Healthcare Analytics 4 (2023) 100210

Contents lists available at ScienceDirect

Healthcare Analytics

journal homepage: www.elsevier.com/locate/health

A fractional-order mathematical model for malaria and COVID-19 co-infection dynamics

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ARTICLE INFO

Keywords:
Fractional-order
Malaria
COVID-19
Co-infection
Atangana–Baleanu derivative
Lyapunov function

ABSTRACT

This study proposes a fractional-order mathematical model for malaria and COVID-19 co-infection using the Atangana–Baleanu Derivative. We explain the various stages of the diseases together in humans and mosquitoes, and we also establish the existence and uniqueness of the fractional order co-infection model solution using the fixed point theorem. We conduct the qualitative analysis along with an epidemic indicator, the basic reproduction number R0 of this model. We investigate the global stability at the disease and endemic free equilibrium of the malaria-only, COVID-19-only, and co-infection models. We run different simulations of the fractional-order co-infection model using a two-step Lagrange interpolation polynomial approximate method with the aid of the Maple software package. The results reveal that reducing the risk of malaria and COVID-19 by taking preventive measures will reduce the risk factor for getting COVID-19 after contracting malaria and will also reduce the risk factor for getting malaria after contracting COVID-19 even to the point of extinction.

1. Introduction

Malaria is a life-threatening disease spread by mosquitoes. Fever, chills, and flu-like symptoms are frequently experienced by malaria patients [1]. Individuals infected with the disease may experience serious problems and eventually pass away if untreated. Infected female Anopheles mosquitoes, particularly those carrying Plasmodium falciparum, transmit malaria to humans when they are feeding on blood. According to estimates, there are 241 million instances of malaria worldwide in 2020, and 627,000 people died from it, largely children in sub-Saharan Africa. In the United States, 2,000 incidences of malaria are estimated to occur annually. Africa accounts for more than 90% of malaria deaths, and children make up almost the entire mortality rate. In 2020, children under the age of five made up more than 80% of the malaria deaths in the area [2]. The goal of reducing the burden of malaria has become more challenging as a result of the evolution of treatment resistance to malaria and the absence of an efficient and secure vaccine. Many organizations have long supported the development of potential malaria vaccines in an attempt to prevent malaria transmission with the ultimate objective of eradicating the disease [3].

The SARS-CoV-2 virus is the infectious disease known as coronavirus disease (COVID-19). The infection is referred to as coronavirus 2 severe acute respiratory syndrome (SARS-CoV-2). It creates a condition known as coronavirus disease (COVID-19). The World Health Organization (WHO) declared the COVID-19 outbreak as a pandemic in March 2020 [4]. Two to fourteen days following exposure, COVID-19 symptoms and signs may manifest. The incubation period is the interval between exposure and the onset of symptoms. Coronaviruses is highly contagious and easily transmitted from one person to another. The airborne COVID-19 transmission routes include direct transmissions like close contact and indirect transmissions like coughing and sneezing. Most people who have been infected will have mild to moderate

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https://doi.org/10.1016/j.health.2023.100210
Received 24 April 2023; Received in revised form 23 May 2023; Accepted 11 June 2023

respiratory illness and will recover without needing any special treatment. Some, however, would become critically ill and need medical attention [5–9].

In order to understand how infectious diseases spread and how to prevent them, mathematical models are often used. The dynamical model study is used to examine key parameters, forecast future trends, and assess control methods to offer conclusive information for decision-making [10]. In recent times, a variety of mathematical models have been developed to investigate the transmission dynamics of COVID-19; for examples, see [11–23] and the references listed therein. Malaria mathematical models are also thoroughly examined in [24–32] and references are mentioned. Infected individuals with SARS-CoV-2 who live in malaria-endemic regions run the risk of developing severe COVID-19 or adverse disease outcomes if they fail to take care of their malaria condition. Although the list of COVID-19 symptoms is continually expanding and changing daily, several symptoms of malaria and COVID-19 are similar. The initial signs of malaria are a fever, headache, and chills, which typically show 10 to 15 days after the infective insect bite. On the other hand, those who are infected with COVID-19 typically have symptoms within 5 days, though this is not always the case [33]. Few studies have been conducted on the dynamics of COVID-19 and malaria [34–38]. Studies on disease modelling that use classical integer order operators have drawbacks since they are unable to adequately account for the memory effect. Note that the memory effect implies that the future state of an operator of a given function depends on the state at a given time and the state's past behaviour [39]. This operator's memory capabilities make it possible to include more historical data, improving the predictive ability of the model. This study's motivation is to incorporate this effect.

It is important to note that fractional order derivatives and integrals play an important role in epidemiological modelling and other real-world problems [40–51] because they capture the memory effect and other nonlocal properties. Many researchers have used fractional-order models to investigate the dynamics of various diseases. Furthermore, fractional-order models have been used in research to solve problems in a variety of disciplines. Many researchers have used the Atangana–Baleanu fractional operator in particular to answer various questions. See [52–55] and the references therein for examples of these studies. As a result, we develop and thoroughly investigate a mathematical model for COVID-19 and malaria co-infection that takes into account the main epidemiological and biological traits of each of the two diseases using a fractional-order mathematical model. In this study, we have develop a deterministic model of Malaria and COVID-19 co-dynamics some control strategies by extending the work of Tchoumi, et al. [34] . Thus we incorporated recovered compartment, COVID-19-induced mortality, malaria-induced mortality and co-infection-induced mortality rates of humans respectively to better understand the dynamics and control of the two disease and transforming the model into fractional order using Atangana–Baleanu Derivative. The rest of the paper is structured as follows: Section two deals with the preliminaries of the study, section three deals with the formulation of the model, the model analysis is presented in section four, section five deals with results and discussion while the conclusion of the study is presented in section six.

2. Preliminaries

In this section, we recall some basic concepts such as definitions, theorems and other properties related fractional calculus that will be needed in this study.

Definition 1 ([56]). Let $\omega \in H^1(a,b)$, $a < b, \alpha \in [0,1]$, therefore, the Atangana–Baleanu–Caputo (ABC) fractional derivative of ω with order α is given by

$$ {}^{ABC}_{a}D^{\alpha}_{t}[\omega(t)] = \frac{\mathfrak{L}(\alpha)}{1-\alpha}\int_a^t \dot{\omega}(\gamma)\mathbf{E}_{\alpha}\left[-\alpha\frac{(t-\gamma)^{\alpha}}{1-\alpha}\right]d\gamma, \tag{1}$$

where $\mathfrak{L}(\alpha)$ is positive and is a normalization function fulfilling $\mathfrak{L}(0) = \mathfrak{L}(1) = 1$ and $\mathbf{E}_{\alpha}$ is the Mittag-Leffler function.

Definition 2 ([56]). Let $\omega \in H^1(a,b)$, $a < b, \alpha \in [0,1]$, therefore, the Atangana–Baleanu Riemann–Liouville (ABR) fractional derivative of ω with order α is given by

$$ {}^{ABR}_{a}D^{\alpha}_{t}[\omega(t)] = \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{d}{dt}\int_a^t \omega(\gamma)\mathbf{E}_{\alpha}\left[-\alpha\frac{(t-\gamma)^{\alpha}}{1-\alpha}\right]d\gamma. \tag{2}$$

Definition 3 ([56]). Let $\omega \in H^1(a,b)$, $a < b, \alpha \in [0,1]$, therefore, the Atangana–Baleanu–Caputo (ABC) fractional Integral of a function $\omega(t)$ of order α is given by

$$ {}^{ABC}_{a}I^{\alpha}_{t}[\omega(t)] = \frac{1-\alpha}{\mathfrak{L}(\alpha)}\omega(t) + \frac{\alpha}{\mathfrak{L}(\alpha)\Gamma(\alpha)}\int_a^t \omega(\sigma)(t-\sigma)^{\alpha-1}d\sigma. \tag{3}$$

Definition 4 ([56]). The Laplace transform of Definitions 1 and 2 respectively can be written as

$$ \mathcal{L}\{{}^{ABC}_{0}D^{\alpha}_{t}[\omega(t)]\}(p) = \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^{\alpha}\mathcal{L}\{\omega(t)\}(p) - p^{\alpha-1}\omega(0)}{p^{\alpha} + \frac{\alpha}{1-\alpha}}. \tag{4}$$

$$ \mathcal{L}\{{}^{ABR}_{0}D^{\alpha}_{t}[\omega(t)]\}(p) = \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^{\alpha}\mathcal{L}\{\omega(t)\}(p)}{p^{\alpha} + \frac{\alpha}{1-\alpha}}, \tag{5}$$

where $\mathcal{L}$ is the Laplace transform operator.

Lemma 1 ([56]). *Let $\omega \in H^1(a,b)$, $a < b, \alpha \in [0,1]$, then the following inequality on $[a,b]$ is satisfied.*

$$ {}^{ABC}_{a}I^{\alpha}_{t}\left({}^{ABC}_{a}D^{\alpha}_{t}[\omega(t)]\right) = \omega(t) - \omega(a) \tag{6}$$

Theorem 2 ([56]). *The following inequality holds on a closed interval $[a,b]$ if ω be a continuous function on $[a,b]$*

$$ \|{}^{ABC}_{a}D^{\alpha}_{t}[\omega(t)]\| < \frac{\mathfrak{L}(\alpha)}{1-\alpha}\|\omega(\gamma)\| \tag{7}$$

where

$$\|\omega(\gamma)\| = \max_{a\le t\le b}|\omega(\gamma)|$$

Theorem 3 ([56]). *The ABC and ABR fractional derivatives satisfy Lipschitz condition respectively as follows:*

$$ \|{}^{ABC}_{0}D^{\alpha}_{t}[\omega(t)] - {}^{ABC}_{0}D^{\alpha}_{t}[g(t)]\| \le H\|\omega(t) - g(t)\| \tag{8}$$

$$ \|{}^{ABR}_{0}D^{\alpha}_{t}[\omega(t)] - {}^{ABR}_{0}D^{\alpha}_{t}[g(t)]\| \le H\|\omega(t) - g(t)\| \tag{9}$$

Therefore, according to the Definition 3, the unique solution of the differential equation with fractional order α can be written as

$${}^{ABC}_{a}D^{\alpha}_{t}[\omega(t)] = q(t)$$

which means

$$\omega(t) = \frac{1-\alpha}{\mathfrak{L}(\alpha)}q(t) + \frac{\alpha}{\mathfrak{L}(\alpha)\Gamma(\alpha)}\int_a^t q(\sigma)(t-\sigma)^{\alpha-1}d\sigma \tag{10}$$

3. Model formulation

The model under consideration consists of total population of humans (host) and total population of mosquitoes (vector) denoted by $N_h(t)$ and $N_v(t)$ respectively. Total population comprises of ten compartments. Namely, susceptible humans, $S_h(t)$; exposed humans to COVID-19 only, $E_c(t)$; exposed humans to malaria only, $E_m(t)$; exposed humans to malaria and COVID-19, $E_{mc}(t)$; infected humans with COVID-19 only, $I_c(t)$; infected humans with malaria only, $I_m(t)$; infected humans with both malaria and COVID-19, $I_{mc}(t)$; infected humans with COVID-19 and exposed to malaria, $I_{cEm}(t)$; infected humans with malaria and exposed to COVID-19, $I_{mEc}(t)$ and recovered humans from $I_c(t)$ as well as $I_m(t)$ is $R_h(t)$. Mathematically, the total population of humans is given by

$$\begin{aligned} N_h(t) = S_h(t) + E_c(t) + E_m(t) + E_{mc}(t) + I_m(t) + I_c(t) + I_{mc}(t) \\ + I_{mEc}(t) + I_{cEm}(t) + R_h(t) \end{aligned}.$$

Similarly, total population of mosquitoes (vector) comprises three compartments. Namely, susceptible mosquitoes, $S_v(t)$; exposed mosquitoes, $E_v(t)$ and infected mosquitoes $I_v(t)$. Mathematically, the total population of mosquitoes is given by $N_v(t) = S_v(t) + E_v(t) + I_v(t)$ Λ_h and Λ_v represents the recruitment rates of humans and mosquitoes respectively. σ_m, σ_c, σ_v and σ_{mc} are the progressive rates of humans from exposed to malaria infectious class, progressive rate of humans from exposed to COVID-19 infectious class, progressive rate of mosquitoes from exposed to infectious class and proportion of humans moving to the co-infection class respectively. μ and η are respectively represent natural mortality rates of humans and mosquitoes. Also, λ_c, λ_m, α_r and υ are the recovery rates from COVID-19 infected class, infected malaria class, infected co-infection class and reintegration rate of humans from recovered to susceptible class respectively. α_m, α_v and α_c represents the probability of transmission of malaria per mosquito bite to susceptible humans, from infected humans to susceptible mosquitoes and COVID-19 per contact respectively. δ_c, δ_m and δ_{mc} represent COVID-19-induced mortality, malaria-induced mortality and co-infection-induced mortality rates of humans respectively. The adjustment parameters γ_1 and γ_2 represents the risk factor for getting COVID-19 after contracting malaria and risk factor for getting malaria after contracting COVID-19 respectively where (γ_1, $\gamma_2 > 0$). ϕ_1 and ϕ_2 represents the malaria infection rate of humans already infected with COVID-19 and the COVID-19 infection rate of humans already infected with malaria respectively. Therefore, the population of humans is declined when susceptible humans develop COVID-19 infection at the rate (β_c) defined as $\alpha_c(1-\epsilon\vartheta)\left(\frac{I_c + I_{mc} + I_{cEm}}{N_h}\right)$ the population of humans is declined when susceptible humans develop malaria infection at the rate (β_v) defined as $\alpha_v b\left(\frac{I_m + I_{mc} + I_{mEc}}{N_h}\right)$ and the population of mosquitoes is declined when susceptible mosquitoes develop malaria infection at the rate (β_m) defined as $\alpha_m b\left(\frac{I_v}{N_h}\right)$ where ϵ is the fraction of humans employing personal protection, ϑ is the efficacy of personal protection and b is the biting rate of mosquitoes. From the above formulations with assumptions, the movement for human and mosquito moving from one stage to another at different rates can be shown in the flow chart of the co-infection model below. The Flow chart of the co-infection model can be represented by the system of first order ordinary differential equations written below

$$
\begin{aligned}
\dot{S}_h &= \Lambda_h - \alpha_c(1-\epsilon\vartheta)\left(\frac{I_c + I_{mc} + I_{cEm}}{N_h}\right)S_h - \alpha_m b\left(\frac{I_v}{N_h}\right)S_h \\
&\quad - \mu S_h + \upsilon R_h \\
\dot{E}_c &= \alpha_c(1-\epsilon\vartheta)\left(\frac{I_c + I_{mc} + I_{cEm}}{N_h}\right)S_h - \alpha_m b\left(\frac{I_v}{N_h}\right)E_c - (\sigma_c + \mu)E_c \\
\dot{E}_m &= \alpha_m b\left(\frac{I_v}{N_h}\right)S_h - \alpha_c(1-\epsilon\vartheta)\left(\frac{I_c + I_{mc} + I_{cEm}}{N_h}\right)E_m - (\sigma_m + \mu)E_m \\
\dot{E}_{mc} &= \alpha_m b\left(\frac{I_v}{N_h}\right)E_c + \alpha_c(1-\epsilon\vartheta)\left(\frac{I_c + I_{mc} + I_{cEm}}{N_h}\right)E_m - (\sigma_{mc} + \mu)E_{mc} \\
\dot{I}_c &= \sigma_c E_c - \left(\lambda_c + \gamma_1\alpha_m b\left(\frac{I_v}{N_h}\right) + \delta_c + \mu\right)I_c \\
\dot{I}_m &= \sigma_m E_m - \left(\lambda_m + \gamma_2\alpha_c(1-\epsilon\vartheta)\left(\frac{I_c + I_{mc} + I_{cEm}}{N_h}\right) + \delta_m + \mu\right)I_m \\
\dot{I}_{mc} &= \sigma_{mc}E_{mc} + \phi_1 I_{cEm} + \phi_2 I_{mEc} - (\alpha + \delta_{mc} + \mu)I_{mc} \\
\dot{I}_{cEm} &= \gamma_1\alpha_m b\left(\frac{I_v}{N_h}\right)I_c - (\phi_1 + \mu)I_{cEm} \\
\dot{I}_{mEc} &= \gamma_2\alpha_c(1-\epsilon\vartheta)\left(\frac{I_c + I_{mc} + I_{cEm}}{N_h}\right)I_m - (\phi_2 + \mu)I_{mEc} \\
\dot{R}_h &= \lambda_c I_c + \lambda_m I_m + \alpha I_{mc} - (\upsilon + \mu)R_h \\
\dot{S}_v &= \Lambda_v - \alpha_v b\left(\frac{I_m + I_{mc} + I_{mEc}}{N_h}\right)S_v - \eta S_v \\
\dot{E}_v &= \alpha_v b\left(\frac{I_m + I_{mc} + I_{mEc}}{N_h}\right)S_v - \sigma_v E_v - \eta E_v \\
\dot{I}_v &= \sigma_v E_v - \eta I_v
\end{aligned}
\tag{11}
$$

with initial conditions

$$
\begin{aligned}
&S_h(0) \geq 0, E_c(0) \geq 0, E_m(0) \geq 0, E_{mc}(0) \geq 0, I_c(0) \geq 0, \\
&I_m(0) \geq 0, I_{mc}(0) \geq 0, I_{cEm}(0) \geq 0, I_{mEc}(0) \geq 0, R_h(0) \geq 0, \\
&S_v(0) \geq 0, E_v(0) \geq 0, I_v(0) \geq 0
\end{aligned}
\tag{12}
$$

To normalize Eqs. (11) and (12), we obtain

$$
\begin{aligned}
\dot{S}_h &= \Lambda_h - (\beta_c + \beta_m + \mu)S_h + \upsilon R_h \\
\dot{E}_c &= \beta_c S_h - (\beta_m + \sigma_c + \mu)E_c \\
\dot{E}_m &= \beta_m S_h - (\beta_c + \sigma_m + \mu)E_m \\
\dot{E}_{mc} &= \beta_m E_c + \beta_c E_m - (\sigma_{mc} + \mu)E_{mc} \\
\dot{I}_c &= \sigma_c E_c - (\lambda_c + \gamma_1\beta_m + \delta_c + \mu)I_c \\
\dot{I}_m &= \sigma_m E_m - (\lambda_m + \gamma_2\beta_c + \delta_m + \mu)I_m \\
\dot{I}_{mc} &= \sigma_{mc}E_{mc} + \phi_1 I_{cEm} + \phi_2 I_{mEc} - (\alpha + \delta_{mc} + \mu)I_{mc} \\
\dot{I}_{cEm} &= \gamma_1\beta_m I_c - (\phi_1 + \mu)I_{cEm} \\
\dot{I}_{mEc} &= \gamma_2\beta_c I_m - (\phi_2 + \mu)I_{mEc} \\
\dot{R}_h &= \lambda_c I_c + \lambda_m I_m + \alpha I_{mc} - (\upsilon + \mu)R_h \\
\dot{S}_v &= \Lambda_v - \beta_v S_v - \eta S_v \\
\dot{E}_v &= \beta_v S_v - \sigma_v E_v - \eta E_v \\
\dot{I}_v &= \sigma_v E_v - \eta I_v
\end{aligned}
\tag{13}
$$

where $\beta_c = \alpha_c(1-\epsilon\vartheta)(I_c + I_{mc} + I_{cEm})$; $\beta_v = \alpha_v b\left(I_m + I_{mc} + I_{mEc}\right)$; $\beta_m = \alpha_m b I_v$; $\gamma_1, \gamma_2 \geq 0$ with initial conditions

$$
\begin{aligned}
&S_h(0) \geq 0, E_c(0) \geq 0, E_m(0) \geq 0, E_{mc}(0) \geq 0, I_c(0) \geq 0, \\
&I_m(0) \geq 0, I_{mc}(0) \geq 0, I_{cEm}(0) \geq 0, I_{mEc}(0) \geq 0, R_h(0) \geq 0, \\
&S_v(0) \geq 0, E_v(0) \geq 0, I_v(0) \geq 0
\end{aligned}
\tag{14}
$$

Description of the state variables and the parameters used are shown in the Table 1 and Table 2 below respectively (see Fig. 1).

3.1. Fractional order of malaria-COVID-19 co-infection model

By considering the model in (13) with the initial conditions (14). The co-infection model in fractional order form $\alpha \in [0, 1]$ can be written as

$$
\begin{aligned}
{}^{ABC}_{a}D^{\alpha}_{t} S_h &= \Lambda_h - (\beta_c + \beta_m + \mu)S_h + \upsilon R_h \\
{}^{ABC}_{a}D^{\alpha}_{t} E_c &= \beta_c S_h - (\beta_m + \sigma_c + \mu)E_c \\
{}^{ABC}_{a}D^{\alpha}_{t} E_m &= \beta_m S_h - (\beta_c + \sigma_m + \mu)E_m \\
{}^{ABC}_{a}D^{\alpha}_{t} E_{mc} &= \beta_m E_c + \beta_c E_m - (\sigma_{mc} + \mu)E_{mc} \\
{}^{ABC}_{a}D^{\alpha}_{t} I_c &= \sigma_c E_c - (\lambda_c + \gamma_1\beta_m + \delta_c + \mu)I_c \\
{}^{ABC}_{a}D^{\alpha}_{t} I_m &= \sigma_m E_m - (\lambda_m + \gamma_2\beta_c + \delta_m + \mu)I_m \\
{}^{ABC}_{a}D^{\alpha}_{t} I_{mc} &= \sigma_{mc}E_{mc} + \phi_1 I_{cEm} + \phi_2 I_{mEc} - (\alpha + \delta_{mc} + \mu)I_{mc} \\
{}^{ABC}_{a}D^{\alpha}_{t} I_{cEm} &= \gamma_1\beta_m I_c - (\phi_1 + \mu)I_{cEm} \\
{}^{ABC}_{a}D^{\alpha}_{t} I_{mEc} &= \gamma_2\beta_c I_m - (\phi_2 + \mu)I_{mEc} \\
{}^{ABC}_{a}D^{\alpha}_{t} R_h &= \lambda_c I_c + \lambda_m I_m + \alpha I_{mc} - (\upsilon + \mu)R_h \\
{}^{ABC}_{a}D^{\alpha}_{t} S_v &= \Lambda_v - \beta_v S_v - \eta S_v \\
{}^{ABC}_{a}D^{\alpha}_{t} E_v &= \beta_v S_v - \sigma_v E_v - \eta E_v \\
{}^{ABC}_{a}D^{\alpha}_{t} I_v &= \sigma_v E_v - \eta I_v
\end{aligned}
\tag{15}
$$

where ${}^{ABC}_{a}D^{\alpha}_{t}$ shows fractional derivative in ABC sense with initial conditions

$$
\begin{aligned}
&S_h(0) = S_{h0}, E_c(0) = E_{c0}, E_m(0) = E_{m0}, E_{mc}(0) = E_{mc0}, \\
&I_c(0) = I_{c0}, I_m(0) = I_{m0}, I_{mc}(0) = I_{mc0}, I_{cEm}(0) = I_{cEm0}, \\
&I_{mEc}(0) = I_{mEc0}, R_h(0) = R_{h0}, S_v(0) = S_{v0}, \\
&E_v(0) = E_{v0}, I_v(0) = I_{v0}
\end{aligned}
\tag{16}
$$

Table 1
Details definition of variables.

Variable	Description
$S_h(t)$	Number of Susceptible humans at time t
$E_c(t)$	Number of Exposed humans with COVID-19-only at time t
$E_m(t)$	Number of Exposed humans with malaria-only at time t
$E_{mc}(t)$	Number of Exposed humans with malaria and COVID-19 at time t
$I_c(t)$	Number of Infected humans with COVID-19-only at time t
$I_m(t)$	Number of Infected humans with malaria-19-only at time t
$I_{mc}(t)$	Number of co-infection humans with COVID-19 and malaria at time t
$I_{cEm}(t)$	Number of Infected humans with COVID-19 and Exposed to malaria at time t
$I_{mEc}(t)$	Number of Infected humans with malaria and Exposed to COVID-19 at time t
$R_h(t)$	Number of Recovered humans at time t
$S_v(t)$	Number of Susceptible mosquitoes at time t
$E_v(t)$	Number of Exposed mosquitoes at time t
$I_v(t)$	Number of Infected mosquitoes at time t
$N_h(t)$	Total number of humans at time t
$N_v(t)$	Total number of mosquitoes at time t

Table 2
Details definition of parameters.

Parameter	Description
Λ_h	Recruitment rate humans
Λ_v	Recruitment rate mosquitoes
σ_m	Progressive rate of humans from exposed to malaria infectious class
σ_c	Progressive rate of humans from exposed to COVID-19 infectious class
σ_v	Progressive rate of mosquitoes from exposed to infectious class
σ_{mc}	Proportion of humans moving to the co-infection I_{mc} class
λ_c	Recovery rate of humans from infected COVID-19 class to recovered class
λ_m	Recovery rate of humans from infected malaria class to recovered class
υ	Reintegration rate of humans from recovered to susceptible class
α_r	Recovery rate of humans from infected co-infection class to recovered class
α_m	Probability of transmission of malaria per mosquito bite to susceptible humans
α_c	Probability of transmission of COVID-19 per contact
α_v	Probability of transmission of malaria per mosquito bite from infected humans to susceptible mosquitoes
b	Mosquito biting rate
ϵ	Fraction of humans employing personal protection
ϑ	Efficacy of personal protection
ϕ_1	Malaria infection rate of humans already infected with COVID-19
ϕ_2	COVID-19 infection rate of humans already infected with Malaria
δ_c	COVID-19-induced mortality rate of humans
δ_m	Malaria-induced mortality rate of humans
δ_{mc}	Co-infection-induced mortality rate of humans
μ	Natural mortality rate of humans
η	Natural mortality rate of mosquitoes
γ_1	A risk factor for getting COVID-19 after contracting malaria.
γ_2	A risk factor for getting malaria after contracting COVID-19

4. Model analysis

In this section, we first examine the Existence and Uniqueness of Atangana–Baleanu–Caputo (ABC) with time fractional order co-infection model solution. Also, we will consider the sub-models fractional order of malaria only and COVID-19 only. Each of these comprise the study of positivity and boundedness of the solutions, invariant region, condition of existence of equilibrium points and basic reproduction number ($\mathcal{R}_0$) of the model.

4.1. Existence and uniqueness of ABC with time fractional order co-infection model solution

In this subsection, it is important to verify the existence and uniqueness of solution by applying some basic results from fixed point theory to the fractional order ABC derivative of the co-infection model (15) so that it can modify in the following form [57],

$$\begin{cases} {}^{ABC}_{a}\mathcal{D}^{\alpha}_{t}\omega(t) = G(t,\omega(t)), \\ \omega(0) = \omega_0, \quad 0 < t < \mathcal{F} < \infty. \end{cases} \tag{17}$$

where the vector $\omega = (S_h, E_m, E_c, E_{mc}, I_m, I_c, I_{mc}, I_{cEm}, I_{mEc}, R_h, S_v, E_v, I_v)$ denotes state variables corresponding to the co-infection model and G represent a continuous vector function as follows:

$$G = \begin{pmatrix} G_1 \\ G_2 \\ G_3 \\ G_4 \\ G_5 \\ G_6 \\ G_7 \\ G_8 \\ G_9 \\ G_{10} \\ G_{11} \\ G_{12} \\ G_{13} \end{pmatrix} = \begin{pmatrix} \Lambda_h - (\beta_c + \beta_m + \mu)S_h + \upsilon R_h \\ \beta_c S_h - (\beta_m + \sigma_c + \mu)E_c \\ \beta_m S_h - (\beta_c + \sigma_m + \mu)E_m \\ \beta_m E_c + \beta_c E_m - (\sigma_{mc} + \mu)E_{mc} \\ \sigma_c E_c - (\lambda_c + \gamma_1\beta_m + \delta_c + \mu)I_c \\ \sigma_m E_m - (\lambda_m + \gamma_2\beta_c + \delta_m + \mu)I_m \\ \sigma_{mc}E_{mc} + \phi_1 I_{cEm} + \phi_2 I_{mEc} - (\alpha + \delta_{mc} + \mu)I_{mc} \\ \gamma_1\beta_m I_c - (\phi_1 + \mu)I_{cEm} \\ \gamma_2\beta_c I_m - (\phi_2 + \mu)I_{mEc} \\ \lambda_c I_c + \lambda_m I_m + \alpha I_{mc} - (\upsilon + \mu)R_h \\ \Lambda_v - \beta_v S_v - \eta S_v \\ \beta_v S_v - \sigma_v E_v - \eta E_v \\ \sigma_v E_v - \eta I_v \end{pmatrix}$$

whereas

$$\omega_0 = (S_h(0), E_m(0), E_c(0), E_{mc}(0), I_m(0), I_c(0), I_{mc}(0), I_{cEm}(0), I_{mEc}(0), R_h(0), S_v(0), E_v(0), I_v(0)).$$

Furthermore, the function G satisfy the Lipschitz condition which can be written below as

$$\|G(t,\omega_1(t)) - G(t,\omega_2(t))\| \leq H\|\omega_1(t) - \omega_2(t)\|, H > 0. \tag{18}$$

The existence of a unique solution is proven in the following theorems:

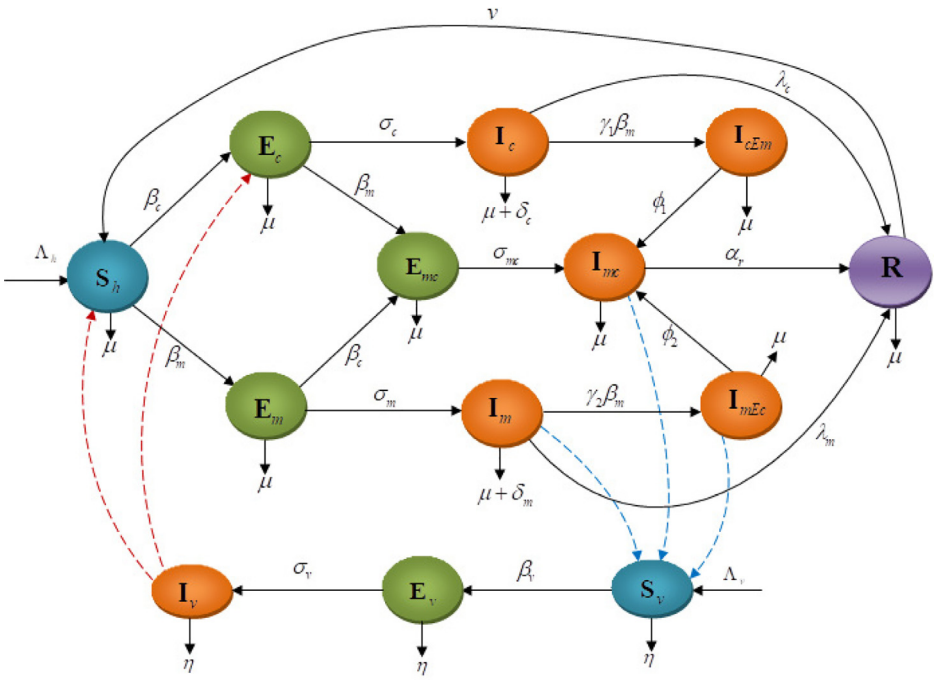

Fig. 1. Flow chart of the co-infection model.

Theorem 4. *There exists a unique solution of the fractional order of co-infection model (17), if the condition shown in Eq. (19) satisfied:*

$$\left(\frac{1-\alpha}{\mathfrak{L}(\alpha)}H+\frac{\alpha H}{\mathfrak{L}(\alpha)\Gamma(\alpha+1)}\mathcal{T}^{\alpha}_{max}\right)<1 \tag{19}$$

Proof. Taking the Atangana–Baleanu–Caputo integral on the both sides of Eq. (19), which provides a non-linear Volterra Integral equation written as follows:

$$\omega(t)=\omega_0+\frac{1-\alpha}{\mathfrak{L}(\alpha)}G(t,\omega(t))+\frac{\alpha}{\mathfrak{L}(\alpha)\Gamma(\alpha)}\int_0^t\omega(\sigma)(t-\omega)^{\alpha-1}d\sigma \tag{20}$$

Let $\mathcal{J}=(0,\mathcal{T})$, and the operator $\mathcal{G}:(\mathcal{J},\mathbb{R}^{13})\to(\mathcal{J},\mathbb{R}^{13})$ be expressed as

$$\mathcal{G}[\omega(t)]=\omega_0+\frac{1-\alpha}{\mathfrak{L}(\alpha)}G(t,\omega(t))+\frac{\alpha}{\mathfrak{L}(\alpha)\Gamma(\alpha)}\int_0^t\omega(\sigma)(t-\omega)^{\alpha-1}d\sigma \tag{21}$$

Thus, Eq. (21) becomes

$$\omega(t)=\mathcal{G}[\omega(t)] \tag{22}$$

Additional, let $\|.\|_{\mathcal{J}}$ represent the supremum norm over $\mathcal{J}$ and define as:

$$\|\omega(t)\|_{\mathcal{J}}=\sup_{t\in\mathcal{J}}\|\omega(t)\|,\ \omega(t)\in C. \tag{23}$$

It is obvious that $C(\mathcal{J},\mathbb{R}^{13})$ with the corresponding norm $\|.\|_{\mathcal{J}}$ is a Banach space. In addition, the inequality expressed as follows:

$$\left\|\int_0^t\mathcal{W}(t,x)\omega(t)dx\right\|\le\mathcal{T}\|\mathcal{W}(t,x)\|_{\mathcal{J}}\|\omega(t)\|_{\mathcal{J}}, \tag{24}$$

with $\omega(t)\in C(\mathcal{J},\mathbb{R}^{13})$, $\mathcal{W}(t,x)\in C(\mathcal{J}^2,\mathbb{R})$ that is,

$$\|\mathcal{W}(t,x)\|_{\mathcal{J}}=\sup_{t,x\in\mathcal{J}}|\mathcal{W}(t,x)|.$$

Using Eq. (22) as well as Eqs. (18) and (24), we can say that

$$\begin{aligned}
&\|G\left[\omega_1(t)\right]-G\left[\omega_2(t)\right]\|_{\mathcal{J}}\\
&\le\|\frac{(1-\alpha)}{\mathfrak{L}(\alpha)}\left(G(t,\omega_1(t))-G(t,\omega_2(t))\right)+\frac{\alpha}{\mathfrak{L}(\alpha)\Gamma(\alpha)}\times\\
&\int_0^t(t-x)^{\alpha-1}\left(G(x,\omega_1(x))-G(x,\omega_2(x))\right)dx\|_{\mathcal{J}},\\
&\le\frac{(1-\alpha)\mathtt{D}}{\mathfrak{L}(\alpha)}\|\omega_1(t)-\omega_2(t)\|_{\mathcal{J}}+\frac{\alpha\mathtt{D}}{\mathfrak{L}(\alpha)\Gamma(\alpha)}\times\\
&\int_0^t(t-x)^{\alpha-1}\left\|\omega_1(x)-\omega_2(x)dx\right\|_{\mathcal{J}},\\
&\le\frac{(1-\alpha)\mathtt{D}}{\mathfrak{L}(\alpha)}\sup_{\omega\in\mathcal{J}}\|\omega_1(t)-\omega_2(t)\|+\frac{\alpha\mathtt{D}}{\mathfrak{L}(\alpha)\Gamma(\alpha)}\times\\
&\left(\int_0^t(t-x)^{\alpha-1}\right)dx\sup_{\omega\in\mathcal{J}}\left\|\omega_1(x)-\omega_2(x)\right\|\\
&\le\left(\frac{(1-\alpha)\mathtt{D}}{\mathfrak{L}(\alpha)}+\frac{\alpha\mathtt{D}}{\mathfrak{L}(\alpha)\Gamma(\alpha+1)}\mathcal{T}^{\alpha}_{\max}\right)\|\omega_1(t)-\omega_2(t)\|_{\mathcal{J}}
\end{aligned} \tag{25}$$

In conclusion, Eq. (25) can be written as follows:

$$\|G(t,\omega_1(t))-G(t,\omega_2(t))\|\le H\|\omega_1(t)-\omega_2(t)\|,. \tag{26}$$

where, $H=\frac{(1-\alpha)\mathtt{D}}{\mathfrak{L}(\alpha)}+\frac{\alpha\mathtt{D}}{\mathfrak{L}(\alpha)\Gamma(\alpha+1)}\mathcal{T}^{\alpha}_{\max}$.

If condition given in (19) satisfies then the operator G becomes a contradiction. Thus, the operator G has a unique fixed point in (17) which is a solution subject to the initial value problem in (17) and for this reason it is a solution to the fractional order ABC derivative of the co-infection model (15). □

4.2. Fractional order of malaria-only model

To obtain fractional order of malaria model only, we set $E_c(t)=E_{mc}(t)=I_c(t)=I_{mc}(t)=I_{cEm}(t)=I_{mEc}(t)=0$ and substitute into model (15), thus,

$$\begin{aligned}
{}^{ABC}_{a}D^{\alpha}_{t}S_h&=\Lambda_h-(\beta_m+\mu)S_h+\upsilon R_h\\
{}^{ABC}_{a}D^{\alpha}_{t}E_m&=\beta_m S_h-(\sigma_m+\mu)E_m\\
{}^{ABC}_{a}D^{\alpha}_{t}I_m&=\sigma_m E_m-(\lambda_m+\delta_m+\mu)I_m\\
{}^{ABC}_{a}D^{\alpha}_{t}R_h&=\lambda_m I_m-(\upsilon+\mu)R_h\\
{}^{ABC}_{a}D^{\alpha}_{t}S_{\mathrm{v}}&=\Lambda_{\mathrm{v}}-\beta_{\mathrm{v}}S_{\mathrm{v}}-\eta S_{\mathrm{v}}\\
{}^{ABC}_{a}D^{\alpha}_{t}E_{\mathrm{v}}&=\beta_{\mathrm{v}}S_{\mathrm{v}}-\sigma_{\mathrm{v}}E_{\mathrm{v}}-\eta E_{\mathrm{v}}\\
{}^{ABC}_{a}D^{\alpha}_{t}I_{\mathrm{v}}&=\sigma_{\mathrm{v}}E_{\mathrm{v}}-\eta I_{\mathrm{v}}
\end{aligned} \tag{27}$$

where $\beta_{\mathrm{v}}=\alpha_{\mathrm{v}}bI_m$; $\beta_m=\alpha_m bI_{\mathrm{v}}$ and ${}^{ABC}_{a}D^{\alpha}_{t}$ shows fractional derivative in ABC sense with initial conditions

$$\begin{aligned}
S_h(0)=S_{h0},E_m(0)=E_{m0},I_m(0)=I_{m0},R_h(0)=R_{h0},\\
S_{\mathrm{v}}(0)=S_{\mathrm{v}0},E_{\mathrm{v}}=E_{\mathrm{v}0},I_{\mathrm{v}}(0)=I_{\mathrm{v}0}(t),
\end{aligned} \tag{28}$$

4.2.1. Non-negativity of the solution for malaria-only

For the fractional order of malaria model only in (27) subject to initial conditions be biologically meaningful and positively invariant in the region Ω_m, we state the theorem below,

Theorem 5. *The region* $\Omega_m = \{(S_h, E_m, I_m, R_h, S_v, E_v, I_v) \in \mathbb{R}^7_+ : N_{hm} \leq \frac{\Lambda_h}{\mu}.\frac{\Lambda_v}{\eta}\}$ *is positively invariant for the fractional order of malaria only model in (27) subject to non-negative initial conditions* $\mathbb{R}^7_+$ *in (28).*

Proof. Let N_{hm} represent the total population of humans for malaria-only and N_v represent the total population of mosquitoes. Since $N_{hm} = S_h+E_m+I_m+R_h$ and $N_v = S_v+E_v+I_v$, applying fractional derivative on both sides of the total population of humans and the total population of mosquitoes respectively and substituting Eq. (27) into them, we obtain ${}^{ABC}_{a}D^{\alpha}_{t} N_{hm} = \Lambda_h - \mu(S_h + E_m + I_m + R_h) - \delta_m I_m$ and ${}^{ABC}_{a}D^{\alpha}_{t} N_v = \Lambda_v - \eta(S_v + E_v + I_v)$ which can be re-written respectively as

$$ {}^{ABC}_{a}D^{\alpha}_{t} N_{hm} \leq \Lambda_h - \mu N_{hm} \tag{29} $$

$$ {}^{ABC}_{a}D^{\alpha}_{t} N_v \leq \Lambda_v - \eta N_v \tag{30} $$

Applying the Laplace transform on both Eqs. (29) and (30), and the inverse Laplace expressed as Mittag-Leffler function and taking the limit as $t \to \infty$ the Eqs. (29) and (30) can be written respectively as $N_{hm} \leq \frac{\Lambda_h}{\mu}$ and $N_v \leq \frac{\Lambda_v}{\eta}$. For this reason, the fractional order of malaria-only model in Eq. (27) has the solution in Ω_m. Therefore, the feasible region for the malaria-only model in Eq. (27) is

$$ \Omega_m = \left\{ (S_h, E_m, I_m, R_h, S_v, E_v, I_v) \in \mathbb{R}^7_+ : N_{hm}(t) \leq \frac{\Lambda_h}{\mu}.N_v \leq \frac{\Lambda_v}{\eta} \right\} $$

which is positively invariant. □

4.2.2. Existence of the malaria-only-free equilibrium

The disease-free equilibrium of the fractional ABC for the malaria-only in model (27) can be obtained by setting the right hand side of the model (27) as well as $E_m = I_m = R_h = E_v = I_v = 0$ and we obtain

$$ \mathbf{E}_{0m} = (S_h, E_m, I_m, R_h, S_v, E_v, I_v) = \left(\frac{\Lambda_h}{\mu}, 0, 0, 0, \frac{\Lambda_v}{\eta}, 0, 0\right) \tag{31} $$

4.2.3. Basic reproduction number of malaria-only ($\mathcal{R}_{0m}$) model

We derive the basic reproduction number of malaria-only ($\mathcal{R}_{0m}$) from malaria-only-free equilibrium (MFE) using next generation matrix method [58]. Also, the transfer rate of humans infection $\mathcal{F}(X)$ to the compartments $\mathcal{V}(X)$ is given by

$$ \mathcal{F}(X) = \begin{pmatrix} b\alpha_m I_v S_h \\ 0 \\ b\alpha_v I_m S_v \\ 0 \end{pmatrix} $$

and

$$ \mathcal{V}(X) = \begin{pmatrix} (\sigma_m + \mu)E_m \\ (\lambda_m + \delta_m + \mu)I_m - \sigma_m E_m \\ (\sigma_v + \eta)E_v \\ \eta I_v - \sigma_v \end{pmatrix} $$

Therefore, if $\mathbf{F}(X)$ is the new infection and $\mathbf{V}(X)$ is the residual transfer then $\mathcal{F}(X)$ and $\mathcal{V}(X)$ can be written by using Jacobian Matrix respectively as

$$ \mathbf{F} = \begin{pmatrix} 0 & 0 & 0 & \frac{b\alpha_m \Lambda_h}{\mu} \\ 0 & 0 & 0 & 0 \\ 0 & \frac{b\alpha_v \Lambda_v}{\eta} & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix} \tag{32} $$

and

$$ \mathbf{V} = \begin{pmatrix} (\sigma_m + \mu) & 0 & 0 & 0 \\ -\sigma_m & (\lambda_m + \delta_m + \mu) & 0 & 0 \\ 0 & 0 & (\sigma_v + \eta) & 0 \\ 0 & 0 & -\sigma_v & \eta \end{pmatrix} \tag{33} $$

According to [58], since the matrix of $\mathbf{F}$ and the inverse matrix of $\mathbf{V}$ (that is $\mathbf{V}^{-1}$) are non-negative as well as the matrix $\mathbf{FV}^{-1}$ which is the next generation matrix is non-negative. Therefore, the basic reproduction number $\mathcal{R}_0$ is the dominant or largest eigenvalue corresponding to the Spectral radius of matrix $\mathbf{FV}^{-1}$. Mathematically, it can be written as $\mathcal{R}_0 = \rho(\mathbf{FV}^{-1})$ where ρ is the Spectral radius. Thus;

$$ \mathcal{R}_{0m} = \sqrt{\frac{b^2 \alpha_v \Lambda_v \sigma_m \alpha_m \Lambda_h \sigma_v}{\eta^2 (\sigma_m + \mu)(\lambda_m + \delta_m + \mu)\mu (\sigma_v + \eta)}} \tag{34} $$

4.2.4. Existence of endemic equilibrium for malaria-only

The endemic equilibrium of the fractional ABC for the malaria-only in model (27) can be obtained by setting the right hand side of the model (27) to be zero and putting $S_h = S^*_h$, $E_m = E^*_m$, $I_m = I^*_m$, $R_h = R^*_h$, $S_v = S^*_v$, $E_v = E^*_v$, $I_v = I^*_v$ and we obtain

$$ \mathbf{E}_{1m} = (S_h, E_m, I_m, R_h, S_v, E_v, I_v) = (S^*_h, E^*_m, I^*_m, R^*_h, S^*_v, E^*_v, I^*_v) \tag{35} $$

by simplification, Eq. (35) can be written as

$$ \begin{aligned} S^*_h &= \frac{\upsilon R^*_h + \Lambda_h}{\alpha_m b I^*_v + \mu} \qquad E^*_m = \frac{\alpha_m b I^*_v S^*_h}{\sigma_m + \mu} \qquad I^*_m = \frac{\sigma_m E^*_m}{\lambda_m + \delta_m + \mu} \\ R^*_h &= \frac{\lambda_m I^*_m}{\upsilon + \mu} \qquad S^*_v = \frac{\Lambda_v}{\alpha_v b I^*_m + \eta} \qquad E^*_v = \frac{\alpha_v b I^*_m S^*_v}{\sigma_v + \eta} \qquad I^*_v = \frac{E^*_v \sigma_v}{\eta} \end{aligned} \tag{36} $$

The Eq. (36) can be simplified further as

$$ \begin{aligned} S^*_h &= \frac{\eta\, k_1\, k_2\, k_4 \left(b k_3 \Lambda_h \alpha_v \sigma_m + \eta\, k_1\, k_2\, k_3\, \mu - \eta\, \upsilon\, \lambda_m \sigma_m\right)}{k_5 \sigma_m} \\ E^*_m &= \frac{k_2\, k_3 \left(b^2 \Lambda_h \Lambda_v \alpha_m \alpha_v \sigma_m \sigma_v - \eta^2 k_2\, k_4\, \mu^2 - \eta^2 k_2\, k_4\, \mu\, \sigma_m\right)}{k_5 \sigma_m} \\ I^*_m &= \frac{k_3 \left(b^2 \Lambda_h \Lambda_v \alpha_m \alpha_v \sigma_m \sigma_v - \eta^2 k_2\, k_4\, \mu^2 - \eta^2 k_2\, k_4\, \mu\, \sigma_m\right)}{k_5} \\ R^*_h &= \frac{\left(b^2 \Lambda_h \Lambda_v \alpha_m \alpha_v \sigma_m \sigma_v - \eta^2 k_2\, k_4\, \mu^2 - \eta^2 k_2\, k_4\, \mu\, \sigma_m\right) \lambda_m}{k_5} \\ S^*_v &= \frac{k_1\, k_2\, k_3 \left(b\, \Lambda_v \alpha_m \sigma_v + \eta\, k_4\, \mu\right) - b\, \Lambda_v \alpha_m \sigma_v \upsilon\, \lambda_m \sigma_m}{b \alpha_m \sigma_v k_6} \\ E^*_v &= \frac{k_3 \left(b^2 \Lambda_h \Lambda_v \alpha_m \alpha_v \sigma_m \sigma_v - \eta^2 k_2\, k_4\, \mu^2 - \eta^2 k_2\, k_4\, \mu\, \sigma_m\right)}{\sigma_v k_4 k_6} \\ I^*_v &= \frac{k_3 \left(b^2 \Lambda_h \Lambda_v \alpha_m \alpha_v \sigma_m \sigma_v - \eta^2 k_2\, k_4\, \mu^2 - \eta^2 k_2\, k_4\, \mu\, \sigma_m\right)}{k_4\, k_6\, \eta} \end{aligned} \tag{37} $$

where $k_1 = (\sigma_m + \mu), k_2 = (\lambda_m + \delta_m + \mu), k_3 = (\upsilon + \mu), k_4 = (\sigma_v + \eta)$,

$$ \begin{aligned} k_5 = b\alpha_v (&b k_2\, k_3\, \mu\, \Lambda_v \alpha_m \sigma_v + b k_2\, k_3\, \Lambda_v \alpha_m \sigma_m \sigma_v - b\upsilon\, \Lambda_v \alpha_m \lambda_m \sigma_m \sigma_v \\ &+ \eta\, k_2\, k_3\, k_4\, \mu^2 + \eta\, k_2\, k_3\, k_4\, \mu\, \sigma_m) \end{aligned} $$

$$ k_6 = b\alpha_m \left(b k_3\, \Lambda_h \alpha_v \sigma_m + \eta\, k_2\, k_3\, \mu + \eta\, k_2\, k_3\, \sigma_m - \eta\, \upsilon\, \lambda_m \sigma_m\right) $$

4.2.5. Global stability of Malaria-only-Free Equilibrium (MFE)

Theorem 6. *If* $\mathcal{R}_{0m} \leq 1$ *then the malaria-only-free equilibrium* (E_{0m}) *given by Eq. (31) is globally asymptotically stable. Otherwise, it is unstable.*

Proof. Using the Lyapunov function of the type [57,59,60],

$$ \mathfrak{M} = a_{1m} E_m + a_{2m} I_m + a_{3m} E_v + a_{4m} I_v $$

where $a_{1m} = \frac{\sigma_m}{(\sigma_m + \mu)(\lambda_m + \delta_m + \mu)}$, $a_{2m} = \frac{1}{(\lambda_m + \delta_m + \mu)}$, $a_{3m} = \frac{\eta \mathcal{R}_{0m}}{\alpha_m b \Lambda_v}$ and $a_{4m} = \frac{\eta(\sigma_v + \eta)\mathcal{R}_{0m}}{\alpha_v b \sigma_v \Lambda_v}$. Thus, a_{1m}, a_{2m}, a_{3m} and a_{4m} are all positive. Therefore, the fractional order derivative of $\mathfrak{M}$ can be written as

$$ \begin{aligned} {}^{ABC}_{a}D^{\alpha}_{t}\mathfrak{M} = &a_{1m} \left({}^{ABC}_{a}D^{\alpha}_{t} E_m\right) + a_{2m} \left({}^{ABC}_{a}D^{\alpha}_{t} I_m\right) + a_{3m} \left({}^{ABC}_{a}D^{\alpha}_{t} E_v\right) \\ &+ a_{4m} \left({}^{ABC}_{a}D^{\alpha}_{t} I_v\right) \end{aligned} \tag{38} $$

By substituting Eq. (27) into Eq. (38) and simplifying to obtain

$$\begin{aligned}{}_{a}^{ABC}D_t^{\alpha}\mathfrak{M} &= \frac{b\sigma_m\alpha_m\Lambda_h I_v}{(\sigma_m+\mu)(\lambda_m+\delta_m+\mu)} - \frac{\eta(\sigma_v+\eta)\mathcal{R}_{0m}I_v}{b\alpha_v\Lambda_v\sigma_v} \\ &\quad + \mathcal{R}_{0m}I_m - I_m \\ &\le \left(\frac{b\sigma_m\alpha_m\Lambda_h}{\mu(\sigma_m+\mu)(\lambda_m+\delta_m+\mu)} - \frac{\eta(\sigma_v+\eta)\mathcal{R}_{0m}}{b\alpha_v\Lambda_v\sigma_v}\right) I_v \\ &\quad + \left(\mathcal{R}_{0m}-1\right) I_m \\ &= \left[\left(\sqrt{\frac{\eta^2\Lambda_h\sigma_m\alpha_m}{\Lambda_v\sigma_v\alpha_v\mu(\sigma_m+\mu)(\lambda_m+\delta_m+\mu)}}\right) I_v + I_m\right]\left(\mathcal{R}_{0m}-1\right)\end{aligned} \tag{39}$$

From the above result, ${}_{a}^{ABC}D_t^{\alpha}\mathfrak{M} \le 0$ on condition that $\mathcal{R}_{0m} \le 1$ in addition to ${}_{a}^{ABC}D_t^{\alpha}\mathfrak{M} = 0$ on condition that $\mathcal{R}_{0m} = 1$ or $I_m = 0$ and $I_v = 0$. It shows that the highest invariance set in

$$\left\{\left(S_h, E_m, I_m, R_h, S_v, E_v, I_v\right) \in \mathbb{R}_+^7 : {}_{a}^{ABC}D_t^{\alpha}\mathfrak{M} = 0\right\}$$

which is the singleton MFE (E_{0m}) and by LaSalle's invariance principle according to [61], MFE (E_{0m}) is globally asymptotically stable in $\mathbb{R}_+^7$. The proof of Theorem 6 shows that, malaria would become extinct in the neighbourhood whenever $\mathcal{R}_{0m} \le 1$ regardless of the number of humans in model (27) at initial stage of the population. □

4.3. Global stability of endemic equilibrium for malaria only

Theorem 7. *If $\mathcal{R}_{0m} > 1$ then model (27) has a unique endemic equilibrium (E_{1m}) whenever $\mathcal{R}_{0m} > 1$ and no endemic equilibrium otherwise.*

Proof. If the existence of endemic equilibrium point for malaria-only in Eq. (35) form Eq. (36) as well as (44) then by substituting I_v^* in Eq. (44) into the force infection of humans for malaria-only $\left(\beta_m^* = b\alpha_m I_v^*\right)$ becomes

$$\mathcal{A}_m\beta_m^* + \mathcal{B}_m = 0 \tag{40}$$

where $\mathcal{A}_m = \eta\upsilon\lambda_m\sigma_m - k_3\Lambda_h\alpha_v\alpha_m - \eta k_1k_2k_3$ and $\mathcal{B}_m = \eta k_1k_2k_3\mu\left(\mathcal{R}_{0m}^2 - 1\right)$. Hence, Eq. (40) can be defined as $\beta_m^* = -\dfrac{\mathcal{B}_m}{\mathcal{A}_m} \le 0$ if $\mathcal{B}_m \ge 0$ at $\mathcal{R}_{0m} \le 1$, and endemic equilibrium does not exist. Moreover, $\beta_m^* = \dfrac{\mathcal{B}_m}{\mathcal{A}_m} > 0$ if $\mathcal{B}_m < 0$ at $\mathcal{R}_{0m} > 1$. Thus, ∃ the endemic equilibrium only at $\mathcal{R}_{0m} > 1$. This shows that model (27) has a unique endemic which is non-negative equilibrium whenever $\mathcal{R}_{0m} > 1$. □

Theorem 8. *If $\mathcal{R}_{0m} > 1$, then the endemic equilibrium of model (35) given by $E_{1m} = (S_h^*, E_m^*, I_m^*, R_h^*, S_v^*, E_v^*, I_v^*)$ is globally asymptotically stable in the interior of the region $\mathbb{R}_+^7$.*

Proof. Following the approach of [60,62,63], the equation below consists of the following Goh-Volterra type Lyapunov function:

$$\begin{aligned}\mathfrak{A}_m &= S_h - S_h^* - S_h^*\ln\frac{S_h}{S_h^*} + E_m - E_m^* - E_m^*\ln\frac{E_m}{E_m^*} \\ &\quad + d_{m1}(I_m - I_m^* - I_m^*\ln\frac{I_m}{I_m^*}) + d_{m2}(S_v - S_v^* - S_v^*\ln\frac{S_v}{S_v^*}) \\ &\quad + d_{m3}(E_v - E_v^* - E_v^*\ln\frac{E_v}{E_v^*}) + d_{m4}(I_v - I_v^* - I_v^*\ln\frac{I_v}{I_v^*})\end{aligned} \tag{41}$$

where $d_{m1} = \dfrac{\alpha_m S_h^* I_v^*}{\sigma_m E_m^*}$, $d_{m2} = \dfrac{\alpha_m S_h^* I_v^*}{\alpha_v S_m^* I_m^*}$, $d_{m3} = \dfrac{\alpha_m S_h^* I_v^*}{\alpha_v S_m^* I_m^*}$ and $d_{m4} = \dfrac{\alpha_m S_h^* I_v^*}{\sigma_v E_v^*}$. Applying fractional order derivative with time on Eq. (41), we have

$$\begin{aligned}{}_{a}^{ABC}D_t^{\alpha}\mathfrak{A}_m &= \left(1 - \frac{S_h^*}{S_h}\right){}_{a}^{ABC}D_t^{\alpha}S_h + \left(1 - \frac{E_m^*}{E_m}\right){}_{a}^{ABC}D_t^{\alpha}E_m \\ &\quad + d_{m1}\left(1 - \frac{I_m^*}{I_m}\right){}_{a}^{ABC}D_t^{\alpha}I_m + d_{m2}\left(1 - \frac{S_v^*}{S_v}\right){}_{a}^{ABC}D_t^{\alpha}S_v \\ &\quad + d_{m3}\left(1 - \frac{E_v^*}{E_v}\right){}_{a}^{ABC}D_t^{\alpha}E_v + d_{m4}\left(1 - \frac{I_v^*}{I_v}\right){}_{a}^{ABC}D_t^{\alpha}I_v\end{aligned} \tag{42}$$

If $R_h \to R_h^*$ as $t \to \infty$ in Eq. (35) then at a steady-state, the equilibrium relation satisfies

$$\begin{aligned}&\Lambda_h = \alpha_m b S_h^* I_v^* + \mu S_h^*;\ (\sigma_m+\mu) = \frac{\alpha_m b S_h^* I_v^*}{E_m^*};\ \Lambda_v = \alpha_v b S_v^* I_m^* + \eta S_v^*; \\ &(\lambda_m+\delta_m+\mu) = \frac{\sigma_m E_m^*}{I_m^*};\quad (\sigma_v+\eta) = \frac{\alpha_v b I_m^* S_v^*}{E_v^*};\quad \eta = \frac{E_v^*\sigma_v}{I_v^*}.\end{aligned} \tag{43}$$

Substituting Eq. (43) into model (27) simplifying eq. model (41), we obtain

$${}_{a}^{ABC}D_t^{\alpha}\mathfrak{A}_m = \mu S_h^*\left(2 - \frac{S_h^*}{S_h} - \frac{S_h}{S_h^*}\right) + \frac{\alpha_m\eta S_h^* I_v^*}{\alpha_v I_m^*}\left(2 - \frac{S_v^*}{S_v} - \frac{S_v}{S_v^*}\right) + \alpha_m b S_h^* I_v^* \left(6 - \frac{S_h^*}{S_h} - \frac{E_m I_m^*}{E_m^* I_m} - \frac{S_h E_m^* I_v}{S_h^* E_m I_v^*} - \frac{S_v^*}{S_v} - \frac{E_v I_v^*}{E_v^* I_v} - \frac{S_v E_v^* I_m}{S_v^* E_v I_m^*}\right) \le 0$$

Finally, since geometric mean is less than arithmetic mean, then the following inequalities holds:

$$\begin{aligned}&2 - \frac{S_h^*}{S_h} - \frac{S_h}{S_h^*} \le 0,\quad 2 - \frac{S_v^*}{S_v} - \frac{S_v}{S_v^*} \le 0; \\ &\left(6 - \frac{S_h^*}{S_h} - \frac{E_m I_m^*}{E_m^* I_m} - \frac{S_h E_m^* I_v}{S_h^* E_m I_v^*} - \frac{S_v^*}{S_v} - \frac{E_v I_v^*}{E_v^* I_v} - \frac{S_v E_v^* I_m}{S_v^* E_v I_m^*}\right) \le 0\end{aligned}$$ □

Appropriately, ${}_{a}^{ABC}D_t^{\alpha}\mathfrak{A}_m \le 0$ for $\mathcal{R}_{0m} > 1$. In view of the fact that all the parameters are positive with ${}_{a}^{ABC}D_t^{\alpha}\mathfrak{A}_m = 0$ provided that $S_h = S_h^*$, $E_m = E_m^*$, $I_m = I_m^*$, $S_v = S_v^*$, $E_v = E_v^*$ and $I_v = I_v^*$. Since, it has been said that $R_h \to R_h^*$ as time, $t \to \infty$ and by LaSalle's invariance principle [61] then the endemic equilibrium E_{1m} is globally asymptotically stable whenever $\mathcal{R}_{0m} > 1$. Epidemiologically, Theorem 8 means that malaria would establish itself in the neighbourhood whenever $\mathcal{R}_{0m} > 1$ irrespective of the number of infectious humans at initial stage of the population.

4.4. Fractional order of COVID-19 only model

To obtain fractional order of COVID-19 model, we substitute $E_m(t) = E_{mc}(t) = I_m(t) = I_{mc}(t) = I_{cEm}(t) = I_{mEc}(t) = S_v(t) = E_v(t) = I_v(t) = 0$ into model (15)

$$\begin{aligned}{}_{a}^{ABC}D_t^{\alpha}S_h &= \Lambda_h - (\beta_C+\mu)S_h + \upsilon R_h \\ {}_{a}^{ABC}D_t^{\alpha}E_c &= \beta_c S_h - (\sigma_c+\mu)E_c \\ {}_{a}^{ABC}D_t^{\alpha}I_c &= \sigma_c E_c - (\lambda_c+\delta_c+\mu)I_c \\ {}_{a}^{ABC}D_t^{\alpha}R_h &= \lambda_c I_c - (\upsilon+\mu)R_h,\end{aligned} \tag{44}$$

where $\beta_c = \alpha_c(1-\epsilon\vartheta)I_c$ and ${}_{a}^{ABC}D_t^{\alpha}$ shows fractional derivative in ABC sense with initial conditions

$$S_h(0) = S_{h0}, E_c(0) = E_{c0}, I_c(0) = I_{c0}, R_h(0) = R_{h0}. \tag{45}$$

4.4.1. Non-negativity of the solution for COVID-19 model

To make the fractional order of COVID-19 only model in (44) subject to initial conditions be meaningful mathematically, biologically, epidemiologically and positively invariant in the region Ω_m.

Theorem 9. *The region $\Omega_m = \{(S_h, E_c, I_c, R_h) \in \mathbb{R}_+^4 : N_{hc} \le \dfrac{\Lambda_h}{\mu}\}$ is positively invariant for the fractional order of COVID-19 only model in (44) subject to non-negative initial conditions $\mathbb{R}_+^4$ in (45).*

Proof. Let N_{hc} represent the total population of humans for COVID-19 only. Since $N_{hc} = S_h + E_c + I_c + R_h$, using ABC fractional derivative on the total population of humans for COVID-19 only and substituting Eq. (44) into it, we have, ${}_{a}^{ABC}D_t^{\alpha}N_{hc} = \Lambda_h - \mu(S_h + E_c + I_c + R_h) - \delta_c I_c$ which is given by

$${}_{a}^{ABC}D_t^{\alpha}N_{hc} \le \Lambda_h - \mu N_{hc}. \tag{46}$$

By applying Laplace transform in Eq. (46), and the inverse Laplace expressed as Mittag-Leffler function, we deduce that taking the limit as $t \to \infty$ the Eq. (46) is given as $N_{hc} \le \dfrac{\Lambda_h}{\mu}$ and $N_v \le \dfrac{\Lambda_v}{\eta}$, therefore, the

fractional order of COVID-19 only model in Eq. (44) has the solution in Ω_c. Therefore, the feasible region of COVID-19 only model in Eq. (44) is

$\Omega_c = \left\{(S_h, E_c, I_c, R_h) \in \mathbb{R}^4_+ : N_{hc}(t) \leq \frac{\Lambda_h}{\mu}\right\}$ which is positively invariant. □

4.4.2. Existence of COVID-19 only-free equilibrium

The disease-free equilibrium of the fractional ABC for the COVID-19 model in (44) can be obtain by setting the right hand side of the model (44) as well as $E_c = I_c = R_h = 0$ and we obtain

$$\mathbf{E}_{0c} = (S_h, E_c, I_c, R_h) = \left(\frac{\Lambda_h}{\mu}, 0, 0, 0\right) \tag{47}$$

4.4.3. Basic reproduction number of COVID-19-only ($\mathcal{R}_{0c}$) model

We derive the basic reproduction number of COVID-19 model ($\mathcal{R}_{0c}$) from the COVID-19 Free Equilibrium (CFE) using next generation matrix method [58]. The transfer rate of humans infection $\mathcal{F}(X)$ to the compartments $\mathcal{V}(X)$ is given by

$$\mathcal{F}(X) = \begin{pmatrix} \alpha_c(1-\epsilon\vartheta)I_c S_h \\ 0 \end{pmatrix};$$

$$\mathcal{V}(X) = \begin{pmatrix} (\sigma_c+\mu)E_c \\ (\lambda_c+\delta_c+\mu)I_c - \sigma_c E_c \end{pmatrix}$$

Therefore, if $\mathbf{F}(X)$ is the new infection and $\mathbf{V}(X)$ is the residual transfer, then, $\mathcal{F}(X)$ and $\mathcal{V}(X)$ can be written by using Jacobian Matrix respectively as

$$\mathbf{F} = \begin{pmatrix} 0 & \alpha_c(1-\epsilon\vartheta) \\ 0 & 0 \end{pmatrix}; \tag{48}$$

$$\mathbf{V} = \begin{pmatrix} (\sigma_c+\mu) & 0 \\ -\sigma_c & (\lambda_c+\delta_c+\mu) \end{pmatrix} \tag{49}$$

According to [58], since the matrix of $\mathbf{F}$ and the inverse matrix of $\mathbf{V}$ that is, $\mathbf{V}^{-1}$ are non-negative as well as the matrix $\mathbf{FV}^{-1}$ which is the next generation matrix is non-negative, therefore, the basic reproduction number $\mathcal{R}_0$ is the dominant or largest eigenvalue corresponding to the Spectral radius of matrix $\mathbf{FV}^{-1}$. This can be written as $\mathcal{R}_0 = \rho(\mathbf{FV}^{-1})$ where ρ is the Spectral radius. Thus;

$$\mathcal{R}_{0c} = \frac{\Lambda_h \alpha_c \sigma_c (1-\epsilon\vartheta)}{\mu(\sigma_c+\mu)(\lambda_c+\delta_c+\mu)} \tag{50}$$

4.4.4. Existence of endemic equilibrium for COVID-19-only

The endemic equilibrium of the fractional*ABC* for the COVID-19-only in model (44) can be obtained by setting the right hand side of the model (44) to be zero and substituting $S_h = S_h^*$, $E_c = E_c^*$, $I_c = I_c^*$, $R_h = R_h^*$. Thus,

$$\mathbf{E}_{1c} = (S_h, E_c, I_c, R_h) = (S_h^*, E_c^*, I_c^*, R_h^*), \tag{51}$$

by simplification, Eq. (51) can be written as

$$\begin{aligned} S_h^* &= \frac{\upsilon R_h^* + \Lambda_h}{\alpha_c(1-\epsilon\vartheta)I_c^* + \mu} \qquad E_c^* = \frac{\alpha_c(1-\epsilon\vartheta)I_c^* S_h^*}{\sigma_c+\mu} \\ I_c^* &= \frac{\sigma_c E_c^*}{\lambda_c+\delta_c+\mu} \qquad R_h^* = \frac{\lambda_c I_c^*}{\upsilon+\mu}. \end{aligned} \tag{52}$$

Also, Eq. (52) can be simplified further as,

$$\begin{aligned} S_h^* &= \frac{b_1 b_2}{b_3\alpha_c\sigma_c} = \frac{\Lambda_h}{\mu}\frac{1}{\mathcal{R}_{0c}} \\ E_c^* &= \frac{b_2 k_3 (b_3\Lambda_h\alpha_c\sigma_c - b_1 b_2\mu)}{b_3\alpha_c\sigma_c(b_1 b_2 k_3 - \upsilon\lambda_c\sigma_c)} = \frac{b_2 k_3\Lambda_h}{b_4}\frac{(\mathcal{R}_{0c}-1)}{\mathcal{R}_{0c}} \\ I_c^* &= \frac{k_3(b_3\Lambda_h\alpha_c\sigma_c - b_1 b_2\mu)}{b_3\alpha_c(b_1 b_2 k_3 - \upsilon\lambda_c\sigma_c)} = \frac{k_3\Lambda_h\sigma_c}{b_4}\frac{(\mathcal{R}_{0c}-1)}{\mathcal{R}_{0c}} \\ R_h^* &= \frac{\lambda_c(b_3\Lambda_h\alpha_c\sigma_c - b_1 b_2\mu)}{b_3\alpha_c(b_1 b_2 k_3 - \upsilon\lambda_c\sigma_c)} = \frac{\Lambda_h\sigma_c\lambda_c}{b_4}\frac{(\mathcal{R}_{0c}-1)}{\mathcal{R}_{0c}}, \end{aligned} \tag{53}$$

where $b_1 = (\sigma_c+\mu), b_2 = (\lambda_c+\delta_c+\mu), b_3 = (1-\epsilon\vartheta), b_4 = (b_1 b_2 k_3 - \upsilon\lambda_c\sigma_c)$ and recall that $k_3 = (\upsilon+\mu)$

4.4.5. Global stability of the COVID-19 free equilibrium (CFE)

Theorem 10. *If $\mathcal{R}_{0c} \leq 1$, then the COVID-19-only free equilibrium in Eq. (47) is globally asymptotically stable. Otherwise, it is unstable.*

Proof. Following the approach of [57,59,60], we construct the Lyapunov function of the type

$$\mathfrak{C} = b_{1c}E_c + b_{2c}I_c,$$

where $b_{1c} = (\lambda_c+\delta_c+\mu)$ and $b_{2c} = (\sigma_c+\mu)$. This can be seen that b_{1c} and b_{2c} are all positive. Thus, the fractional order derivative of $\mathfrak{C}$ can be written as

$${}^{ABC}_{a}D^{\alpha}_{t}\mathfrak{C} = b_{1c}\left({}^{ABC}_{a}D^{\alpha}_{t}\right)E_c + b_{2c}\left({}^{ABC}_{a}D^{\alpha}_{t}\right)I_c \tag{54}$$

By substituting Eq. (44) into Eq. (54). Thus,

$$\begin{aligned} {}^{ABC}_{a}D^{\alpha}_{t}\mathfrak{C} &= \alpha_c\sigma_c(1-\epsilon\vartheta)S_h I_c - (\sigma_c+\mu)(\lambda_c+\delta_c+\mu)I_c \\ &\leq \left(\frac{\alpha_c\sigma_c(1-\epsilon\vartheta)\Lambda_h}{\mu} - (\sigma_c+\mu)(\lambda_c+\delta_c+\mu)\right)I_c \\ &= (\sigma_c+\mu)(\lambda_c+\delta_c+\mu)(\mathcal{R}_{0c}-1)I_c. \end{aligned} \tag{55}$$

From the above result, ${}^{ABC}_{a}D^{\alpha}_{t}\mathfrak{C} \leq 0$ provided that $\mathcal{R}_{0c} \leq 1$ in addition to ${}^{ABC}_{a}D^{\alpha}_{t}\mathfrak{C} = 0$ on condition that $\mathcal{R}_{0c} = 1$ or $I_c = 0$. It shows that the highest invariance set in $\{(S_h, E_c, I_c, R_h) \in \mathbb{R}^4_+\}$ which is the singleton CFE (E_{0c}) and by LaSalle's invariance principle according to [61], CFE (E_{0c}) is globally asymptotically stable in $\mathbb{R}^4_+$. Epidemiologically, Theorem 10 show that, COVID-19 would die out in the neighbourhood whenever $\mathcal{R}_{0c} \leq 1$ regardless of the number of humans in model (44) at the initial stage of the population. □

4.5. Global stability of endemic equilibrium for COVID-19-only

Theorem 11. *If $\mathcal{R}_{0c} > 1$, then model (44) has a unique endemic equilibrium (E_{1c}) whenever $\mathcal{R}_{0c} > 1$ and no endemic equilibrium otherwise.*

Proof. If the existence of endemic equilibrium point for COVID-19-only in Eq. (51) form Eq. (52) as well as Eq. (53) then by substituting I_c^* in Eq. (53) into the force infection of humans for COVID-19-only $(\beta_c^* = b\alpha_c I_c^*)$ becomes

$$\mathcal{A}_c\beta_c^* + \mathcal{B}_c = 0 \tag{56}$$

where $\mathcal{A}_c = (\upsilon\lambda_C\sigma_c - b_1 b_2 k_3)\mathcal{R}_{0c}$ and $\mathcal{B}_c = k_3 b\Lambda_h\sigma_c\alpha_c(\mathcal{R}_{0c}-1)$. Hence, Eq. (56) can be defined as $\beta_c^* = -\frac{\mathcal{B}_c}{\mathcal{A}_c} \leq 0$ if $\mathcal{B}_c \geq 0$ at $\mathcal{R}_{0c} \leq 1$, and endemic equilibrium does not exist. Moreover, $\beta_c^* = \frac{\mathcal{B}_c}{\mathcal{A}_c} > 0$ if $\mathcal{B}_c < 0$ at $\mathcal{R}_{0c} > 1$. Thus, there exists the endemic equilibrium only at $\mathcal{R}_{0c} > 1$. This shows that model (44) has a unique endemic which is non-negative equilibrium whenever $\mathcal{R}_{0c} > 1$. □

Theorem 12. *If $\mathcal{R}_{0c} > 1$, then the endemic equilibrium of COVID-19-only in model (51) given by $E_{1c} = (S_h^*, E_c^*, I_c^*, R_h^*)$ is globally asymptotically stable in the interior of the region $\mathbb{R}^4_+$.*

Proof. Following the approach of [60,62,63], the equation below consists of the following Goh-Volterra type Lyapunov function:

$$\begin{aligned} \mathfrak{A}_c &= S_h - S_h^* - S_h^*\ln\frac{S_h}{S_h^*} + E_c - E_c^* - E_c^*\ln\frac{E_c}{E_c^*} \\ &\quad + d_{c1}(I_c - I_c^* - I_c^*\ln\frac{I_c}{I_c^*}) \end{aligned} \tag{57}$$

where $d_{c1} = \frac{\alpha_c(1-\epsilon\vartheta)S_h^* I_c^*}{\sigma_c E_c^*}$. Applying fractional order derivative with respect to time on Eq. (57), we have

$$\begin{aligned} {}^{ABC}_{a}D^{\alpha}_{t}\mathfrak{A}_c &= \left(1-\frac{S_h^*}{S_h}\right){}^{ABC}_{a}D^{\alpha}_{t}S_h + \left(1-\frac{E_c^*}{E_c}\right){}^{ABC}_{a}D^{\alpha}_{t}E_c \\ &\quad + d_{c1}\left(1-\frac{I_c^*}{I_c}\right){}^{ABC}_{a}D^{\alpha}_{t}I_c \end{aligned} \tag{58}$$

If $R_h \to R_h^*$ as time, $t \to \infty$ in Eq. (52) then at a steady-state, the equilibrium relation satisfies as follows

$$\Lambda_h = \alpha_c(1-\epsilon\,\vartheta)S_h^*I_c^* + \mu S_h^*;\ (\sigma_c+\mu) = \frac{\alpha_c\,(1-\epsilon\,\vartheta)\,S_h^*I_c^*}{E_c^*};\quad (\lambda_c+\delta_c+\mu) = \frac{\sigma_c E_c^*}{I_c^*}. \tag{59}$$

Substituting Eq. (59) into model (44) and simplifying Eq. (58), we obtain

$${}_a^{ABC}\mathcal{D}_t^{\alpha}\mathfrak{A}_c = \mu S_h^*\left(2-\frac{S_h^*}{S_h}-\frac{S_h}{S_h^*}\right)+\alpha_c\,(1-\epsilon\,\vartheta)\,S_h^*I_c^* \left(3-\frac{S_h^*}{S_h}-\frac{E_cI_c^*}{E_c^*I_c}-\frac{S_hE_c^*I_c}{S_h^*E_cI_c^*}\right)$$

Finally, since geometric mean is less than arithmetic mean, then the following inequalities holds:

$$\left(2-\frac{S_h^*}{S_h}-\frac{S_h}{S_h^*}\right)\le 0;\quad \left(3-\frac{S_h^*}{S_h}-\frac{E_cI_c^*}{E_c^*I_c}-\frac{S_hE_c^*I_c}{S_h^*E_cI_c^*}\right)\le 0 \quad \square$$

Appropriately, ${}_a^{ABC}\mathcal{D}_t^{\alpha}\mathfrak{A}_c \le 0$ for $\mathcal{R}_{0c} > 1$. In view of the fact that all the parameters are positive with ${}_a^{ABC}\mathcal{D}_t^{\alpha}\mathfrak{A}_c = 0$ provided that $S_h = S_h^*$, $E_c = E_c^*$ and $I_c = I_c^*$. Since it is established that $R_h \to R_h^*$ as $t \to \infty$ and by LaSalle's invariance principle [61], then the endemic equilibrium E_{1c} is globally asymptotically stable whenever $\mathcal{R}_{0c} > 1$. Epidemiologically, Theorem 12 means that COVID-19 would establish itself in the neighbourhood whenever $\mathcal{R}_{0c} > 1$ irrespective of the number of infectious humans at initial stage of the population.

4.6. Fractional order of malaria-COVID-19 model

The fractional order of Malaria-COVID-19 model in (15) subject to initial conditions is positively invariant in the region $\Omega_{cm} = \Omega_c \times \Omega_m$.

Theorem 13. *The region*

$$\Omega_{cm} = \{(S_h, E_m, E_c, E_{mc}, I_m, I_c, I_{mc}, I_{cEm}, I_{mEc}, R_h, S_v, E_v, I_v) \in \mathbb{R}_+^{13} : N_h \le \frac{\Lambda_h}{\mu}\times\frac{\Lambda_v}{\eta}\}$$

is positively invariant for the fractional order of Malaria-COVID-19 model in (15) subject to non-negative initial conditions $\mathbb{R}_+^{13}$ in (16)

Proof. Let N_h represent the total population of Malaria-COVID-19. Since $N_h = N_{hcm} + N_v$ that is, $Nh = S_h + E_m + E_c + E_{mc} + I_m + I_c + I_{mc} + I_{cEm} + I_{mEc} + R_h + S_v + E_v + I_v$, using ABC fractional derivative on the total population of Malaria-COVID-19. Next, by substituting Eq. (15) into it, we have ${}_a^{ABC}\mathcal{D}_t^{\alpha}N_{hcm} = \Lambda_h - \mu(S_h + E_m + E_c + E_{mc} + I_m + I_c + I_{mc} + I_{cEm} + I_{mEc} + R_h) - \delta_{cm}I_{cm} - \delta_cI_c - \delta_mI_m$ and ${}_a^{ABC}\mathcal{D}_t^{\alpha}N_v = \Lambda_h - \mu(S_v + E_v + I_v)$. These can be written as

$$\begin{aligned} {}_a^{ABC}\mathcal{D}_t^{\alpha}N_{hcm} &\le \Lambda_h - \mu N_{hcm} \\ {}_a^{ABC}\mathcal{D}_t^{\alpha}N_v &\le \Lambda_h - \mu N_v \end{aligned} \tag{60}$$

By applying Laplace transform in Eq. (15), and the inverse Laplace expressed as Mittag-Leffler function, we deduce that $t \to \infty$ then Eq. (15) is expressed as $N_{hcm} \le \frac{\Lambda_h}{\mu}$ and $N_v \le \frac{\Lambda_v}{\eta}$. Therefore, the fractional order of Malaria-COVID-19 model in Eq. (15) has the solution in Ω_{cm}. Therefore, the feasible region of Malaria-COVID-19 model in Eq. (15) is

$$\Omega_{cm} = \{(S_h, E_m, E_c, E_{mc}, I_m, I_c, I_{mc}, I_{cEm}, I_{mEc}, R_h, S_v, E_v, I_v) \in \mathbb{R}_+^{13} : N_h \le \frac{\Lambda_h}{\mu}\times\frac{\Lambda_v}{\eta}\}$$

which is positively invariant. $\square$

4.6.1. Existence of malaria-COVID-19-free equilibrium

The Malaria-COVID-19-free equilibrium of the fractional ABC for the Malaria-COVID-19 in model (15) can be obtained by setting the right hand side of the model (15) as well as $E_m = E_c = E_{mc} = I_m = I_c = I_{mc} = I_{cEm} = I_{mEc} = R_h = E_v = I_v = 0$ and we obtain

$$\begin{aligned} \mathbf{E}_{0cm} &= (S_h, E_m, E_c, E_{mc}, I_m, I_c, I_{mc}, I_{cEm}, I_{mEc}, R_h, S_v, E_v, I_v) \\ &= (\frac{\Lambda_h}{\mu}, 0, 0, 0, 0, 0, 0, 0, 0, \frac{\Lambda_v}{\eta}, 0, 0) \end{aligned} \tag{61}$$

4.6.2. Existence of endemic equilibrium for malaria-COVID-19

The endemic equilibrium of the fractional ABC for the Malaria-COVID-19 in model (15) can be obtained by setting the right hand side of the model (15) to be zero and putting $S_h = S_h^*$, $E_c = E_c^*$, $I_c = I_c^*$, $R_h = R_h^*$ and we obtain

$$\begin{aligned} \mathbf{E}_{1cm} &= (S_h, E_m, E_c, E_{mc}, I_m, I_c, I_{mc}, I_{cEm}, I_{mEc}, R_h, S_v, E_v, I_v) \\ &= (S_h^*, E_m^*, E_c^*, E_{mc}^*, I_m^*, I_c^*, I_{mc}^*, I_{cEm}^*, I_{mEc}^*, R_h^*, S_v^*, E_v^*, I_v^*) \end{aligned} \tag{62}$$

4.6.3. Basic reproduction number of COVID-19-only ($\mathcal{R}_{0c}$) model

Recall that, we have derived the basic reproduction number for COVID-19 only ($\mathcal{R}_{0c}$) and Malaria-19 only ($\mathcal{R}_{0m}$) then according to [58] the related basic reproduction number for Malaria-COVID-19 ($\mathcal{R}_{0cm}$) in model (15) is given by

$$\mathcal{R}_{0cm} = max\{\mathcal{R}_{0c}, \mathcal{R}_{0m}\}. \tag{63}$$

The subsequent result follows from Theorem 2 in [58].

Theorem 14. *If $\mathcal{R}_{0cm} \le 1$ then the Malaria-COVID-19 free equilibrium in Eq. (61) is globally asymptotically stable. Otherwise, it is unstable.*

Theorem 15. *If $\mathcal{R}_{0cm} > 1$ then model (15) has a unique endemic equilibrium (E_{1cm}) whenever $\mathcal{R}_{0cm} > 1$ and no endemic equilibrium otherwise.*

Theorem 16. *If $\mathcal{R}_{0cm} > 1$ then the endemic equilibrium of Malaria-COVID-19 co-infection in model (15) given by*

$$E_{1cm} = \left(S_h^*, E_m^*, E_c^*, E_{mc}^*, I_m^*, I_c^*, I_{mc}^*, I_{cEm}^*, I_{mEc}^*, R_h^*, S_v^*, E_v^*, I_v^*\right)$$

is globally asymptotically stable in the interior of the region $\mathbb{R}_+^{13}$

4.7. Procedure for solution

There are many numerical methods that can be used to tackle the solution of fractional order numerically and as a result of this, we will consider one of the approximate methods. According to [64], we will combine fundamental theorem fractional calculus mentioned in the preliminaries and two-step Lagrange interpolation polynomial. To write the scheme for the developed model, let us consider the fractional order of the co-infection model (15) subject to the initial conditions in Eq. (16). Applying the Laplace transform from the Definition 4 of Eq. (4) on both sides of Eq. (15). Thus,

$$\begin{aligned} \mathfrak{Y}_1 &= \mathcal{L}\{\Lambda_h - (\beta_c+\beta_m+\mu)S_h + \upsilon R_h\} \\ \mathfrak{Y}_2 &= \mathcal{L}\{\beta_cS_h - (\beta_m+\sigma_c+\mu)E_c\} \\ \mathfrak{Y}_3 &= \mathcal{L}\{\beta_mS_h - (\beta_c+\sigma_m+\mu)E_m\} \\ \mathfrak{Y}_4 &= \mathcal{L}\{\beta_mE_c + \beta_cE_m - (\sigma_{mc}+\mu)E_{mc}\} \\ \mathfrak{Y}_5 &= \mathcal{L}\{\sigma_cE_c - (\lambda_c+\gamma_1\beta_m+\delta_c+\mu)I_c\} \\ \mathfrak{Y}_6 &= \mathcal{L}\{\sigma_mE_m - (\lambda_m+\gamma_2\beta_c+\delta_m+\mu)I_m\} \\ \mathfrak{Y}_7 &= \mathcal{L}\{\sigma_{mc}E_{mc} + \phi_1I_{cEm} + \phi_2I_{mEc} - (\alpha+\delta_{mc}+\mu)I_{mc}\} \end{aligned} \tag{64}$$

$$
\begin{aligned}
\mathfrak{Y}_8 &= \mathcal{L}\{\gamma_1\beta_m I_c - (\phi_1+\mu)I_{cEm}\}\\
\mathfrak{Y}_9 &= \mathcal{L}\{\gamma_2\beta_c I_m - (\phi_2+\mu)I_{mEc}\}\\
\mathfrak{Y}_{10} &= \mathcal{L}\{\lambda_c I_c + \lambda_m I_m + \alpha I_{mc} - (\upsilon+\mu)R_h\}\\
\mathfrak{Y}_{11} &= \mathcal{L}\{\Lambda_v - \beta_v S_v - \eta S_v\}\\
\mathfrak{Y}_{12} &= \mathcal{L}\{\beta_v S_v - \sigma_v E_v - \eta E_v\}\\
\mathfrak{Y}_{13} &= \mathcal{L}\{\sigma_v E_v - \eta I_v\}
\end{aligned}
$$

where

$$
\begin{aligned}
\mathfrak{Y}_1 &= \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^\alpha\mathcal{L}\{S_h(t)\} - p^{\alpha-1}S_h(0)}{p^\alpha + \frac{\alpha}{1-\alpha}}\\
\mathfrak{Y}_2 &= \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^\alpha\mathcal{L}\{E_c(t)\} - p^{\alpha-1}E_c(0)}{p^\alpha + \frac{\alpha}{1-\alpha}}\\
\mathfrak{Y}_3 &= \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^\alpha\mathcal{L}\{E_m(t)\} - p^{\alpha-1}E_m(0)}{p^\alpha + \frac{\alpha}{1-\alpha}}\\
\mathfrak{Y}_4 &= \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^\alpha\mathcal{L}\{E_{mc}(t)\} - p^{\alpha-1}E_{mc}(0)}{p^\alpha + \frac{\alpha}{1-\alpha}}\\
\mathfrak{Y}_5 &= \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^\alpha\mathcal{L}\{I_c(t)\} - p^{\alpha-1}I_c(0)}{p^\alpha + \frac{\alpha}{1-\alpha}}\\
\mathfrak{Y}_6 &= \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^\alpha\mathcal{L}\{I_m(t)\} - p^{\alpha-1}I_m(0)}{p^\alpha + \frac{\alpha}{1-\alpha}}\\
\mathfrak{Y}_7 &= \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^\alpha\mathcal{L}\{I_{mc}(t)\} - p^{\alpha-1}I_{mc}(0)}{p^\alpha + \frac{\alpha}{1-\alpha}}\\
\mathfrak{Y}_8 &= \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^\alpha\mathcal{L}\{I_{cEm}(t)\} - p^{\alpha-1}I_{cEm}(0)}{p^\alpha + \frac{\alpha}{1-\alpha}}\\
\mathfrak{Y}_9 &= \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^\alpha\mathcal{L}\{I_{mEc}(t)\} - p^{\alpha-1}I_{mEc}(0)}{p^\alpha + \frac{\alpha}{1-\alpha}}\\
\mathfrak{Y}_{10} &= \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^\alpha\mathcal{L}\{R_h(t)\} - p^{\alpha-1}R_h(0)}{p^\alpha + \frac{\alpha}{1-\alpha}}\\
\mathfrak{Y}_{11} &= \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^\alpha\mathcal{L}\{S_v(t)\} - p^{\alpha-1}S_v(0)}{p^\alpha + \frac{\alpha}{1-\alpha}}\\
\mathfrak{Y}_{12} &= \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^\alpha\mathcal{L}\{E_v(t)\} - p^{\alpha-1}E_v(0)}{p^\alpha + \frac{\alpha}{1-\alpha}}\\
\mathfrak{Y}_{13} &= \frac{\mathfrak{L}(\alpha)}{1-\alpha}\frac{p^\alpha\mathcal{L}\{I_v(t)\} - p^{\alpha-1}I_v(0)}{p^\alpha + \frac{\alpha}{1-\alpha}}.
\end{aligned}
\tag{65}
$$

Recall that $k_1 = (\sigma_m+\mu), k_2 = (\lambda_m+\delta_m+\mu), k_3 = (\upsilon+\mu), b_1 = (\sigma_c+\mu), b_2 = (\lambda_c+\delta_c+\mu)$. Thus, Eqs. (64) and (65) can be written as

$$
\begin{aligned}
\mathcal{L}\{S_h(t)\} &= \frac{S_h(0)}{p} + \frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\Lambda_h - k_7 S_h + \upsilon R_h\}\\
\mathcal{L}\{E_c(t)\} &= \frac{E_c(0)}{p} + \frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\beta_c S_h - (\beta_m+b_1)E_c\}\\
\mathcal{L}\{E_m(t)\} &= \frac{E_m(0)}{p} + \frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\beta_m S_h - (\beta_c+k_1)E_m\}\\
\mathcal{L}\{E_{mc}(t)\} &= \frac{E_{mc}(0)}{p} + \frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\beta_m E_c + \beta_c E_m - k_8 E_{mc}\}\\
\mathcal{L}\{I_c(t)\} &= \frac{I_c(0)}{p} + \frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\sigma_c E_c - (\gamma_1\beta_m + b_2)I_c\}\\
\mathcal{L}\{I_m(t)\} &= \frac{I_m(0)}{p} + \frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\sigma_m E_m - (\gamma_2\beta_c + k_2)I_m\}\\
\mathcal{L}\{I_{mc}(t)\} &= \frac{I_{mc}(0)}{p} + \frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\sigma_{mc} E_{mc} + \phi_1 I_{cEm} + k_9\}\\
\mathcal{L}\{I_{cEm}(t)\} &= \frac{I_{cEm}(0)}{p} + \frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\gamma_1\beta_m I_c - (\phi_1+\mu)I_{cEm}\}\\
\mathcal{L}\{I_{mEc}(t)\} &= \frac{I_{mEc}(0)}{p} + \frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\gamma_2\beta_c I_m - (\phi_2+\mu)I_{mEc}\}\\
\mathcal{L}\{R_h(t)\} &= \frac{R_h(0)}{p} + \frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\lambda_c I_c + \lambda_m I_m + k_{10} - k_3 R_h\}\\
\mathcal{L}\{S_v(t)\} &= \frac{S_v(0)}{p} + \frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\Lambda_v - \beta_v S_v - \eta S_v\}\\
\mathcal{L}\{E_v(t)\} &= \frac{E_v(0)}{p} + \frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\beta_v S_v - \sigma_v E_v - \eta E_v\}\\
\mathcal{L}\{I_v(t)\} &= \frac{I_v(0)}{p} + \frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\sigma_v E_v - \eta I_v\}
\end{aligned}
\tag{66}
$$

where $k_7 = (\beta_c+\beta_m+\mu), k_8 = (\sigma_{mc}+\mu), k_9 = \phi_2 I_{mEc} - (\alpha+\delta_{mc}+\mu)I_{mc}, k_{10} = \alpha I_{mc}$.

By applying the inverse Laplace transform in Eq. (66), we obtain

$$
\begin{aligned}
S_h(t) &= S_h(0) + \mathcal{L}^{-1}\left[\frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\Lambda_h - k_7 S_h + \upsilon R_h\}\right]\\
E_c(t) &= E_c(0) + \mathcal{L}^{-1}\left[\frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\beta_c S_h - (\beta_m+b_1)E_c\}\right]\\
E_m(t) &= E_m(0) + \mathcal{L}^{-1}\left[\frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\beta_m S_h - (\beta_c+k_1)E_m\}\right]\\
E_{mc}(t) &= E_{mc}(0) + \mathcal{L}^{-1}\left[\frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\beta_m E_c + \beta_c E_m - k_8 E_{mc}\}\right]\\
I_c(t) &= I_c(0) + \mathcal{L}^{-1}\left[\frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\sigma_c E_c - (\gamma_1\beta_m + b_2)I_c\}\right]\\
I_m(t) &= I_m(0) + \mathcal{L}^{-1}\left[\frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\sigma_m E_m - (\gamma_2\beta_c + k_2)I_m\}\right]\\
I_{mc}(t) &= I_{mc}(0) + \mathcal{L}^{-1}\left[\frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\sigma_{mc} E_{mc} + \phi_1 I_{cEm} + k_9\}\right]\\
I_{cEm}(t) &= I_{cEm}(0) + \mathcal{L}^{-1}\left[\frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\gamma_1\beta_m I_c - (\phi_1+\mu)I_{cEm}\}\right]\\
I_{mEc}(t) &= I_{mEc}(0) + \mathcal{L}^{-1}\left[\frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\gamma_2\beta_c I_m - (\phi_2+\mu)I_{mEc}\}\right]\\
R_h(t) &= R_h(0) + \mathcal{L}^{-1}\left[\frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\lambda_c I_c + \lambda_m I_m + k_{10} - k_3 R_h\}\right]\\
S_v(t) &= S_v(0) + \mathcal{L}^{-1}\left[\frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\Lambda_v - \beta_v S_v - \eta S_v\}\right]\\
E_v(t) &= E_v(0) + \mathcal{L}^{-1}\left[\frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\beta_v S_v - \sigma_v E_v - \eta E_v\}\right]\\
I_v(t) &= I_v(0) + \mathcal{L}^{-1}\left[\frac{p^\alpha(1-p)+p}{p^\alpha(\mathfrak{L}(\alpha))}\mathcal{L}\{\sigma_v E_v - \eta I_v\}\right]
\end{aligned}
\tag{67}
$$

The series solutions can be achieved following the expressions below:

$$
S_h = \sum_{n=0}^{\infty} S_{hn};\ E_c = \sum_{n=0}^{\infty} E_{cn};\ E_m = \sum_{n=0}^{\infty} E_{mn};\ E_{mc} = \sum_{n=0}^{\infty} E_{mcn};\ I_c = \sum_{n=0}^{\infty} I_{cn};
$$

$$
I_m = \sum_{n=0}^{\infty} I_{mn};\ I_{mc} = \sum_{n=0}^{\infty} I_{mcn};\ I_{cEm} = \sum_{n=0}^{\infty} I_{cEmn};\ I_{mEc} = \sum_{n=0}^{\infty} E_{mEcn};
$$

$$
R_h = \sum_{n=0}^{\infty} R_{hn};\ S_v = \sum_{n=0}^{\infty} S_{vn};\ E_v = \sum_{n=0}^{\infty} E_{vn};\ I_v = \sum_{n=0}^{\infty} I_{vn}
$$

and the non-linear terms from the above can be written as

$$S_h I_c = \sum_{n=0}^{\infty} A_n;\ S_h I_{mc} = \sum_{n=0}^{\infty} B_n;\ S_h I_{cEm} = \sum_{n=0}^{\infty} C_n;\ S_h I_{\mathrm{v}} = \sum_{n=0}^{\infty} F_n;$$
$$S_{\mathrm{v}} I_m = \sum_{n=0}^{\infty} J_n;\ S_{\mathrm{v}} I_{mc} = \sum_{n=0}^{\infty} P_n;\ S_{\mathrm{v}} I_{mEc} = \sum_{n=0}^{\infty} Q_n$$

Although $A_n, B_n, C_n, F_n, J_n, P_n$ and Q_n are further decomposed as follows

$$A_n = \sum_{i=0}^{n} S_{hi} \sum_{i=0}^{n} I_{ci} - \sum_{i=0}^{n-1} S_{hi} \sum_{i=0}^{n-1} I_{ci};\ B_n = \sum_{i=0}^{n} S_{hi} \sum_{i=0}^{n} I_{mci} - \sum_{i=0}^{n-1} S_{hi} \sum_{i=0}^{n-1} I_{mci};$$
$$C_n = \sum_{i=0}^{n} S_{hi} \sum_{i=0}^{n} I_{cEmi} - \sum_{i=0}^{n-1} S_{hi} \sum_{i=0}^{n-1} I_{cEmi};\ F_n = \sum_{i=0}^{n} S_{hi} \sum_{i=0}^{n} I_{\mathrm{v}i} - \sum_{i=0}^{n-1} S_{hi} \sum_{i=0}^{n-1} I_{\mathrm{v}i};$$
$$J_n = \sum_{i=0}^{n} S_{\mathrm{v}i} \sum_{i=0}^{n} I_{mi} - \sum_{i=0}^{n-1} S_{\mathrm{v}i} \sum_{i=0}^{n-1} I_{mi};\ P_n = \sum_{i=0}^{n} S_{\mathrm{v}i} \sum_{i=0}^{n} I_{mci} - \sum_{i=0}^{n-1} S_{\mathrm{v}i} \sum_{i=0}^{n-1} I_{mci};$$
$$Q_n = \sum_{i=0}^{n} S_{\mathrm{v}i} \sum_{i=0}^{n} I_{mEci} - \sum_{i=0}^{n-1} S_{\mathrm{v}i} \sum_{i=0}^{n-1} I_{mEci}$$

Thus, recursive formula can be written as

$$\begin{aligned}
S_{h(n+1)}(t) &= S_{hn}(0) + \mathcal{L}^{-1}\left[\frac{p^{\alpha}(1-p)+p}{p^{\alpha}(\mathfrak{L}(\alpha))}\mathcal{L}\{\Lambda_h - k_7 S_h + \upsilon R_h\}\right]\\
E_{c(n+1)}(t) &= E_{cn}(0) + \mathcal{L}^{-1}\left[\frac{p^{\alpha}(1-p)+p}{p^{\alpha}(\mathfrak{L}(\alpha))}\mathcal{L}\{\beta_c S_h - (\beta_m + b_1)E_c\}\right]\\
E_{m(n+1)}(t) &= E_{mn}(0) + \mathcal{L}^{-1}\left[\frac{p^{\alpha}(1-p)+p}{p^{\alpha}(\mathfrak{L}(\alpha))}\mathcal{L}\{\beta_m S_h - (\beta_c + k_1)E_m\}\right]\\
E_{mc(n+1)}(t) &= E_{mcn}(0) + \mathcal{L}^{-1}\left[\frac{p^{\alpha}(1-p)+p}{p^{\alpha}(\mathfrak{L}(\alpha))}\mathcal{L}\{\beta_m E_c + \beta_c E_m - k_8 E_{mc}\}\right]\\
I_{c(n+1)}(t) &= I_{cn}(0) + \mathcal{L}^{-1}\left[\frac{p^{\alpha}(1-p)+p}{p^{\alpha}(\mathfrak{L}(\alpha))}\mathcal{L}\{\sigma_c E_c - (\gamma_1\beta_m + b_2)I_c\}\right]\\
I_{m(n+1)}(t) &= I_{mn}(0) + \mathcal{L}^{-1}\left[\frac{p^{\alpha}(1-p)+p}{p^{\alpha}(\mathfrak{L}(\alpha))}\mathcal{L}\{\sigma_m E_m - (\gamma_2\beta_c + k_2)I_m\}\right]\\
I_{mc(n+1)}(t) &= I_{mcn}(0) + \mathcal{L}^{-1}\left[\frac{p^{\alpha}(1-p)+p}{p^{\alpha}(\mathfrak{L}(\alpha))}\mathcal{L}\{\sigma_{mc} E_{mc} + \phi_1 I_{cEm} + k_9\}\right]\\
I_{cEm(n+1)}(t) &= I_{cEmn}(0) + \mathcal{L}^{-1}\left[\frac{p^{\alpha}(1-p)+p}{p^{\alpha}(\mathfrak{L}(\alpha))}\mathcal{L}\{\gamma_1\beta_m I_c - (\phi_1 + \mu)I_{cEm}\}\right]
\end{aligned} \tag{68}$$

$$\begin{aligned}
I_{mEc(n+1)}(t) &= I_{mEcn}(0) + \mathcal{L}^{-1}\left[\frac{p^{\alpha}(1-p)+p}{p^{\alpha}(\mathfrak{L}(\alpha))}\mathcal{L}\{\gamma_2\beta_c I_m - (\phi_2 + \mu)I_{mEc}\}\right]\\
R_{h(n+1)}(t) &= R_{hn}(0) + \mathcal{L}^{-1}\left[\frac{p^{\alpha}(1-p)+p}{p^{\alpha}(\mathfrak{L}(\alpha))}\mathcal{L}\{\lambda_c I_c + \lambda_m I_m + k_{10} - k_3 R_h\}\right]\\
S_{\mathrm{v}(n+1)}(t) &= S_{\mathrm{v}n}(0) + \mathcal{L}^{-1}\left[\frac{p^{\alpha}(1-p)+p}{p^{\alpha}(\mathfrak{L}(\alpha))}\mathcal{L}\{\Lambda_{\mathrm{v}} - \beta_{\mathrm{v}} S_{\mathrm{v}} - \eta S_{\mathrm{v}}\}\right]\\
E_{\mathrm{v}(n+1)}(t) &= E_{\mathrm{v}n}(0) + \mathcal{L}^{-1}\left[\frac{p^{\alpha}(1-p)+p}{p^{\alpha}(\mathfrak{L}(\alpha))}\mathcal{L}\{\beta_{\mathrm{v}} S_{\mathrm{v}} - \sigma_{\mathrm{v}} E_{\mathrm{v}} - \eta E_{\mathrm{v}}\}\right]\\
I_{\mathrm{v}(n+1)}(t) &= I_{\mathrm{v}n}(0) + \mathcal{L}^{-1}\left[\frac{p^{\alpha}(1-p)+p}{p^{\alpha}(\mathfrak{L}(\alpha))}\mathcal{L}\{\sigma_{\mathrm{v}} E_{\mathrm{v}} - \eta I_{\mathrm{v}}\}\right],
\end{aligned}$$

where

$$S_h(0) = S_{h0}, E_c(0) = E_{c0}, E_m(0) = E_{m0}, E_{mc}(0) = E_{mc0},$$
$$I_c(0) = I_{c0}, I_m(0) = I_{m0}, I_{mc}(0) = I_{mc0}, I_{cEm}(0) = I_{cEm0},$$
$$I_{mEc}(0) = I_{mEc0}, R_h(0) = R_{h0}, S_{\mathrm{v}}(0) = S_{\mathrm{v}0},$$
$$E_{\mathrm{v}}(0) = E_{\mathrm{v}0}, I_{\mathrm{v}}(0) = I_{\mathrm{v}0}$$

5. Results and discussion

In this section, we consider the numerical solution of the model (15) using the parameters values given in Table 3 to achieve the graphical results. We have considered seven different values of fractional order α to stimulate all the five infectious classes of humans in model (15). We notice that as we increase the fractional order α so also the solution converges to the integer order. We use Maple 2018 software package to carry out the simulation and the initial values for the model in (15) are listed as follows: $S_h(0) = 2,500, E_c(0) = 1, E_m(0) = 1, E_{mc}(0) = 1, I_c(0) = 20, I_m(0) = 10, I_{mc}(0) = 3, I_{cEm}(0) = 3, I_{mEc}(0) = 1, R_h(0) = 20, S_{\mathrm{v}}(0) = 10,000, E_{\mathrm{v}}(0) = 8, I_{\mathrm{v}}(0) = 10$. We demonstrate the effect of γ_1 and γ_2 parameters which represent A risk factor for getting COVID-19 after contracting malaria and A risk factor for getting malaria after contracting COVID-19 respectively, where $\{\gamma_1 \in [0,1]$ and $\gamma_2 \in [0,1]\}$ as well as the effect of $\alpha \in [0,1]$.

Table 3
Details definition of variables and parameters.

Parameter	Value	Source	Parameter	Value	Source
Λ_h	$\frac{10000}{(59\times365)}$	[34]	α_c	0.4531	[34]
Λ_{υ}	$\frac{10000}{21}$	[34]	α_{v}	0.48	[34]
ϕ_1	0.0833	[34]	ϕ_2	0.4	[34]
σ_m	0.8333	[34]	b	$4.3 * 0.33$	[34]
σ_c	0.6	[34]	δ_c	0.00286	[34]
σ_{v}	0.1	[34]	δ_m	0.068	[34]
σ_{mc}	0.333	[34]	$\delta_m c$	0.0383	[34]
λ_c	0.3	[34]	μ	$\frac{1}{(59\times365)}$	[34]
λ_m	0.25	[34]	η	$\frac{1}{21}$	[34]
υ	0.025	[34]	γ_1	$[0-1]$	[34]
ϵ	0.5	[34]	ϑ	0.5	[34]
α_m	0.125	[34]	γ_2	$[0-1]$	[34]
α_r	0.5	Assumed			

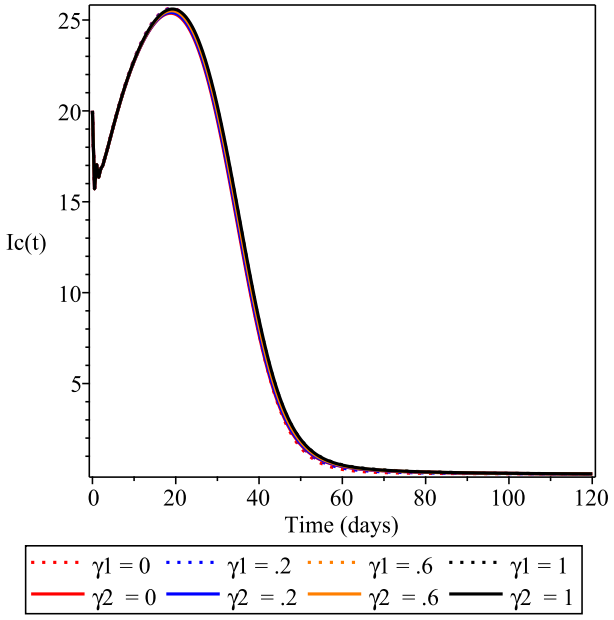

Fig. 2. Simulation of $I_c(t)$ with respect to time t in days, at different values of γ_1 and γ_2 where $\alpha = 0.98$ and other parameters listed in Table 3.

Fig. 2 is the simulation of the number of humans infected with COVID-19-only ($I_c(t)$) with respect to time t in days, at different values of the risk factor for getting COVID-19 after contracting malaria (γ_1) and A risk factor for getting malaria after contracting COVID-19 (γ_2) where $\alpha = 0.98$ and other parameters listed in Table 3. This shows that the number of humans infected COVID-19-only decreases from 20 to 16 in less than 1 day thereafter, it increases rapidly for 40 days to reach the maximum number of 26 people before a rapid decrease until after 55 days when the number of infected COVID-19-only becomes extinct.

Fig. 3 is the simulation of the number of humans infected with Malaria-only ($I_m(t)$) with respect to time t in days, at different values (γ_1) and (γ_2) where $\alpha = 0.98$ and other parameters listed in Table 3. This shows that the number of humans infected with malaria-only decrease from 10 to 7 in less than 3 days thereafter, it increases rapidly from 39 days to reach the maximum number of 320 people before a rapid

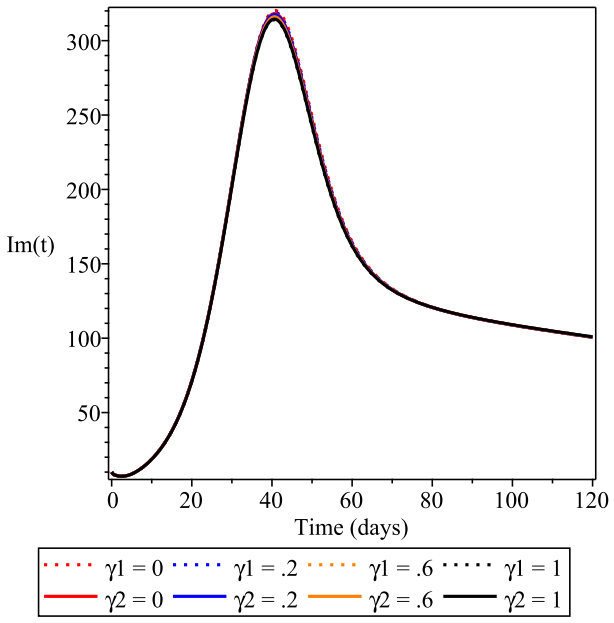

Fig. 3. Simulation of $I_m(t)$ with respect to time t in days, at different values of γ_1 and γ_2 where $\alpha = 0.98$ and other parameters listed in Table 3.

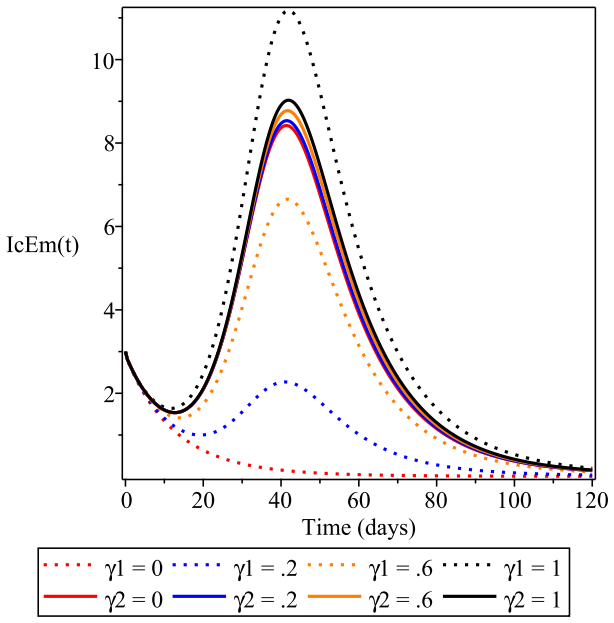

Fig. 5. Simulation of $I_{cEm}(t)$ with respect to time t in days, at different values of γ_1 and γ_2 where $\alpha = 0.98$ and other parameters listed in Table 3.

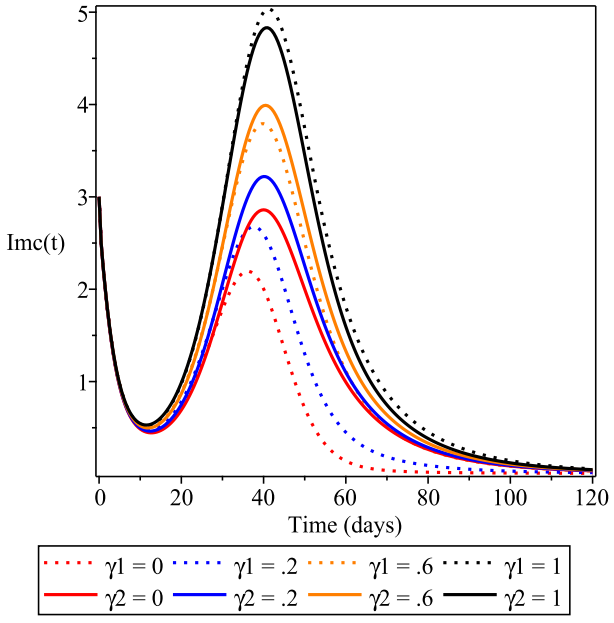

Fig. 4. Simulation of $I_{mc}(t)$ with respect to time t in days, at different values of γ_1 and γ_2 where $\alpha = 0.98$ and other parameters listed in Table 3.

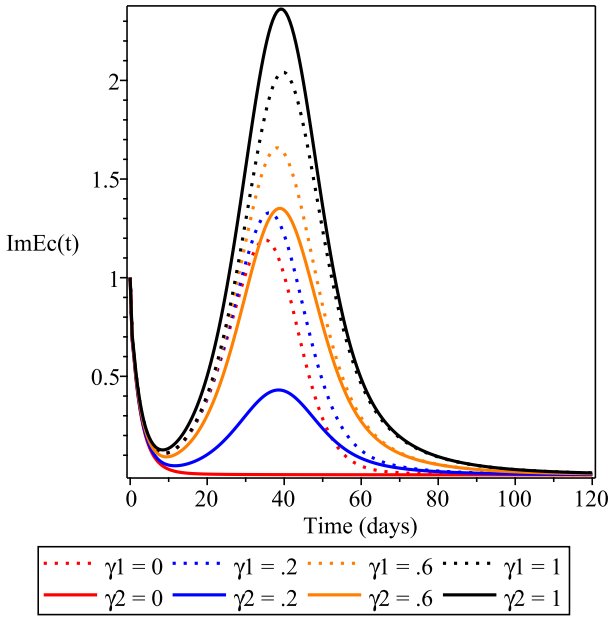

Fig. 6. Simulation of $I_{mEc}(t)$ with respect to time t in days, at different values of γ_1 and γ_2 where $\alpha = 0.98$ and other parameters listed in Table 3.

decrease until after 60 days when the number of people infected with malaria-only decreases.

Fig. 4 is the simulation of the number of humans infected with malaria and COVID-19 ($I_{mc}(t)$) with respect to time t in days, at different values of (γ_1) (γ_2) where $\alpha = 0.98$ and other parameters listed in Table 3. This shows that the number of humans infected with malaria and COVID-19 decrease rapidly from 3 to below 1 in less than 10 days and increases rapidly for 40 days to reach the maximum number of 5 people before a rapid decrease until after 60 days when the number of infected with malaria and COVID-19 becomes extinct.

Fig. 5 is the simulation of the number of humans infected with COVID-19 and Exposed to malaria ($I_{cEm}(t)$) with respect to time t in days, at different values of (γ_1) and (γ_2) where $\alpha = 0.98$ and other parameters listed in Table 3. This shows that the number of humans infected humans with COVID-19 and Exposed to malaria decrease gradually from 3 to below 2 in less than 30 days thereafter, $\gamma_1 = 0$ continues to decrease until it becomes extinct. Meanwhile others increase at different values to reach their maximum number of people and $\gamma_1 = 1$ has highest number of 12 people before a rapid decrease as well as others until after 60 days when the number of infected humans with COVID-19 and Exposed to malaria becomes extinct.

Fig. 6 is the simulation of the number of humans infected humans with malaria and Exposed to COVID-19 ($I_{mEc}(t)$) with respect to time t in days, at different values of the relative infectiousness humans

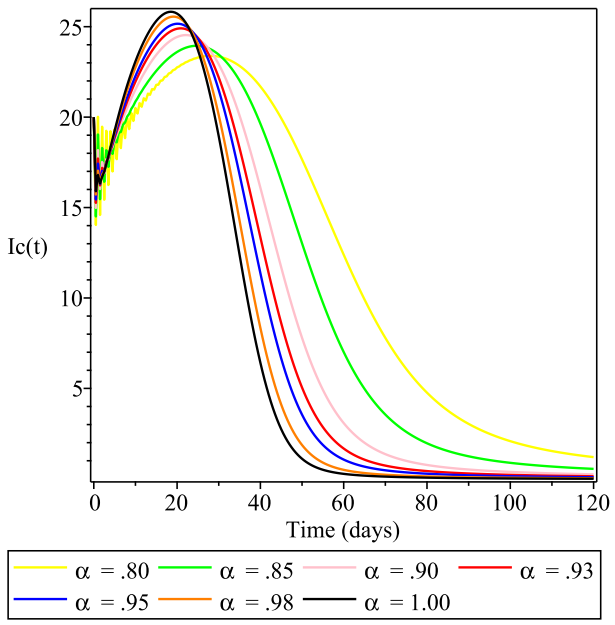

Fig. 7. Simulation of $I_c(t)$ with respect to time t in days, at seven different fractional order between 0 and 1. All other parameters listed in Table 3.

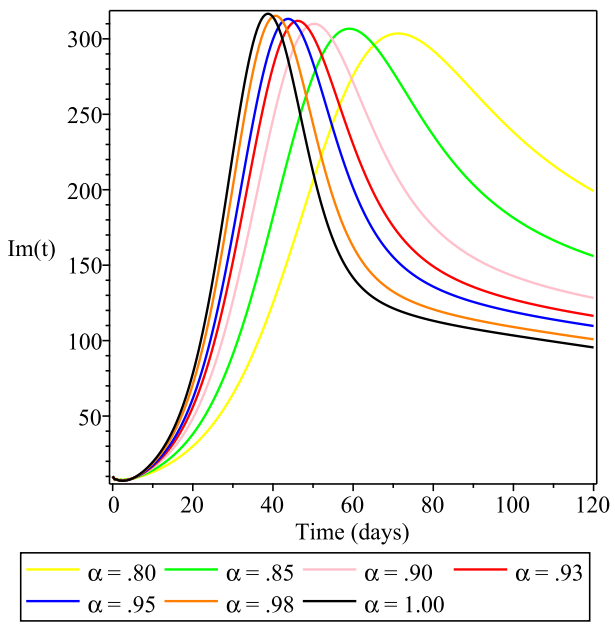

Fig. 8. Simulation of $I_m(t)$ with respect to time t in days, at seven different fractional order between 0 and 1. All other parameters listed in Table 3.

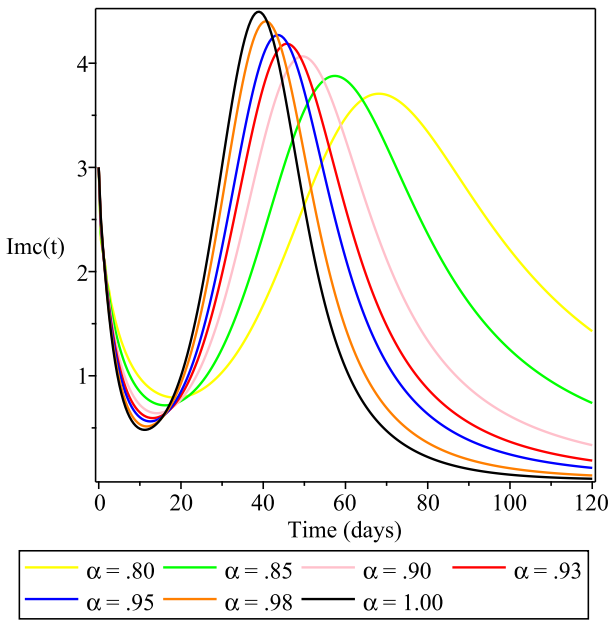

Fig. 9. Simulation of $I_{mc}(t)$ with respect to time t in days, at seven different fractional order between 0 and 1. All other parameters listed in Table 3.

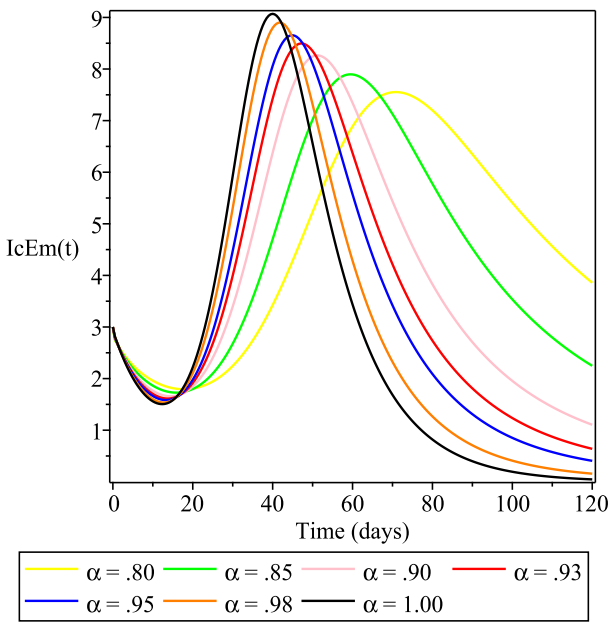

Fig. 10. Simulation of $I_{cEm}(t)$ with respect to time t in days, at seven different fractional order between 0 and 1. All other parameters listed in Table 3.

developing COVID-19 subsequent malaria disease (γ_1) and relative infectiousness humans developing malaria subsequent COVID-19 disease (γ_2) where $\alpha = 0.98$ and other parameters listed in Table 3. This shows that the number of humans infected humans with malaria and Exposed to COVID-19 decrease gradually from 1 person to nearly 0 in less than 8 days thereafter, $\gamma_2 = 0$ continues to decrease until it becomes extinct. Meanwhile others increase at different values to reach their maximum number of people and $\gamma_2 = 1$ has highest number of over 2 people before a rapid decrease as well as others until after 50 days when the number of infected humans with malaria and Exposed to COVID-19 becomes extinct.

The dynamics of co-infection of malaria and COVID-19 with seven different values of fractional order (α) as well as different classes are given in Figs. 7, 8, 9, 10 and 11.

6. Conclusion

In this paper, we have studied the co-infection of malaria and COVID-19 model under Atangana–Baleanu–Caputo fractional order derivative. Existence and the uniqueness of the co-infection have been proved. We also considered the dynamics of malaria-only and COVID-19-only, and their basic reproduction numbers. We have carried out

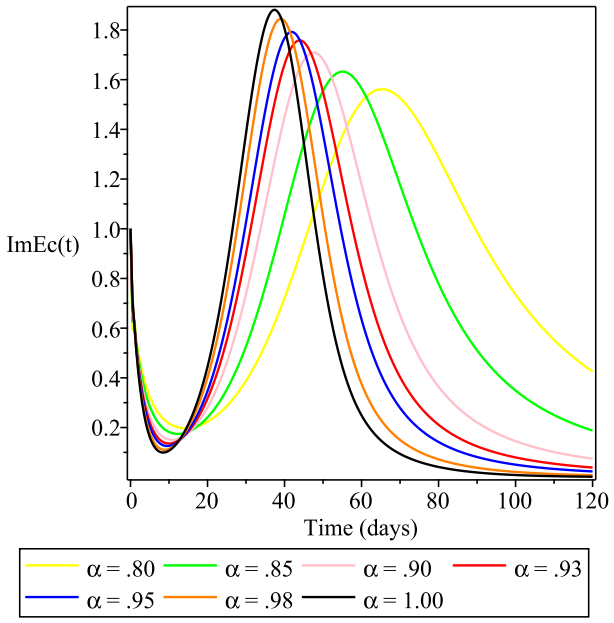

Fig. 11. Simulation of $I_{mEc}(t)$ with respect to time t in days, at seven different fractional order between 0 and 1. All other parameters listed in Table 3.

global stabilities of malaria-only-free, COVID-19-only-free and their co-infection-free for both existences and endemics equilibria by means of Lyapunov function. From our analysis, we have shown risk factor for getting COVID-19 after contracting malaria and risk factor for getting malaria after contracting COVID-19 in order to understand the dynamics and control of the two disease. It can be deduced from our simulations that, reducing the risk of malaria and COVID-19 by taking preventive measures will reduce the risk factor for getting COVID-19 after contracting malaria and will also reduce the risk factor for getting malaria after contracting COVID-19 even, to the point of extinction. The findings of our study suggest the significance of control techniques in reducing the prevalence of two diseases.

Declaration of competing interest

There are no conflicts of interest to declare.

Code Availability The code that support the findings of this study are available from the corresponding author upon reasonable request

Data availability

Data used to support the findings of this study are included in the article. The authors used a set of parameter values whose sources are from the literature as shown in Table 1.

Acknowledgement

All authors have read and agreed to the proofs of the manuscript.

References

[1] E. Mtisi, H. Rwezaura, J.M. Tchuenche, A mathematical analysis of malaria and tuberculosis co-dynamics, Discrete Contin. Dyn. Syst. Ser. B 12 (4) (2009) 827.
[2] Z. Mukandavire, A.B. Gumel, W. Garira, J.M. Tchuenche, Mathematical analysis of a model for HIV-malaria co-infection, Math. Biosci. Eng. 6 (2) (2009) 333.
[3] J.M. Tchuenche, C. Chiyaka, D. Chan, A. Matthews, G. Mayer, A mathematical model for antimalarial drug resistance, Math. Med. Biol.: J. IMA 28 (4) (2011) 335–355.
[4] WHO, World Malaria Report 2021, 2021, https://www.who.int/teams/global-malaria-programme/reports/world-malaria-report-2021, Online; accessed 02-February-2022.
[5] S.S. Nadim, J. Chattopadhyay, Occurrence of backward bifurcation and prediction of disease transmission with imperfect lockdown: A case study on COVID-19, Chaos Solitons Fractals 140 (2020) 110163.
[6] J.T. Wu, K. Leung, G.M. Leung, Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: A modelling study, Lancet 395 (10225) (2020) 689–697.
[7] Q. Li, X. Guan, P. Wu, X. Wang, L. Zhou, Y. Tong, R. Ren, K.S. Leung, E.H. Lau, J.Y. Wong, et al., Early transmission dynamics in Wuhan, China, of novel coronavirus–infected pneumonia, N. Engl. J. Med. (2020).
[8] L.-X. Feng, S.-L. Jing, S.-K. Hu, D.-F. Wang, H.-F. Huo, Modelling the effects of media coverage and quarantine on the COVID-19 infections in the UK, Math. Biosci. Eng. 17 (4) (2020) 3618–3636.
[9] H. Sharma, M. Mathur, S. Purohit, K. Owolabi, K. Nisar, Parameter estimation and early dynamics of COVID-19 disease, in: Proceedings of International Conference on Data Science and Applications: ICDSA 2021, Vol. 2, Springer, 2022, pp. 783–795.
[10] M. Park, A.R. Cook, J.T. Lim, Y. Sun, B.L. Dickens, A systematic review of COVID-19 epidemiology based on current evidence, J. Clin. Med. 9 (4) (2020) 967.
[11] D. Okuonghae, A. Omame, Analysis of a mathematical model for COVID-19 population dynamics in Lagos, Nigeria, Chaos Solitons Fractals 139 (2020) 110032.
[12] O.J. Peter, S. Qureshi, A. Yusuf, M. Al-Shomrani, A.A. Idowu, A new mathematical model of COVID-19 using real data from Pakistan, Results Phys. 24 (2021) 104098.
[13] M. Ayana, T. Hailegiorgis, K. Getnet, The impact of infective immigrants and self isolation on the dynamics and spread of COVID-19 pandemic: A mathematical modeling study, Pure Appl. Math. J. 9 (6) (2020) 109–117.
[14] C.T. Deressa, G.F. Duressa, Modeling and optimal control analysis of transmission dynamics of COVID-19: The case of Ethiopia, Alex. Eng. J. 60 (1) (2021) 719–732.
[15] A.I. Abioye, M.D. Umoh, O.J. Peter, H.O. Edogbanya, F.A. Oguntolu, O. Kayode, S. Amadiegwu, Forecasting of COVID-19 pandemic in Nigeria using real statistical data, Commun. Math. Biol. Neurosci. 2021 (2021) Article–ID.
[16] D.K. Mamo, Model the transmission dynamics of COVID-19 propagation with public health intervention, Results Appl. Math. 7 (2020) 100123.
[17] O.J. Peter, A.S. Shaikh, M.O. Ibrahim, K.S. Nisar, D. Baleanu, I. Khan, A.I. Abioye, Analysis and dynamics of fractional order mathematical model of COVID-19 in Nigeria using atangana-baleanu operator, Comput., Mater. Continua 66 (2) (2021) 1823–1848.
[18] K.G. Mekonen, T.G. Habtemicheal, S.F. Balcha, Modeling the effect of contaminated objects for the transmission dynamics of COVID-19 pandemic with self protection behavior changes, Results Appl. Math. 9 (2021) 100134.
[19] T.T. Ega, M.Y. Dawed, B.K. Gebremeskel, T.T. Tegegn, Mathematical model for estimating unconfirmed cases of COVID-19 in ethiopia, and targeting sensitive parameters, J. Math. Comput. Sci. 10 (6) (2020) 2853–2870.
[20] L. Lemecha Obsu, S. Feyissa Balcha, Optimal control strategies for the transmission risk of COVID-19, J. Biol. Dyn. 14 (1) (2020) 590–607.
[21] I.U. Haq, N. Ullah, N. Ali, K.S. Nisar, A new mathematical model of COVID-19 with quarantine and vaccination, Mathematics 11 (1) (2022) 142.
[22] M. Shoaib, A. Haider, M.A.Z. Raja, K.S. Nisar, Artificial intelligence knacks-based computing for stochastic COVID-19 SIRC epidemic model with time delay, Internat. J. Modern Phys. B 36 (26) (2022) 2250174.
[23] M.A. Noor, A. Raza, M.S. Arif, M. Rafiq, K.S. Nisar, I. Khan, S.F. Abdelwahab, Non-standard computational analysis of the stochastic COVID-19 pandemic model: An application of computational biology, Alex. Eng. J. 61 (1) (2022) 619–630.
[24] A.I. Abioye, M.O. Ibrahim, O.J. Peter, S. Amadiegwu, F.A. Oguntolu, Differential transform method for solving mathematical model of SEIR and SEI spread of malaria, Int. J. Sci.: Basic Appl. Res. (IJSBAR) 40 (1) (2018) 197–219.
[25] D. Khamis, C. El Mouden, K. Kura, M.B. Bonsall, Optimal control of malaria: combining vector interventions and drug therapies, Malar. J. 17 (1) (2018) 1–18.
[26] S. Olaniyi, K.O. Okosun, S.O. Adesanya, E.A. Areo, Global stability and optimal control analysis of malaria dynamics in the presence of human travelers, Open Infect. Dis. J. 10 (1) (2018).
[27] O. Koutou, B. Traoré, B. Sangaré, Mathematical modeling of malaria transmission global dynamics: taking into account the immature stages of the vectors, Adv. Difference Equ. 2018 (1) (2018) 1–34.
[28] A.A. Ayoade, O.J. Peter, A.I. Abioye, T.F. Aminu, O.A. Uwaheren, Application of homotopy perturbation method to an SIR mumps model, Adv. Math.: Sci. J. 9 (3) (2020) 329–1340.
[29] Z. Zhao, S. Li, Y. Lu, Mathematical models for the transmission of malaria with seasonality and ivermectin, Electron. J. Differential Equations 2022 (28) (2022).
[30] W.A. Woldegerima, R. Ouifki, J. Banasiak, Mathematical analysis of the impact of transmission-blocking drugs on the population dynamics of malaria, Appl. Math. Comput. 400 (2021) 126005.
[31] A.I. Abioye, O.J. Peter, A.A. Ayoade, O.A. Uwaheren, M.O. Ibrahim, Application of adomian decomposition method on a mathematical model of malaria, Adv. Math.: Sci. J. 9 (1) (2020) 417–435.
[32] E. Ndamuzi, P. Gahungu, Mathematical modeling of malaria transmission dynamics: case of Burundi, J. Appl. Math. Phys. 9 (10) (2021) 2447–2460.

[33] P. Wilairatana, F.R. Masangkay, K.U. Kotepui, G.D.J. Milanez, M. Kotepui, Prevalence and characteristics of malaria among COVID-19 individuals: A systematic review, meta-analysis, and analysis of case reports, PLoS Negl. Trop. Dis. 15 (10) (2021) e0009766.
[34] S. Tchoumi, M. Diagne, H. Rwezaura, J. Tchuenche, Malaria and COVID-19 co-dynamics: A mathematical model and optimal control, Appl. Math. Model. 99 (2021) 294–327.
[35] D.J. Weiss, A. Bertozzi-Villa, S.F. Rumisha, P. Amratia, R. Arambepola, K.E. Battle, E. Cameron, E. Chestnutt, H.S. Gibson, J. Harris, et al., Indirect effects of the COVID-19 pandemic on malaria intervention coverage, morbidity, and mortality in Africa: A geospatial modelling analysis, Lancet Infect. Dis. 21 (1) (2021) 59–69.
[36] E. Sherrard-Smith, A.B. Hogan, A. Hamlet, O.J. Watson, C. Whittaker, P. Winskill, T.S. Churcher, The potential public health consequences of COVID-19 on malaria in Africa, Lancet Infect. Dis. 26 (9) (2020) 1411–1416.
[37] S.J. Rogerson, J.G. Beeson, M. Laman, J.R. Poespoprodjo, T. William, J.A. Simpson, R.N. Price, Identifying and combating the impacts of COVID-19 on malaria, BMC Med. 18 (1) (2020) 1–7.
[38] A. Hogan, B. Jewell, E. Sherrard-Smith, O. Watson, C. Whittaker, A. Hamlet, J. Smith, P. Winskill, R. Verity, M. Baguelin, et al., Potential impact of the COVID-19 pandemic on HIV, TB and malaria in low-and middle-income countries: A modelling study, Lancet Global Health 8 (9) (2020) e1132–e1141.
[39] N. Sene, SIR epidemic model with Mittag–Leffler fractional derivative, Chaos Solitons Fractals 137 (2020) 109833.
[40] M.M. Raja, V. Vijayakumar, R. Udhayakumar, A new approach on approximate controllability of fractional evolution inclusions of order 1< r< 2 with infinite delay, Chaos Solitons Fractals 141 (2020) 110343.
[41] O.J. Peter, A. Yusuf, K. Oshinubi, F.A. Oguntolu, J.O. Lawal, A.I. Abioye, T.A. Ayoola, Fractional order of pneumococcal pneumonia infection model with Caputo fabrizio operator, Results Phys. 29 (2021) 104581.
[42] N.J. Vickers, Animal communication: when i'm calling you, will you answer too? Curr. Biol. 27 (14) (2017) R713–R715.
[43] C. Ravichandran, K. Munusamy, K.S. Nisar, N. Valliammal, Results on neutral partial integrodifferential equations using monch-krasnosel'skii fixed point theorem with nonlocal conditions, Fractal Fract. 6 (2) (2022) 75.
[44] K.S. Nisar, K. Logeswari, V. Vijayaraj, H.M. Baskonus, C. Ravichandran, Fractional order modeling the gemini virus in capsicum annuum with optimal control, Fractal Fract. 6 (2) (2022) 61.
[45] O.J. Peter, Transmission dynamics of fractional order brucellosis model using caputo–fabrizio operator, Int. J. Differ. Equ. Appl. 2020 (2020).
[46] T. Yuvaraj, K. Ravi, Multi-objective simultaneous DG and DSTATCOM allocation in radial distribution networks using cuckoo searching algorithm, Alex. Eng. J. 57 (4) (2018) 2729–2742.
[47] M. Farman, A. Akgül, K.S. Nisar, D. Ahmad, A. Ahmad, S. Kamangar, C.A. Saleel, Epidemiological analysis of fractional order COVID-19 model with Mittag-Leffler kernel, AIMS Math. 7 (1) (2022) 756–783.
[48] U. Ihtisham, A. Nigar, K.S. Nisar, An optimal control strategy and Grünwald-Letnikov finite-difference numerical scheme for the fractional-order COVID-19 model, Math. Model. Numer. Simul. Appl. 2 (2) (2022) 108–116.
[49] A.S. Shaikh, I.N. Shaikh, K.S. Nisar, A mathematical model of COVID-19 using fractional derivative: outbreak in India with dynamics of transmission and control, Adv. Difference Equ. 2020 (1) (2020) 373.
[50] K.M. Owolabi, A. Shikongo, Mathematical modelling of multi-mutation and drug resistance model with fractional derivative, Alex. Eng. J. 59 (4) (2020) 2291–2304.
[51] B. Karaagac, K.M. Owolabi, E. Pindza, A computational technique for the Caputo fractal-fractional diabetes mellitus model without genetic factors, Int. J. Dyn. Control (2023) 1–18.
[52] O.A. Arqub, B. Maayah, Numerical solutions of integrodifferential equations of Fredholm operator type in the sense of the Atangana–Baleanu fractional operator, Chaos Solitons Fractals 117 (2018) 117–124.
[53] O.A. Arqub, M. Al-Smadi, Atangana–Baleanu fractional approach to the solutions of Bagley–Torvik and Painlevé equations in Hilbert space, Chaos Solitons Fractals 117 (2018) 161–167.
[54] S. Momani, O. Abu Arqub, B. Maayah, Piecewise optimal fractional reproducing kernel solution and convergence analysis for the Atangana–Baleanu–Caputo model of the Lienard's equation, Fractals 28 (08) (2020) 2040007.
[55] S. Momani, B. Maayah, O.A. Arqub, The reproducing kernel algorithm for numerical solution of Van der Pol damping model in view of the Atangana–Baleanu fractional approach, Fractals 28 (08) (2020) 2040010.
[56] A. Atangana, D. Baleanu, New fractional derivatives with nonlocal and non-singular kernel: theory and application to heat transfer model, 2016, arXiv preprint arXiv:1602.03408.
[57] A.I. Abioye, M.O. Ibrahim, O.J. Peter, H.A. Ogunseye, Optimal control on a mathematical model of malaria, Sci. Bull., Ser. A: Appl. Math. Phys. (2020) 178–190.
[58] P. Van den Driessche, J. Watmough, Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission, Math. Biosci. 180 (1–2) (2002) 29–48.
[59] V. Lakshmikantham, S. Leela, A.A. Martynyuk, Stability Analysis of Nonlinear Systems, Author, 1989.
[60] A.I. Abioye, O.J. Peter, F.A. Oguntolu, A.F. Adebisi, T.F. Aminu, Global stability of seir-sei model of malaria transmission, Adv. Math., Sci. J. 9 (2020) 5305–5317.
[61] J. La Salle, S. Lefschetz, The Stability of Dynamical Systems, Author, 1976.
[62] O.J. Peter, A.F. Adebisi, M.O. Ajisope, F.O. Ajibade, A.I. Abioye, F.A. Oguntolu, Global stability analysis of typhoid fever model, Adv. Syst. Sci. Appl. 20 (2) (2020) 20–31.
[63] A.I. Abioye, O.J. Peter, H.A. Ogunseye, F.A. Oguntolu, K. Oshinubi, A.A. Ibrahim, I. Khan, Mathematical model of COVID-19 in Nigeria with optimal control, Results Phys. 28 (2021) 104598.
[64] M. Toufik, A. Atangana, New numerical approximation of fractional derivative with non-local and non-singular kernel: application to chaotic models, Eur. Phys. J. Plus 132 (10) (2017) 1–16.