frac{1}{\Gamma(\alpha)} \sum_{j=0}^{n} b_{j,n+1}\left(p y_j - \delta z_j\right)$$

where

$$a_{j,n+1} = \begin{cases} n^{\alpha+1} - (n-\alpha)(n+1)^\alpha, & \text{if } j = 0, \\ (n-j+2)^{\alpha+1} + (n-j)^{\alpha+1} - 2(n-j+1)^{\alpha+1}, & \text{if } 0 \le j \le n, \\ 1, & \text{if } j = 1, \end{cases}$$

$$b_{j,n+1} = \frac{h^\alpha}{\alpha}\left((n+1-j)^\alpha - (n-j)^\alpha\right), \quad 0 \le j \le n.$$

6.2 Numerical simulations

The purpose of the numerical simulation is to examine the influence of order change on the dynamic action of the system. For this reason, we use predictor-corrector method developed by Adam-Bashforth-Moulton (see [15]) based on the iterative scheme of fractional derivative in Caputo sense ([31]).

Now, we have performed some numerical simulations to corroborate the theoretical work in the disease-free case and in the endemic case.
Depending on whether the number of basic reproduction is less or greater than unity, the dynamics of the different states are observed using the Python version 3.7 programming software.

For the case of $\mathcal{R}_0 < 1$, the values of the others parameters are estimated : $b = 14, \beta_1 = 0.01, \beta_2 = 0.003, \mu = 0.1, \eta = 0.2, p = 0.1$ and $\delta = 0.9$. With theses values, we obtained the following curves :

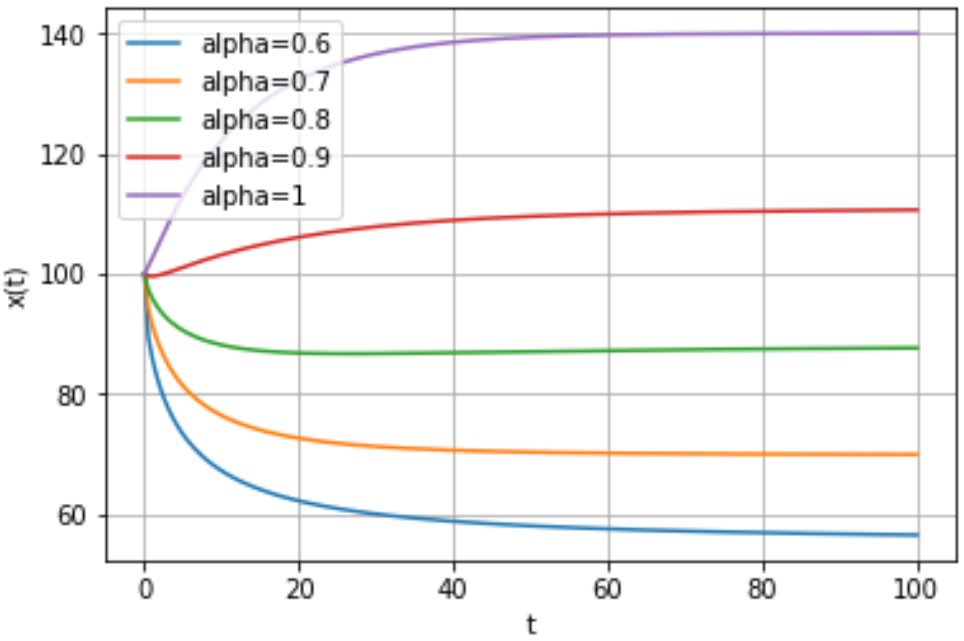

Figure 1. Susceptible humans x when $\mathcal{R}_0 < 1$.

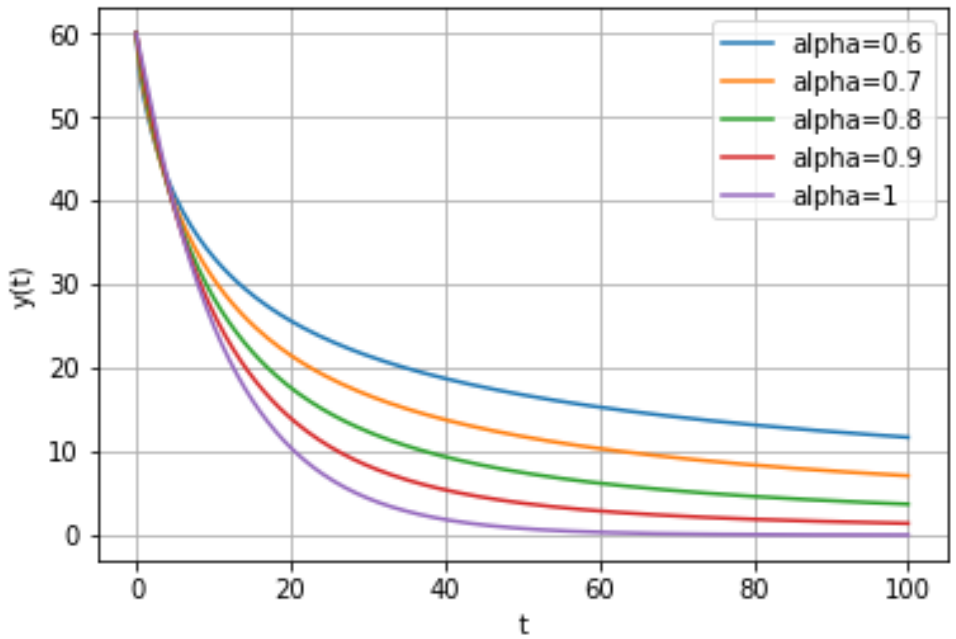

Figure 2. Infected humans y when $\mathcal{R}_0 < 1$.

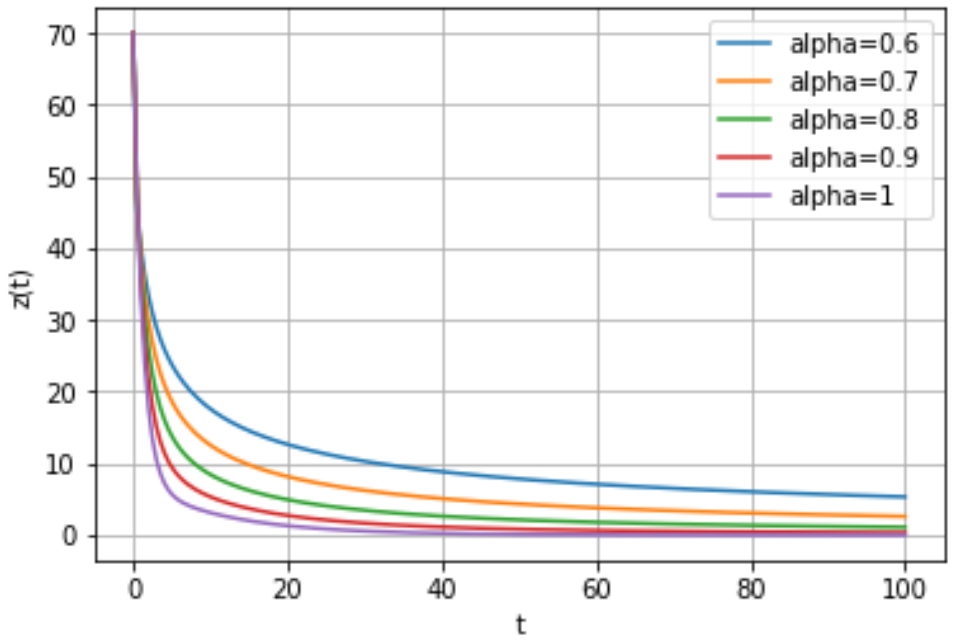

Figure 3. Infected humans z when $\mathcal{R}_0 < 1$.

The figures 1, 2, 3 show the evolution of the population of susceptible individuals (x), infected individuals (y), infected vectors (z) respectively when the basic reproduction number is less than 1 with the fractional order values $\alpha = 0.6, 0.7, 0.8, 0.9, 1$.
In each figure 1, 2, 3 we have a comparison of states dynamics under different orders. We can see clearly from the images that the state of the system depends on the fractional order. Indeed, for different orders, each state variable shows the same change trend. However, the time to converge to the equilibrium point is slightly different. With the increase of the order, the model converges to the equilibrium point faster. For example, it can be see in figure 2 that when $\alpha = 0.9, 1$ the compartment y converges to zero faster than when $\alpha = 0.6, 0.7, 0.8$. That means the fractional order operator shows interesting properties of convergence that the integer order operator doesn't have, and it can predict the model more accurately.
Theses different curves point out that the disease tends to disappear in the population. Indeed, the individual and vector infectious classes y, z are getting closer and closer to zero with the evolution of time t. This implies the disappearance of the disease in the population when $\mathcal{R}_0 < 1$ for all the fractional order.

For the case of $\mathcal{R}_0 > 1$, the values of the others parameters are estimated : $b = 14, \beta_1 = 0.3, \beta_2 = 0.2, \mu = 1/55, \eta = 1/10, p = 0.2$ and $\delta = 0.19$. With theses values, we obtained the following curves :

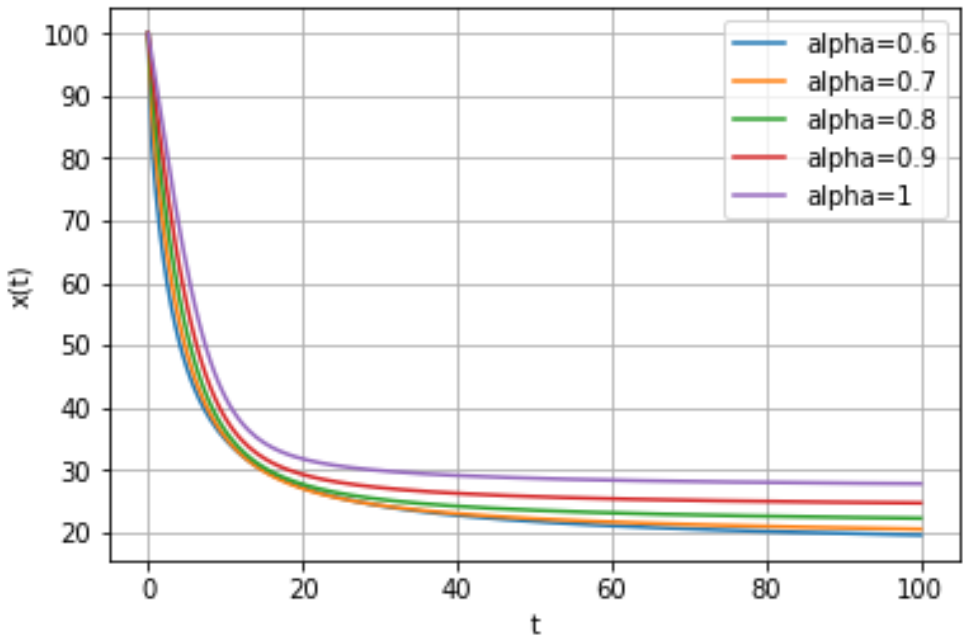

Figure 4. Susceptible humans x when $\mathcal{R}_0 > 1$.

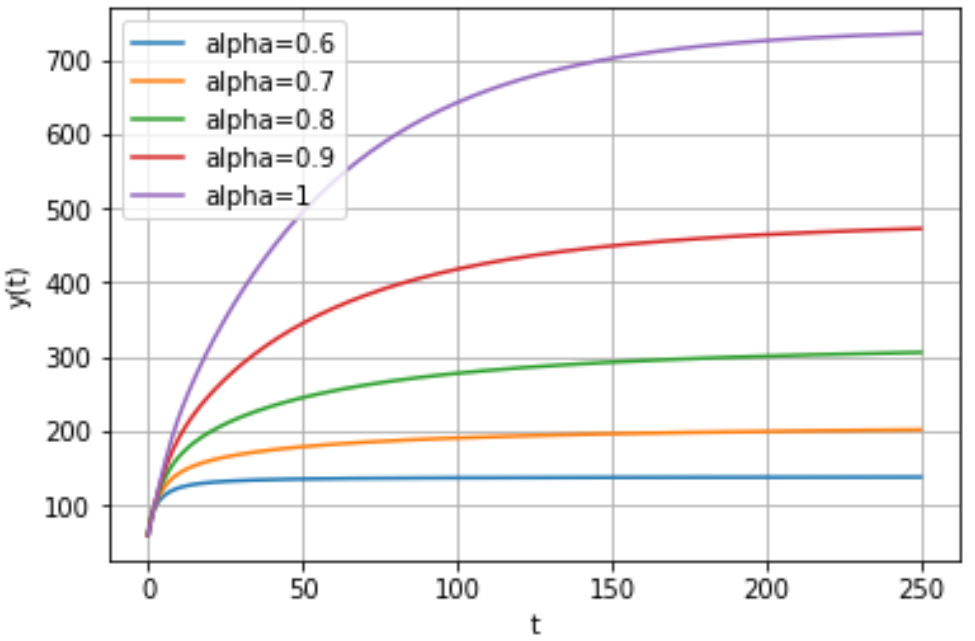

Figure 5. Infected humans y when $\mathcal{R}_0 > 1$.

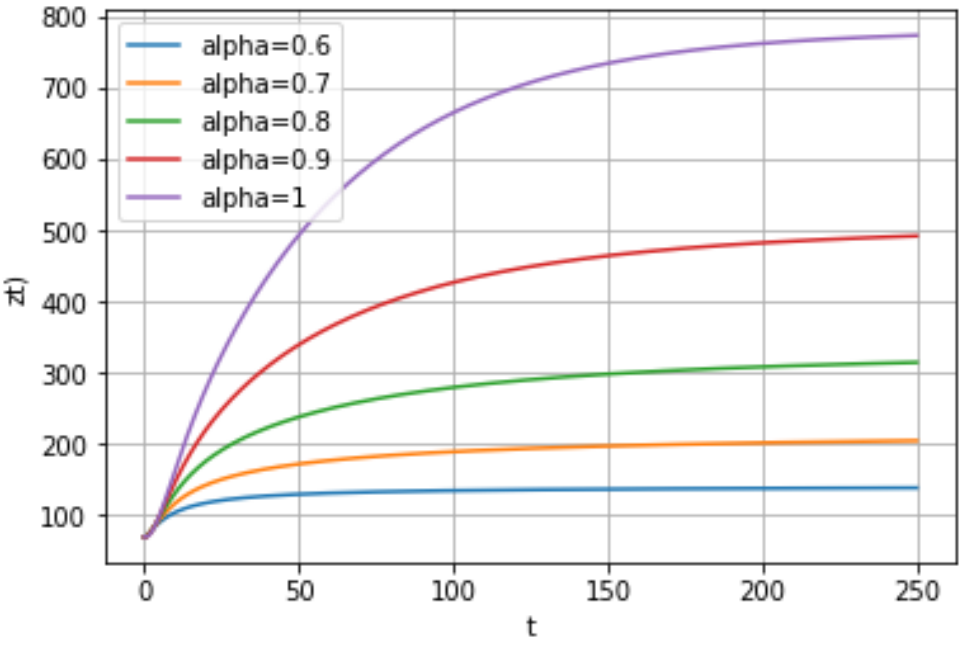

Figure 6. Infected humans z when $\mathcal{R}_0 > 1$.

By the figures 4, 5, 6 we present the dynamics as a function of time (days) of the population of susceptible individuals(x), infected individuals (y) and infected vectors (z) respectively when the basic reproduction number is greater than 1 with the fractional order values $\alpha = 0.6, 0.7, 0.8, 0.9, 1$.
For each value of the fractional order α, we observe that the susceptible classe (x) and the infectious classes (y, z) stabilize after a certain time. By changing the alpha value, we observe that the shapes of the curves are similar. In fact, the different stabilization are observed around the endemic equilibrium point x^*, y^*, z^* which are a function of α. We also observe that for the values of α we have taken, the different curves of the infectious classes (x, y, z) stabilize around a non-zero point. That situation numerically proves the persistence of the disease in the population when the basic reproduction number is greater than 1 and corroborate our mathematical work.

7 Conclusion

HIV and Zikas virus have become a worldwide public health problem. Thus, a well-developed mathematical model is crucial for understanding the dynamics of its transmission. In our paper, we used the Caputo fractional order model with direct and indirect incidence function of transmission to study the dynamics of diseases such as dengue, Zikas virus and HIV. This model has provided flexibility to researchers in designing the transmission model by associating memory into the model. Then, we presented the dynamics of the transmission for some values of $\alpha \in \{0.6, 0.7, 0.8, 0.9, 1\}$. We also studied the stabilization of the disease transmission dynamic system. We have obtained that when $\mathcal{R}_0 < 1$, the disease-free equilibrium point θ^0 is unique and globally asymptotically stable. So, we found that when $\mathcal{R}_0 > 1$, the endemic equilibrium point θ^* is unique. Moreover, if $p \leqslant \eta$ and $sgn(x^* - x) = sgn(y^* - y) = sgn(z^* - z)$, the endemic equilibrium point θ^* is globally asymptotically stable. Finally, we presented curves showing the possible dynamics of our fractional differential equation system using Python version 3.7 software and the predictor-corrector method.
From this study, we note that when the fractional order is less than 1, we can get more precision, more details and more realistic dynamics with a shorter convergence time towards the equilibrium points. We intend to study the stochastic version of this fractional model a perspective.

References

[1] I. A. Baba and B. A. Nasidi. Fractional order model for the role of mild cases in the transmission of covid-19. *Chaos, Solitons & Fractals*, 142:110374, 2021.

[2] S. Boulaaras, R. Jan, A. Khan, and M. Ahsan. Dynamical analysis of the transmission of dengue fever via caputo-fabrizio fractional derivative. *Chaos, Solitons & Fractals: X*, 8:100072, 2022.

[3] L. Cai, S. Guo, X. Li, and M. Ghosh. Global dynamics of a dengue epidemic mathematical model. *Chaos, Solitons & Fractals*, 42(4):2297–2304, 2009.

[4] L. F. Chaves, L. C. Harrington, C. L. Keogh, A. M. Nguyen, and U. D. Kitron. Blood feeding patterns of mosquitoes: random or structured? *Frontiers in zoology*, 7:1–11, 2010.

[5] H. Delavari, D. Baleanu, and J. Sadati. Stability analysis of caputo fractional-order nonlinear systems revisited. *Nonlinear Dynamics*, 67:2433–2439, 2012.

[6] O. Diekmann, J. A. P. Heesterbeek, and J. A. Metz. On the definition and the computation of the basic reproduction ratio r 0 in models for infectious diseases in heterogeneous populations. *Journal of mathematical biology*, 28:365–382, 1990.

[7] K. Diethelm and N. Ford. The analysis of fractional differential equations. *Lect. Notes Math*, 2004:3–12, 2010.

[8] K. Diethelm and N. J. Ford. Analysis of fractional differential equations. *Journal of Mathematical Analysis and Applications*, 265(2):229–248, 2002.

[9] Eiman, K. Shah, M. Hleili, and T. Abdeljawad. Two strains model of infectious diseases for mathematical analysis and simulations. *Mathematical and Computer Modelling of Dynamical Systems*, 30(1):477–495, 2024.

[10] A. Guiro, B. Koné, and S. Ouaro. Mathematical model of the spread of the coronavirus disease 2019 (covid-19) in burkina faso. *Applied Mathematics*, 11(11):1204–1218, 2020.

[11] A. Guiro, S. Ouaro, and A. Traore. Stability analysis of a schistosomiasis model with delays. *Advances in Difference Equations*, 2013(1):1–15, 2013.

[12] N. Hamdan and A. Kilicman. Stability and sensitivity analysis of the fractional order dengue model. *ASM Science Journal*, 13, 2020.

[13] J. Huo, H. Zhao, and L. Zhu. The effect of vaccines on backward bifurcation in a fractional order hiv model. *Nonlinear Analysis: Real World Applications*, 26:289–305, 2015.

[14] B. Ivorra, M. R. Ferrández, M. Vela-Pérez, and A. M. Ramos. Mathematical modeling of the spread of the coronavirus disease 2019 (covid-19) taking into account the undetected infections. the case of china. *Communications in nonlinear science and numerical simulation*, 88:105303, 2020.

[15] S. R. Iyengar and R. Jain. *Numerical Methods (As Per Anna University)*. New Age International, 2009.

[16] W. O. Kermack and A. G. McKendrick. A contribution to the mathematical theory of epidemics. *Proceedings of the royal society of london. Series A, Containing papers of a mathematical and physical character*, 115(772):700–721, 1927.

[17] A. Kilicman et al. A fractional order sir epidemic model for dengue transmission. *Chaos, Solitons & Fractals*, 114:55–62, 2018.

[18] M. Kumar and S. Abbas. Stability and optimal control of age-structured cell-free and cell-to-cell transmission model of hiv. *Mathematical Methods in the Applied Sciences*, 2023.

[19] M. Kumar, S. Abbas, and A. Tridane. Optimal control and stability analysis of an age-structured seirv model with imperfect vaccination. *Mathematical Biosciences and Engineering*, 20(8):14438–14463, 2023.

[20] V. Lakshmikantham, S. Leela, and A. A. Martynyuk. *Stability analysis of nonlinear systems*. Springer, 1989.

[21] Y. Li, Y. Chen, and I. Podlubny. Stability of fractional-order nonlinear dynamic systems: Lyapunov direct method and generalized mittag–leffler stability. *Computers & Mathematics with Applications*, 59(5):1810–1821, 2010.

[22] K. S. Miller and B. Ross. An introduction to the fractional calculus and fractional differential equations. *New York : Wiley*, 1993.

[23] Z. M. Odibat and N. T. Shawagfeh. Generalized taylor's formula. *Applied Mathematics and Computation*, 186(1):286–293, 2007.

[24] A. S. Perelson, A. U. Neumann, M. Markowitz, J. M. Leonard, and D. D. Ho. Hiv-1 dynamics in vivo: virion clearance rate, infected cell life-span, and viral generation time. *Science*, 271(5255):1582–1586, 1996.

[25] W. Rahou, A. Salim, J. Lazreg, and M. Benchohra. Implicit caputo tempered fractional differential equations with retarded and advanced arguments in banach spaces. *Palestine Journal of Mathematics*, 14(1), 2025.

[26] S. Salwahan, S. Abbas, A. Tridane, and M. A. Hajji. Optimal control of the treatment and the vaccination in an epidemic switched system using polynomial approach. *Alexandria Engineering Journal*, 74:187–193, 2023.

[27] N. Sene. Fractional advection-dispersion equation described by the caputo left generalized fractional derivative. *Palestine Journal of Mathematics*, 10(2):562–579, 2021.

[28] K. Shah, H. Naz, T. Abdeljawad, and B. Abdalla. Study of fractional order dynamical system of viral infection disease under piecewise derivative. *CMES-Computer Modeling in Engineering & Sciences*, 136(1), 2023.

[29] K. Shah, M. Sarwar, T. Abdeljawad, et al. On mathematical model of infectious disease by using fractals fractional analysis. *Discrete and Continuous Dynamical Systems-S*, 17(10):3064–3085, 2024.

[30] K. Shah, M. Sarwar, T. Abdeljawad, et al. On rotavirus infectious disease model using piecewise modified *abc* fractional order derivative. *Networks & Heterogeneous Media*, 19(1), 2024.

[31] A. Shloof, N. Senu, A. Ahmadian, M. Pakdaman, and S. Salahshour. A new iterative technique for solving fractal-fractional differential equations based on artificial neural network in the new generalized caputo sense. *Engineering with Computers*, 39(1):505–515, 2023.

[32] H. Shu and X.-S. Wang. Global dynamics of a coupled epidemic model. *Discrete & Continuous Dynamical Systems-Series B*, 22(4), 2017.

[33] P. Van den Driessche and J. Watmough. Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission. *Mathematical biosciences*, 180(1-2):29–48, 2002.

[34] R. S. Varga. Iterative analysis. *New Jersey*, 322, 1962.

[35] C. Vargas-De-León. Volterra-type lyapunov functions for fractional-order epidemic systems. *Communications in Nonlinear Science and Numerical Simulation*, 24(1-3):75–85, 2015.

[36] C. Vinauger, L. Buratti, and C. R. Lazzari. Learning the way to blood: first evidence of dual olfactory conditioning in a blood-sucking insect, rhodnius prolixus. i. appetitive learning. *Journal of Experimental Biology*, 214(18):3032–3038, 2011.

[37] X.-S. Wang, J. Wu, and Y. Yang. Richards model revisited: Validation by and application to infection dynamics. *Journal of theoretical biology*, 313:12–19, 2012.

[38] Y. Yoda, D. Ouedraogo, M. Barro, and A. Guiro. Analysis of dengue transmission taking into account hemorrhagic cases through caputo fractional order derivatives. *SeMA Journal*, pages 1–31, 2025.

[39] Y. Yoda, D. Ouedraogo, H. Ouedraogo, and A. Guiro. Optimal control of seihr mathematical model of covid-19. *Electronic Journal of Mathematical Analysis and Applications*, 11(1):134–161, 2023.

[40] Y. Yoda, H. Ouedraogo, D. Ouedraogo, and A. Guiro. Mathematical analysis and optimal control of dengue fever epidemic model. *Advances in Continuous and Discrete Models*, 2024(1):1–33, 2024.

[41] D. Zwilling. Fractional differential equations. *Handbook of Differential Equations*, pages 258–262, 1992.

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