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Analysis of Caputo fractional SEIR model for Covid-19 pandemic

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Abstract

In this paper, we study the spread of COVID-19 and its effect on a population through mathematical models. We propose a Caputo time-fractional compartmental model (SEIR) comprising the susceptible, exposed, infected and recovered population for the dynamics of the COVID-19 pandemic. The proposed nonlinear fractional model is an extension of a formulated integer-order COVID-19 mathematical model. The existence of a unique solution for the proposed model was shown by using basic concepts such as continuity and Banach's fixed-point theorem. The uniqueness and boundedness of the solutions of the proposed model are investigated. We calculate a central quantity in epidemiology called the basic reproduction number, R_0 by the concept of the next-generation matrices approach. The equilibrium points of the model are calculated and the local asymptotic stability for the derived disease-free equilibrium point is discussed.

Keywords: Time-fractional model, SEIR epidemic model, Covid-19, Banach fixed-point, Stability Analysis.
2022 MSC: 34A08, 26A33, 92D30, 34D20

1 Introduction

The name "corona virus," coined in 1968, is derived from the "corona" like or crown-like morphology observed for these viruses in the electron microscope. The families of this viruses are circulating among animals and sometimes can also be found in humans [3]. The novel corona virus (COVID-19) was initially identified in late December of 2019 in Wuhan, China. It is an infectious disease caused by severe acute respiratory syndrome corona virus 2 (SARS-CoV-2) a beta corona virus [15, 48]. COVID-19 also has similarities to the severe acute respiratory syndrome (SARS) of 2003 [49]. With SARS there were more than 8,000 cases and 774 deaths [49]. However, within 2 months of the COVID-19 outbreak, there were more than 82,000 cases and more than 2,800 deaths [49].

Most of the initial stages were usually incorporated to the wholesale Human seafood market, which also traded live animals. The continuing novel corona virus or SARS-CoV-2 epidemic has been declared a pandemic by the World Health Organization (WHO) on March 11, 2020 [19, 35, 45]. Novel corona virus has already exceeded the earlier records of two life-threatening outbreaks, namely Severe Acute Respiratory Syndrome Corona virus (SARS-CoV) and Middle East Respiratory Syndrome Corona virus (MERS-CoV), posing the major warning to the global public health and economy after the 2nd world war [42].

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With little information about this new virus, no known cure or effective therapies, and an incubation period of approximately 14 days, the virus rapidly spread globally [16]. The virus can be transmitted from an infected person to other people, through direct contact with handshakes and by touching surfaces contaminated with the disease, and then it affects parts of the body such as the eyes, nose and mouth [47]. Due to heavy mobility of human from continent to continent through air transportation, the disease has extremely spread throughout the world [51].

This communicable corona virus disease has traits like fever, dry cough, sore throat, breathlessness and fatigue [53]. While COVID-19 can be deadly, symptoms, however, vary greatly from person to person [17].

While some may experience mild symptoms such as fever, coughing, and shortness of breath, others may face more severe complications, including damage to the lungs, acute respiratory failure, or sometimes even death [30, 37]. Other symptoms may also include difficulty breathing, fatigue, muscle or body aches, headaches, loss of taste or smell, sore throat, congestion, a runny nose, nausea or vomiting, or diarrhea [17]. In addition, COVID-19 can have serious effects on anyone, but tends to have more serious effects on older people or people with compromised immune systems.

With both asymptomatic and symptomatic infectious carriers with a 14-day incubation period, high transmission rate, and high numbers of fatalities, COVID-19 is deadly and extremely hard to track and contain. At the beginning of the pandemic, the number of hospitalizations increased at an alarming level in multiple regions of the world [44, 26, 13].

To control the spread of the virus, governments worldwide started implementing non-pharmaceutical interventions. These included temporary closures of schools and non-essential businesses, the use of face masks, and social distancing while the world waited for a vaccine that could be used to minimize the spread of the virus [14, 50].

Although the spread of COVID-19 began to slow as a result of these new containment measures, the fight against the virus was far from over. Having a vaccine seems to be the only long-term solution that can stop the virus from devastating people's lives and the global economy further.

Researchers from fields such as epidemiology, genetics, and related fields have been working diligently since the disease outbreak to gain a thorough understanding of the virus's mechanism [27, 39, 8]. This helps medical teams understand how the virus spreads biologically, which can lead to the development of viable therapeutic treatments such as vaccines. On the other hand, mathematical models have been shown to be effective methods for imparting knowledge about the nature of infectious diseases. They also contribute insights to help develop optimal controls and facilitate non-pharmaceutical interventions to minimize the spread of a virus [30].

In other words, through epidemiological models we are able to get a better understanding of the disease, how it works, how to contain it, and how it can be cured. In fact, since the outbreak of COVID-19, numerous mathematical studies by fractional calculus have been carried out and provided predictions of the spreading of COVID-19 [7].

The study of disease dynamics has been made to models described by fractional differential equations, recently receive many attentions [5, 40, 34, 27, 32, 39]. Many biological problems have been modelled by fractional-order derivatives and various mathematical modelling have been proposed and analysed to explore the consequence of transmission dynamics of COVID-19 among population. The most essential property for using fractional order systems is their memory, history and non local effects which exist in many biological systems [23]. These effects can be seen as a hereditary property or a variety on strains and genomes of viruses, which is useful for epidemic model. In recent years, the fractional extensions of mathematical models of Corona virus are show the natural fact in a very systematic way. (see, for examples [5, 40, 34, 41, 7, 4, 1, 28, 8, 6, 10, 22]). Many researchers have been worked on the subject of Caputo fractional derivative. Mathematical models by fractional system of ordinary differential equations are used to simulate the transmission of corona virus [10, 22, 29, 18, 9, 36, 43, 52].

As identified by the World Health Organization (WHO), the mathematical models, mainly those formulated in a timely manner, can play a crucial role in allowing public health decision and policy makers with evidence based statistics [24, 31].

The progression of any outbreak depends on the infectivity of pathogens as well as the available uninfected individuals. For a novel infection, when the transmission dynamics of an epidemiological disease is unknown, mathematical models play a crucial role to estimate the worst and best scenarios [2, 11].

It can also aid in estimating the effect of precautionary measures adopted against disease. With preventive techniques, the main object is to preserve the basic reproduction number R_0 below 1, to control further development of infection, whereas in a mitigation policy, the main object is indelicate the effect of outbreak [25].

The structure of the paper is organized as follows: In Section 2, we give the essential preliminary results and definitions from fractional calculus. Section 3 is devoted to the formulation of the SEIR model of Caputo fractional order for Covid-19 transmission by considering four compartments: Susceptible-Exposed- Infected and Recovered

populations. In Section 4, the properties and theoretical analysis of the proposed model such as existence and uniqueness of the solution to the proposed model and positivity and boundedness of solutions are investigated. In Section 5, the basic reproduction number R_0 and the equilibrium points are calculated. Also the stability analysis of the disease-free equilibrium point is analysed therein. Conclusions are included in Section 6.

2 Preliminaries

In this section, preliminary definitions and results in fractional calculus are given.

2.1 Definition

For any t¿0, the Caputo-fractional derivative of order α, $(n < \alpha \leq n-1, n \in N)$ of function $f(t)$ is defined as [12]:

$$ {}_{t_0}D_t^{\alpha} f(t) = \frac{1}{\Gamma(\tau - \alpha)} \int_{t_0}^{t} (t-\tau)^{n-\alpha-1} f^{(n)}(\tau) d\tau, $$

where $\Gamma(.)$ is gamma function.

2.2 Definition

The two parameter Mittag-Leffler function is defined as [38]:

$$ E_{\alpha,\beta}(z) = \sum_{\kappa=0}^{\alpha} \frac{z^{\kappa}}{\Gamma(\alpha\kappa + \beta)}, \qquad \alpha \in \mathbb{R}^t, \beta \in \mathbb{R}^t, z \in \mathbb{C} $$

Remark 2.1. The Mittag-Leffler function has the following preperties

1. $E_{\alpha,\beta}(z) = zE_{\alpha,\alpha+\beta}(z) + \frac{1}{\Gamma(\beta)}$
2. ${}_0D_t^{\alpha} e^{\lambda t} = t^{-\alpha} E_{1,1-\alpha}(\lambda t)$
3. ${}_0D_t^{\alpha} E_{\alpha,1}(\lambda t^{\alpha}) = \lambda E_{\alpha,1}(\lambda t^{\alpha})$

3 Fractional Model Formulation

In this section, we consider the fractional order $SEIR$ model to study the spread of corona virus on a population. Here, S, E, I and R represent the susceptible, exposed, infected and recovered compartments, respectively. The model is designed based on the following assumptions.

(i) The size of the total population remains constant.

(ii) Susceptible individuals are recruited into the S compartment at a constant rate Λ.

(iii) The transmission rate from an exposed person to a susceptible is β_1 and the transmission rate from an infectious person to susceptible person is β_2. Also, we assume that $\beta_1 < \beta_2$.

(iv) The transmission rate from an exposed compartment to the infected compartment is γ and the transmission rate from exposed compartment to recovered compartment is σ.

(v) The transmission rate from an infectious person to recovered person is κ. Some people in infectious compartment perish by the virus at the rate δ.

(vi) Recoveries are assume to be permanent.

(vii) Natural morality occur in all compartment at the rate μ.

(viii) All parameters in this model are positive.

By given the above assumptions, we propose a fractional order model using the following system of $oDEs$

$$\begin{cases} {}_0D_t^\alpha S(t) &= \Lambda - \beta_1 S(t)E(t) - \beta_2 S(t)I(t) - \mu S(t) \\ {}_0D_t^\alpha E(t) &= \beta_1 S(t)E(t) + \beta_2 S(t)I(t) - \gamma E(t) - \sigma E(t) - \mu E(t) \\ {}_0D_t^\alpha I(t) &= \gamma E(t) - \kappa I(t) - \sigma I(t) - \mu I(t) \\ {}_0D_t^\alpha R(t) &= \sigma E(t) + \kappa I(t) - \mu R(t) \end{cases} \tag{3.1}$$

The system has the associated initial conditions $S(0) = S_0 > 0, E(0) = E_0 > 0, I(0) = I_0 > 0$ and $R(0) = R_0 > 0$. The operator ${}_0D_t^\alpha$ denotes Caputo-fractional derivative of order $0 < \alpha \leq 1$. The diagram for the proposed model is shown in figure 1.

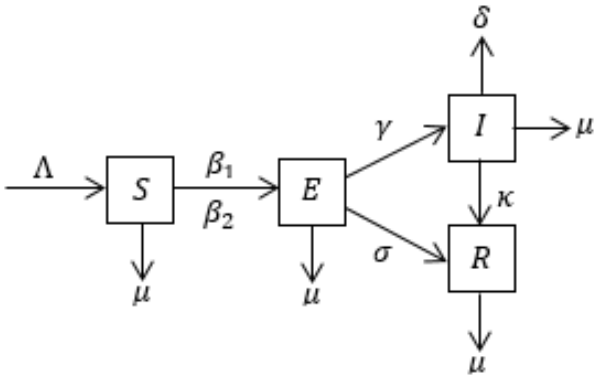

Figure 1: The diagram of $SEIR$ model

4 Qualitative Analysis of the Model

In this section, we study the mathematical and biological properties of the fractional order model. The analysis of the model includes the existence, uniqueness, positivity and boundedness of the solutions of the model (3.1).

4.1 Positivity and Boundedness of Solution

Since the fractional-order model (3.1) to be biologically well-posed, its solution is expected to be positive and bounded at all time.

Theorem 4.1. There exist a unique solution to the system (3.1) and the solution is positive and bounded for any given initial conditions $(S_0, E_0, I_0, R_0) \geq 0 \in \mathbb{R}^4$.

Proof . By applying [33], we prove the existence of the solutions. To show the uniqueness and boundedness of solution, it sufficient to show by [33], if $X(t) = (S, E, I, R)^T$ and $K(t, X(t) = (\phi_1, \phi_2, \phi_3, \phi_4)^T$, the $K(t, X(t))$ is locally Lipschitz continuous where

$$\begin{aligned} \phi_1 &= \Lambda - \beta_1 S(t)E(t) - \beta_2 S(t)I(t) - \mu S(t), \\ \phi_2 &= \beta_1 S(t)E(t) + \beta_2 S(t)I(t) - \gamma E(t) - \sigma E(t) - \mu E(t), \\ \phi_3 &= \gamma E(t) - \kappa I(t) - \sigma I(t) - \mu I(t), \\ \phi_4 &= \sigma E(t) + \kappa I(t) - \mu R(t). \end{aligned}$$

Let $\overline{X}(t) = (\overline{S}, \overline{E}, \overline{I}, \overline{R})^T$ and $\|.\|$ denotes the L_α norm,then

$$\|K(t, X(t)) - K(t, \overline{X}(t))\| \leq L_K \|X - \overline{X}\|$$

and

$$\begin{aligned}&\|K(t,X(t))-K(t,\overline{X}(t))\|\leq\|\phi_1(t,X(t))-\phi_1(t,\overline{X}(t))\|+\|\phi_2(t,X(t))-\phi_2(t,\overline{X}(t))\|\\&+\|\phi_3(t,X(t))-\phi_3(t,\overline{X}(t))\|+\|\phi_4(t,X(t))-\phi_4(t,\overline{X}(t))\|\\&\leq L_1\|X-\overline{X}\|+L_2\|X-\overline{X}\|+L_3\|X-\overline{X}\|+L_4\|X-\overline{X}\|\leq L_K\|X-\overline{X}\|\end{aligned}$$

where $L_K=\max_{1\leq i\leq 4}L_i$ and $L_1=\beta_1+\beta_2+\mu, L_2=\beta_1+\beta_2+\gamma+\sigma, L_3=\gamma+\kappa+\delta+\mu$ and $L_4=\sigma+\kappa+\mu$. Thus K satisfies the local Lipschitz conditions with respect to X, which proves the uniqueness and boundedness of solution.

Now, we prove the positivity of solutions. We start by considering the trajectory of solution along the S-axis where $E(0)=I(0)=R(0)$ and $0<S(0)=S_0\leq N$, then ${}_0D_t^\alpha S(t)=\Lambda-\mu S, S(0)=S_0$, where solution is given by

$$S(t)=S_0E_\alpha(-\mu t^\alpha)+\frac{\Lambda}{\mu}(1-E_\alpha(-\mu t^\alpha))>0$$

since $\Lambda>0$ and $t>0$. In a similar manner, moving along each of the other respective axis yield

$$\begin{aligned}E(t)&=E_0E_\alpha(-(\gamma+\sigma+\mu)t^\alpha)>0,\\I(t)&=I_0E_\alpha(-(\kappa+\delta+\mu)t^\alpha)>0,\\R(t)&=R_0E_\alpha(-\mu t^\alpha)>0,\end{aligned}$$

showing non-negative invariance of the axes. Now, since the solution to the model (3.1) is positive in the $E-I-R$ plane, let $S(t^*)=0$ for $t^*>0$ and $E(t^*)>0$, $I(t^*)>0$, $R(t^*)>0$ and $S(t)<S(t^*)$. On this plane,

$${}_0D_t^\alpha S(t)\mid_{t=t^*}=\Lambda>0 \tag{4.1}$$

By Caputo-fractional mean value theorem [12], it holds $S(t)-S(t^*)=\frac{1}{\Gamma(\alpha)}\,{}_0D_t^\alpha(\tau)(t-t^*)^\alpha, \tau\in[t^*,t]$. Therefore, using equation (4.1) we obtain $S(t)>S(t^*)$, contradicting our assumption for t^*. Thus, any solution $S(t)$ is non-negative for all $t\geq 0$. Other variables can be treated similarly. Hence, solution $X(t)$ remains positive for all $t\geq 0$.

Finally for boundedness, using the fact that $N(t)=S(t)+E(t)+I(t)+R(t)$, it follows from (3.1) that

$$\begin{aligned}{}_0D_t^\alpha N(t)&={}_0D_t^\alpha S(t)+{}_0D_t^\alpha E(t)+{}_0D_t^\alpha I(t)+{}_0D_t^\alpha R(t)\\&=\Lambda-\mu(S(t)+E(t)+I(t)+R(t))-\delta I(t)\\&\leq\Lambda-\mu N.\end{aligned}$$

Thus considering the initial value problem ${}_0D_t^\alpha N(t)=\Lambda-\mu N$, $N(0)=N_0$, and invoking comparison theorem, it follows that

$$N(t)\leq N_0E_\alpha(-\mu t^\alpha)+\frac{\Lambda}{\mu}(1-E_\alpha(-\mu t^\alpha)),$$

and consequently

$$\limsup_{t\to\alpha}N(t)\leq\frac{\Lambda}{\mu}$$

□

5 Stability Analysis

5.1 Equilibria and computation of the basic reproduction number R_0

By setting the left hand side of equation (4.1) to zero, one can obtain the equilibria points. Disease-free equilibrium (DFE) points are these where $I=0$. These immediately imply $E=0$ and $R=0$. Thus, we obtain $\Lambda-\mu S^*=0$ or $S^*=\frac{\Lambda}{\mu}$. Consequently, the DFE point of the fractional model is $\mathrm{Y}^0=(S^0,E^0,I^0,R^0)=(\frac{\Lambda}{\mu},0,0,0)$.

The dynamics and stability of a disease model are governed by the basic reproduction number R_0. It determines the spread a otherwise of the infection into the entire population. The approach to compute the R_0 is based on

next-generation matrices [20, 46, 21]. Now, following the next-generation matrix technique, we consider the two compartments $\mathrm{Y} = (\mathrm{Y}_1, \mathrm{Y}_2) = (E, I)$ containing the infected individuals. We consider the following subsystem

$$
\begin{aligned}
{}_0D_t^{\alpha} E(t) &= \beta_1 S(t)E(t) + \beta_2 S(t)I(t) - \gamma E(t) - \sigma E(t) - \mu E(t),\\
{}_0D_t^{\alpha} I(t) &= \gamma E(t) - \kappa I(t) - \delta I(t) - \mu I(t).
\end{aligned}
$$

The equations can be written in the form ${}_0D_t^{\alpha}\mathrm{Y}_i = \mathrm{F}_i(\mathrm{Y}) - \mathrm{V}_i(\mathrm{Y})$ for $i = 1, 2$, where $\mathrm{F}_i(\mathrm{Y})$ is the rate of appearance of new infections in compartment i, and $\mathrm{V}_i(\mathrm{Y})$ is the rate of other transitions between compartment i and other infected compartments. Then

$$
\begin{aligned}
\mathrm{F}_1 &= \beta_1 S(t)E(t) + \beta_2 S(t)I(t),\\
\mathrm{F}_2 &= 0,
\end{aligned}
$$

and

$$
\begin{aligned}
\mathrm{V}_1 &= \gamma E(t) + \sigma E(t) + \mu E(t),\\
\mathrm{V}_2 &= -\gamma E(t) + \kappa I(t) + \delta I(t) + \mu I(t).
\end{aligned}
$$

Next, we further define

$$
\mathbf{F} = \left[\frac{\partial \mathrm{F}_i(\mathrm{Y})}{\partial \mathrm{Y}_j}\right] \qquad \textit{and} \qquad \mathbf{V} = \left[\frac{\partial \mathrm{V}_i(\mathrm{Y})}{\partial \mathrm{Y}_j}\right], \qquad i, j = 1, 2,
$$

then, the matrices $\mathbf{F}$ and $\mathbf{V}$ evaluated at the disease free equilibrium point are

$$
\begin{aligned}
\mathbf{F} &= \begin{bmatrix} \dfrac{\partial \mathrm{F}_1}{\partial E} & \dfrac{\partial \mathrm{F}_1}{\partial I} \\[2ex] \dfrac{\partial \mathrm{F}_2}{\partial E} & \dfrac{\partial \mathrm{F}_2}{\partial I} \end{bmatrix} = \begin{bmatrix} \beta_1 S^0 & \beta_2 S^0 \\ 0 & 0 \end{bmatrix},\\
\mathbf{V} &= \begin{bmatrix} \dfrac{\partial \mathrm{V}_1}{\partial E} & \dfrac{\partial \mathrm{V}_1}{\partial I} \\[2ex] \dfrac{\partial \mathrm{V}_2}{\partial E} & \dfrac{\partial \mathrm{V}_2}{\partial I} \end{bmatrix} = \begin{bmatrix} \gamma + \sigma + \mu & 0 \\ -\gamma & \kappa + \delta + \mu \end{bmatrix} = \begin{bmatrix} k_1 & 0 \\ -\gamma & k_2 \end{bmatrix},
\end{aligned}
$$

where $k_1 = \gamma + \sigma + \mu$ and $k_2 = \kappa + \delta + \mu$. Then $\rho(\mathbf{F}\mathbf{V}^{-1})$ is the basic reproduction number R_0, where $\rho(x)$ is the spectral radius of x and $\mathbf{F}\mathbf{V}^{-1}$ is the next-generation matrix. Thus, the basic reproduction number is $R_0 = \dfrac{\beta_1}{k_1}S^0 + \dfrac{\beta_2 \gamma}{k_1 k_2}S^0$ or

$$
R_0 = \frac{1}{\gamma + \sigma + \mu}\beta_1 S^0 + \frac{\gamma}{\gamma + \sigma + \mu}\frac{1}{\kappa + \delta + \mu}\beta_2 S^0. \tag{5.1}
$$

Here, $\beta_1 S^0$ is the contraction rate of the virus of S^0 susceptible persons from on exposed person, $\dfrac{1}{\gamma + \sigma + \mu}$ is the meantime in compartment E. In addition, $\beta_2 S^0$ is the contraction rate of the virus of S^0 susceptible from an infectious individual, $\dfrac{\gamma}{\gamma + \sigma + \mu}$ is the fraction progressing from compartment E to I, and $\dfrac{1}{\kappa + \delta + \mu}$ is the meantime in compartment I. Thus R_0 is the expected number of secondary infectious produced in compartment E by an exposed person or an infectious.

5.2 Endemic Equilibrium Point

The endemic equilibrium point denoted as $\mathrm{Y}^* = (S^*, E^*, I^*, R^*)$, where the disease persists in the population. For the endemic equilibrium we consider $I^* \neq 0, E^* \neq 0$ and $R^* \neq 0$. The solution of system (3.1) is

$$\begin{aligned}
S^* &= \frac{\Lambda}{\beta_1 E^* + \beta_2 I^* + \mu}, \\
E^* &= \frac{\Lambda\beta_1 + \Lambda\beta_2 \dfrac{\gamma}{k_1} - k_1\mu}{k_1\beta_1 + k_1\beta_2 \dfrac{\gamma}{k_2}}, \\
I^* &= \frac{\gamma}{k_2}\left[\frac{\Lambda\beta_1 + \Lambda\beta_2 \dfrac{\gamma}{k_2} - k_1\mu}{k_1\beta_1 + k_1\beta_2 \dfrac{\gamma}{k_2}}\right], \\
R^* &= \frac{1}{\mu}\left[\sigma E^* + \kappa I^*\right].
\end{aligned}$$

The endemic point can be written in terms of R_0, as follows

$$\begin{aligned}
S^* &= \frac{\Lambda}{\mu}\frac{1}{R_0}, \\
E^* &= \frac{\Lambda}{k_1}\left(1 - \frac{1}{R_0}\right), \\
I^* &= \frac{\gamma}{k_2}\frac{\Lambda}{k_1}\left(1 - \frac{1}{R_0}\right), \\
R^* &= \frac{\Lambda}{\mu}\frac{1}{k_1}\left(\sigma + \frac{k_1\gamma}{k_2}\right)\left(1 - \frac{1}{R_0}\right).
\end{aligned}$$

By the above equations, the endemic equilibrium point exists only when $R_0 > 1$. When $R_0 < 1$, this point become biologically irrelevant.

5.3 Stability

Theorem 5.1. The DFE point $\mathrm{Y} = (S^0, E^0, I^0, R^0) = \left(\dfrac{\Lambda}{\mu}, 0, 0, 0\right)$ is locally asymptotically stable if $R_o < 1$ and is unstable if $R_0 > 1$.

Proof . The Jacobian matrix evaluated at the DFE point is given as

$$\mathbf{V} = \begin{bmatrix} -\mu & -\beta_1 S^0 & -\beta_2 S^0 & 0 \\ 0 & \beta_1 S^0 - k_1 & \beta_2 S^0 & 0 \\ 0 & \gamma & -k_2 & 0 \\ 0 & \sigma & k_1 & -\mu \end{bmatrix}.$$

The eigenvalues of the Jacobian matrix are given as $\lambda_1 = -\mu < 0$ and the roots of the equation

$$\lambda^2 + \lambda(k_1 + k_2 - \beta_1 S^0) + k_1 k_2 - \beta_1 S^0 k_2 - \beta_2 S^0 \gamma = 0$$

where

$$\lambda_{2,3} = \frac{1}{2}\left[-(k_1 + k_2 - \beta_1 S^0) \pm \sqrt{(k_1 + k_2 - \beta_1 S^0)^2 - 4(k_1 k_2 - \beta_1 S^0 k_2 - \beta_2 S^0 \gamma)}\right].$$

To show that there are real eigenvalues we need to prove that $\Delta \geq 0$. That is

$$\begin{aligned}
\Delta &= (k_1 + k_2 - \beta_1 S^0)^2 - 4(k_1 k_2 - \beta_1 S^0 k_2 - \beta_2 S^0 \gamma), \\
&= (k_1 - k_2)^2 - 2k_1\beta_1 S^0 + 2\beta_1 S^0 k_2 + (\beta_1 S^0)^2 + 4\beta_2 S^0 \gamma, \\
&= (k_1 - k_2)^2 - 2(k_1 - k_2)\beta_1 S^0 + (\beta_1 S^0)^2 + 4\beta_2 S^0 \gamma, \\
&= [(k_1 - k_2) - \beta_1 S^0]^2 + 4\beta_2 S^0 \gamma > 0.
\end{aligned}$$

Since all the parameters are assumed to be positive, the eigenvalues λ_2, λ_3 are distinct real eigenvalues. $\lambda_{2,3} = -(k_1 + k_2 - \beta_1 S^0) \pm \sqrt{\Delta}$.

Finally, we show that λ_2 and λ_3 are negative eigenvalues when $R_0 < 1$. Suppose that $\lambda_2 < 0$, we have

$$
\begin{aligned}
&-(k_1 + k_2 - \beta_1 S^0) + \sqrt{\Delta} > 0,\\
&\sqrt{\Delta} > (k_1 + k_2 - \beta_1 S^0),\\
&(k_1 + k_2 - \beta_1 S^0)^2 - 4(k_1 k_2 - \beta_1 S^0 k_2 - \beta_2 S^0 \gamma) > (k_1 + k_2 - \beta_1 S^0)^2,\\
&-4(k_1 k_2 - \beta_1 S^0 k_2 - \beta_2 S^0 \gamma) > 0,\\
&1 - \frac{\beta_1 S^0}{k_1} - \frac{\beta_2 S^0 \gamma}{k_1 k_2} < 0,\\
&R_0 > 1.
\end{aligned}
$$

So, the DFE is unstable when $R_0 > 1$. □

6 Conclusions

In this work, the SEIR epidemic compartmental model is proposed to the study of transmission of COVID-19 using the Caputo fractional derivative based on the integer order model. The existence of a unique solution for the model by using Banach fixed-point theory has been proved. The basic reproduction number R_0 of the model was computed by the concept of next-generation matrices method and the equilibrium points of the model have been calculated. The model qualitative analysis reconfirm local stability at the disease free equilibrium point for the fractional-order model, whenever the threshold condition $R_0¡ 1$ holds.

For future research efforts in this direction, we can consider the following improvements of the present work:

- extension of the model capture stochastic dynamics;
- parameter estimation of model parameters, including the order of the fractional derivative, based on the available data on COVID-19 and the impact of vaccination process.

References

[1] R.P. Agarwal, D. Baleanu, V. Hedayati, and S. Rezapour, *Two fractional derivative inclusion problems via integral boundary conditions*, Appl. Math. Comput. **257** (2015), 205—212.

[2] L.J. Allen, F. Brauer, P. van den Driessche, and J. Wu, *Mathematical epidemiology*, Volume 1945. Springer, 2008.

[3] A. Al-Jabir, A. Kerwan, M. Nicola, Z. Alsafi, M. Khan, C. Sohrabi, N. O'Neill, C. Iosifidis, M. Griffin, G. Mathew, and R. Agha, *Impact of the coronavirus (covid-19) pandemic on surgical practice-part 2 (surgical prioritisation)*, Int. J. Surgery **79** (2020), 233–248.

[4] A. Alsaedi, D. Baleanu, S. Etemad, and S. Rezapour, *On coupled systems of time-fractional differential problems by using a new fractional derivative*, J. Funct. Spaces **2016** (2016), Article ID 4626940.

[5] H. Al-Sulami, M. El-Shahed, and J.J. Nieto, *On fractional order dengue epidemic model*, Math. Probl. Eng. **4** (2014), 1–6.

[6] D. Baleanu, R.P. Agarwal, H. Mohammadi, and S. Rezapour, *Some existence results for a nonlinear fractional differential equation on partially ordered Banach spaces*, Bound. Value Probl. **2013** (2013), 112.

[7] E. Baleanu, S. Etemad, and S. Rezapour, *On a fractional hybrid integro-differential equation with mixed hybrid integral boundary value conditions by using three operators*, Alex. Eng. J. **59** (2020), no. 5, 3019–3027.

[8] D. Baleanu, V. Hedayati, S. Rezapour, and M.M. Al-Qurashi, *On two fractional differential inclusions*, SpringerPlus **5** (2016), no. 1, 882.

[9] D. Baleanu, H. Mohammadi, and S. Rezapour, *A fractional differential equation model for the COVID-19 transmission by using the Caputo–Fabrizio derivative*, Adv. Differ. Equ. **2020** (2020), 299.

[10] D. Baleanu, A. Mousalou and S. Rezapour, *On the existence of solutions for some infinite coefficient-symmetric Caputo–Fabrizio fractional integro-differential equations*, Bound. Value Probl. **2017** (2017), 145.

[11] F. Brauer, *Mathematical epidemiology: Past, present, and future*, Infect. Disease Model. **2** (2017), no. 2, 113–127.

[12] M. Caputo, *Linear model of dissipation whose q is almost frequency independent, II*, Geophys. J. Int. **13** (1967), no. 5, 529—539.

[13] L. Carenzo, E. Costantini, M. Greco, F. Barra, V. Rendiniello, M. Mainetti, R. Bui, A. Zanella, G. Grasselli, M. Lagioia, and A. and Protti, *Hospital surge capacity in a tertiary emergency referral centre during the COVID-19 outbreak in Italy*, Anaesthesia **75** (2020), no. 7, 928–934.

[14] Centers for Disease Control and Prevention, Trends in COVID-19 Incidence After Implementation of Mitigation Measures — Arizona, January 22-August 7, 2020. https://www.cdc.gov/ mmwr/volumes/69/wr/mm6940e3.htm, 2020. Accessed: 2021-03-20.

[15] Centers for Disease Control and Prevention, About COVID-19. https://www.cdc.gov/ coronavirus/2019-ncov/cdcresponse/about-COVID-19.html, 2020. Accessed: 2021-03-20.

[16] Centers for Disease Control and Prevention, Interim Clinical Guidance for Management of Patients with Confirmed Coronavirus Disease (COVID-19). https://www.cdc.gov/ coronavirus/2019-ncov/hcp/clinical-guidance-management-patients.html, 2021. Accessed: 2021-03-20.

[17] Centers for Disease Control and Prevention, https://www.cdc.gov/coronavirus/2019- ncov/symptoms-testing/symptoms.html. https://www.cdc.gov/coronavirus/2019-ncov/symptoms-testing/symptoms.html, 2021. Accessed: 2021-03-20.

[18] T. Chen, J. Rui, Q. Wang, Z. Zhao, J.A. Cui, and L. Yin, *A mathematical model for simulating the transmission of Wuhan novel coronavirus*, Infect. Dis. Poverty **9** (2020), 24.

[19] D. Cucinotta and M. Vanelli, *Who declares covid-19 a pandemic*, Acta Bio Medica: Atenei Parmensis **91** (2020), no. 1, 157.

[20] O. Diekmann, J. Heesterbeek, and J. Metz, *On the definition and the computation of the basic reproduction ratio R_0 in models for infectious diseases in heterogeneous populations*, J. Math. Biol. **28** (1990), 365-–382.

[21] O. Diekmann, J.A.P. Heesterbeek, and M.G. Roberts, *The construction of next-generation matrices for compartmental epidemic models*, J. R. Soc. Interface **7** (2010), no. 47, 873–885.

[22] A. Dighe, T. Jombart, M.V. Kerkhove, and N. Ferguson, *A mathematical model of the transmission of middle east respiratory syndrome corona virus in dromedary camels (camelus dromedarius)*, Int. J. Infect. Dis. 79 (2019), no. S1, 1-–150.

[23] M. Du, Z. Wang, and H. Hu, *Measuring memory with the order of fractional derivative*, Sci. Rep. **3** (2013), 3431.

[24] M. Egger, L. Johnson, C. Althaus, A. Schöni, G. Salanti, N. Low, and S.L. Norris, *Developing who guidelines: time to formally include evidence from mathematical modelling studies*, F1000Research **6** (2017), 1584.

[25] N. Ferguson, D. Laydon, G. Nedjati Gilani, N. Imai, K. Ainslie, M. Baguelin, S. Bhatia, A. Boonyasiri, Z.U.L.M.A. Cucunuba Perez, G. Cuomo-Dannenburg, and A. Dighe, *Report 9: Impact of non-pharmaceutical interventions (npis) to reduce covid19 mortality and healthcare demand*, Imperial College COVID-19 Response Team, 16 March 2020.

[26] S.M. Garba, J.M.-S. Lubuma, and B. Tsanou, *Modeling the transmission dynamics of the covid-19 pandemic in South Africa*, Mathematical Biosci. **328** (2020), 108441.

[27] F. Haq, K. Shah, G. Rahman, and M. Shahzad, *Numerical analysis of fractional order model of HIV-1 infection of CD4+ T-cells*, Comput. Meth. Differ. Equ. **5** (2017), no. 1, 1—11.

[28] V. Hedayati and S. Rezapour, *The existence of solution for a k-dimensional system of fractional differential inclusions with anti-periodic boundary value problems*, Filomat **30** (2016), no. 6, 1601-–1613.

[29] M. Higazy, *Novel fractional order SIDARTHE mathematical model of COVID-19 pandemic*, Chaos Solitons Fractals **138** (2020), 110007.

[30] E.A. Iboi, C.N. Ngonghala, and A.B. Gumel, *Will an imperfect vaccine curtail the covid-19 pandemic in the us?*,

Infect. Disease Model. **5** (2020), 510–524.

[31] S. Khajanchi, D.K. Das, and T.K. Kar, *Dynamics of tuberculosis transmission with exogenous reinfections and endogenous reactivation*, Phys. A: Statist. Mech. Appl. **497** (2018), 52—71.

[32] I. Koca, *Analysis of rubella disease model with non-local and non-singular fractional derivatives*, Int. J. Optim. Control Theor. Appl. **8** (2018), no. 1, 17-–25.

[33] W. Lin, *Global existence theory and chaos control of fractional differential equations*, J. Math. Anal. Appl. **332** (2007), no. 1, 709—726.

[34] F. Ndaïrou, I. Area, J.J. Nieto, C.J. Silva, and D.F.M. Torres, *Fractional model of COVID-19 applied to Galicia, Spain and Portugal*, Chaos Solitons Fractals **144** (2021), 110652.

[35] F. Ndaïrou, I. Area, J.J. Nieto, and D.F. Torres, *Mathematical modeling of covid-19 transmission dynamics with a case study of Wuhan*, Chaos Solitons Fractals **135** (2010), 109846.

[36] M. Naveed, M. Rafiq, A. Raza, N. Ahmed, I. Khan, K.S. Nisar, and A.H. Soori, *Mathematical analysis of novel Coronavirus (2019-ncov) delay pandemic model*, Comput. Mater. Continua **64** (2020), no. 3, 1401—1414.

[37] N. Ngonghala, E. Iboi, S. Eikenberry, M. Scotch, C.R. MacIntyre, M.H. Bonds, and A.B. Gumel, *Mathematical assessment of the impact of non-pharmaceutical interventions on curtailing the 2019 novel coronavirus*, Math. Biosci. **325** (2020), 108364.

[38] I. Podlubny, *Fractional differential equations*, Mathematics in Science and Engineering, 198, Academic Press, 1999.

[39] S.Z. Rida, A.A.M. Arafa, and Y.A. Gaber, *Solution of the fractional epidemic model by l-adm*, J. Fract. Calc. Appl. **7** (2016), no. 1, 189—195.

[40] S. Rosa and D.F.M. Torres, *Optimal control and sensitivity analysis of a fractional order TB model*, Stat. Optim. Inf. Comput. **7** (2019), 617—625.

[41] M.E. Samei and S. Rezapour, *On a system of fractional q-differential inclusions via sum of two multi-term functions on a time scale*, Bound. Value Probl. **2020** (2020), 135.

[42] P. Samui, J. Mondal, and S. Khajanchi, *A mathematical model for covid-19 transmission dynamics with a case study of india*, Chaos Solitons Fractals **140** (2020), 110173.

[43] A.S. Shaikh, V.S. Jadhav, M.G. Timol, K.S. Nisar, and I. Khan, *Analysis of the covid-19 pandemic spreading in India by an epidemiological model and fractional differential operator*, Preprints 2020050266 (2020). https://doi.org/10.20944/preprints202005.0266.v1

[44] J.E. Tonna, H.A. Hanson, J.N. Cohan, M.L. McCrum, J.J. Horns, B.S. Brooke, R. Das, B.C. Kelly, A.J. Campbell, and J. Hotaling, *Balancing revenue generation with capacity generation: case distribution, nancial impact and hospital capacity changes from cancelling or resuming elective surgeries in the us during covid-19*, BMC Health Services Res. **20** (2020), no. 1, 1–7.

[45] J. Turner-Musa, O. Ajayi, and L. Kemp, *Examining social determinants of health, stigma, and covid-19 disparities*, Healthcare **8** (2020), 168.

[46] P. van den Driessche and J. Watmough, *Reproduction numbers and sub-threshold endemic equilibria for compartmental models of disease transmission*, Math. Biosci. **180** (2002), no. 1, 29—48.

[47] K. Verma, S.C. Sivastava, K. Attur, and A. Kubavat, *Rationale for infection control and its applicability in dental clinics-an overview*, Nat. J. Integ. Res. Med. **11** (2020), no. 4.

[48] C. Wang, P.W. Horby, F.G. Hayden, and E.F. Gao, *A novel coronavirus outbreak of global health concern, Lancet*, **395** (2020), no. 10223, 470—473.

[49] A. Wilder-Smith, C.J. Chiew, and V.J. Lee, *Can we contain the covid-19 outbreak with the same measures as for sars?*, Lancet Infect. Diseases **20** (2020), no. 5, 102–107.

[50] Y. Zhang, B. Jiang, J. Yuan, and Y. Tao, *The impact of social distancing and epicenter lockdown on the covid-19 epidemic in mainland china: A data-driven SEIQR model study*, MedRxiv, 2020, Doi: 10.1101/2020.03.04.20031187.

[51] Y. Zheng, E. Goh, and J. Wen, *The effects of misleading media reports about covid-19 on chinese tourists' mental health: A perspective article*, Anatolia **31** (2020), no. 2, 337-–340.

[52] Y. Zhou, Z. Ma, and F. Brauer, *A discrete epidemic model for SARS transmission and control in China*, Math. Comput. Model. **40** (2004), no. 13, 1491—1506.

[53] L. Zou, F. Ruan, M. Huang, L. Liang, H. Huang, Z. Hong, J. Yu, M. Kang, Y. Song, J. Xia, and Q. Guo, *Sars-cov-2 viral load in upper respiratory specimens of infected patients*, New England J. Med. **382** (2020), no. 2, 1177—1179.