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On the Positivity and Stability Analysis of Conformable Fractional COVID-19 Models

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Abstract: In this paper, we present a novel nonlinear fractional conformable SEIR compartmental model with a vaccination compartment. This SEIHRDV model is one of the next generation models that better explores nonlinear disease behaviour. The main aim of this study is to test when such a model is locally asymptotically stable, respectively, globally asymptotically stable around its equilibrium points: the disease-free state X_0 and the endemic state X_1. To achieve this, we introduce the Sumudu transform as an innovative integral approach to solve the differential equations, compute the basic reproduction number R_0, and construct a Lyapunov function to rigorously establish the stability conditions. Numerical solutions are then obtained using the Rang-Kutta 4th order method, and graphical simulations are performed in MATLAB (version 2023a) to further validate the theoretical findings and illustrate the applicability and the accuracy of the proposed approaches.

Keywords: *nonlinear model; conformable derivative; positivity analysis; local and global stability; Sumudu transform; COVID-19 models.*

Mathematics Subject Classification (2020): 70K75, 93-05, 93-08, 93-10, 93C10, 93D05, 93D20.

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1 Introduction

Epidemiological nonlinear COVID-19 models are associated with a respiratory disease that emerged in December 2019 in Wuhan and other cities in China, which has become a global public health emergency declared by the World Health Organization (WHO) in the first quarter of 2020. The first transmission of the disease was from animal to human. Then, it spreaded rapidly among humans through direct and indirect contact. The most common clinical symptoms of SARS-CoV-2 infections are fever, cough, tiredness, loss of taste or smell, nausea, diarrhea, pneumonia, and respiratory issues.

Mathematical nonlinear models play a crucial role in predicting future trends of epidemics and developing effective strategies to control them based on data and microscopic hypotheses about the population. The Kermack and McKendrick model [6] presented in 1927, was the first SIR model capable of predicting epidemic infections. Since then, researchers have further studied and developed global and local stability of SEIR and SIR models. Recently, the development of mathematical models to predict the evolution of COVID-19 infections has attracted considerable attention. Researchers have explored various aspects of the disease, including its nature, transmission dynamics, basic reproduction number, and stability [3, 5, 9].

The stability of fractional nonlinear epidemiological models is crucial for understanding complex dynamical systems because it allows an accurate representation of natural phenomena by integrating long-term memories and non-local behaviors. Some researchers have examined the stability of fractional conformable pandemic models [7], in particular, simplifying calculations while preserving these advantages, thus facilitating the analysis of local and global stability. The particularity of this derivative is due to its simplicity of handling and interpreting and the use of the simplest initial conditions similar to those of classical derivatives. Some researchers have applied the Sumudu transform in fractional conformable models [2]. Similar to the Laplace and Fourier transforms, the Sumudu transform is an efficient method for solving differential and integral equations. It differs from the Laplace transform in that it also takes into account the units of the original function, making it more suitable in physics and engineering applications. Moreover, its connection with the Laplace transform allows a smooth transition between various analytical techniques, thus increasing its adaptability to different domains.

In this paper, by using the conformable derivative, we study Rabih Ghostine's COVID-19 model focusing on positivity analysis via the Sumudu transformation. Therefore, we apply this technique to understand in detail the local and global stability of this model using the concept of R_0. The results of our study reveal that the Sumudu transformation and the conformable derivative improve these analyses, providing more information about its behaviors as well as possible applications in epidemiological modeling or other related fields.

This paper is organized af follows. In Section 2, we present preliminaries and problem formulation. Section 3 is devoted to the study of the positivity and boundness of the solutions using the Sumudu transform. The choice of this transformation is due to its conservation of units, which facilitates the interpretation of results while simplifying calculations for certain differential and integral equations. Additionally, it provides a direct correspondence with power series and offers a simpler inversion in some cases. The Disease-Free and Endemic Equilibrium and the basic reproduction number are established in Section 4. Stability analysis is presented for the considered class of nonlinear models in Section 5. In Section 6, some numerical examples and simulations are presented to show the effectiveness and applicability of the proposed method.

2 Preliminaries and Problem Formulation

In this section, we present the mathematical formulation of the COVID-19 nonlinear model. We have chosen the conformable derivative for this formulation because it provides a simpler and more intuitive alternative for modelling, manipulating, and interpreting dynamic phenomena. Additionally, it uses simpler initial conditions similar to those of classical derivatives.

2.1 Preliminaries

This subsection presents essential theorems and definitions of conformable fractional operators and the Sumudu transform, which is crucial for the dynamic analysis of the results discussed in this paper.

Definition 2.1 [7] Let a function $x : [0, +\infty) \to \mathbb{R}$ be given. Then the conformable derivative of the function x of order α, with $\alpha \in (0, 1]$, is defined by

$$\mathbf{T}^{\alpha}(x)(t) = \lim_{\epsilon \to 0} \frac{x(t + \epsilon t^{1-\alpha}) - x(t)}{\epsilon}, \quad \forall t > 0.$$

If the conformable derivative of the function x of order α exists for all $t > 0$, then we simply say that x is α-differentiable.

Theorem 2.1 *[7] Let $\alpha \in (0, 1]$ and $x_1, x_2 : \mathbb{R}_+ \to \mathbb{R}$ be α-differentiable functions. Then, $\forall t > 0$,*

(a) $\mathbf{T}^{\alpha}(ax_1(t) + bx_2(t)) = a\mathbf{T}^{\alpha}(x_1)(t) + b\mathbf{T}^{\alpha}(x_2)(t)$ *for all* $a, b \in \mathbb{R}$*;*

(b) $\mathbf{T}^{\alpha}(t^p) = pt^{p-\alpha}$ *for all* $p \in \mathbb{R}$*;*

(c) $\mathbf{T}^{\alpha}(\lambda) = 0$ *for all constant function* $x_1(t) = \lambda$*;*

(d) $\mathbf{T}^{\alpha}(x_1(t)x_2(t)) = x_1(t)\mathbf{T}^{\alpha}(x_2)(t) + x_2(t)\mathbf{T}^{\alpha}(x_1)(t)$*;*

(e) $\mathbf{T}^{\alpha}\left(\dfrac{x_1(t)}{x_2(t)}\right) = \dfrac{x_2(t)\mathbf{T}^{\alpha}(x_1)(t) + x_1(t)\mathbf{T}^{\alpha}(x_2)(t)}{x_2^2(t)}$*;*

(f) If x_1 *is differentiable, then* $\mathbf{T}^{\alpha}(x_1)(t) = t^{1-\alpha}\dfrac{dx_1(t)}{dt}$.

Definition 2.2 [7] We take into account functions with exponential order in the set $\mathcal{A}$ defined by

$$\mathcal{A} = \left\{x(t)\ \exists M, \tau_1, \tau_2 > 0, \mid x(t) \mid < Me^{-\frac{|t|}{\tau_j}},\ \text{if } t \in (-1)^j \times [0, \infty)\right\},$$

the Sumudu transform X of a continuous function x is represented by

$$\mathcal{S}[x(t)] = X(v) = \int_0^{\infty} x(vt)e^{-t}dt, \quad v \in (-\tau_1, \tau_2),$$

or a similar alternative

$$\mathcal{S}[x(t)] = X(v) = \frac{1}{v}\int_0^\infty x(t)e^{-\frac{t}{v}}dt, \quad v > 0.$$

Theorem 2.2 *[1] Let $x : [0,\infty) \to \mathbb{R}$ be a given function, $0 < \alpha \leq 1$. Then we have the following property:*

$$\mathcal{S}_\alpha[\mathbf{T}^\alpha x(t)](v) = \frac{1}{v}\left[\mathcal{S}_\alpha[x(t)](v) - x(0)\right], \quad \forall t > 0.$$

Theorem 2.3 *[1] Let c and $a \in \mathbb{R}$ and $0 < \alpha \leq 1$. Then*

1. $$\mathcal{S}_\alpha[e^{-a\frac{t^\alpha}{\alpha}}x(t)] = \frac{\mathcal{S}_\alpha[x(t)](\frac{1}{v}+a)}{v}, \quad v > 0;$$

2. $$\mathcal{S}_\alpha[c](v) = c;$$

3. $$\mathcal{S}_\alpha\left[\frac{t^{n\alpha}}{\alpha^n}\right](v) = \frac{\Gamma(1+n)^n}{v}, \quad v > 0;$$

4. $$\mathcal{S}_\alpha\left[e^{-\frac{at^\alpha}{\alpha}}\right](v) = \frac{1}{1+av}, \quad v > \frac{1}{a}.$$

2.2 Model formulation

Several models have been developed in the literature to describe and study the dynamics of COVID-19 disease. Rabih Ghostine's nonlinear model has been recognized for its comprehensive yet creative methods used to explain better and understand the outbreak and spread of COVID-19. Several factors contribute to its significance: Accuracy and Predictive Power, Involvement of Different Variables, Adjustability, Transdisciplinarity, Openness and Accessibility, and Influence in Reality. This work focuses on an extended and reformulated version of Ghostine's epidemiological nonlinear model [5], expressed in a fractional form using a conformable derivative, with a subsequent investigation of its global stability.

In our model, the human population denoted by N is composed of seven compartments (subpopulations) according to the status of the disease. The number of susceptible individuals $S(t)$, infected individuals in the incubation period $E(t)$, infectious individuals $I(t)$, hospitalized individuals $H(t)$, recovered $R(t)$, and vaccinated cases $V(t)$ are incorporated. The fractional-order SEIHRDV model, utilizing the conformable fractional derivative of order $0 < \alpha \leq 1$, is given by

$$\begin{aligned}
\mathbf{T}^{\alpha} S(t) &= \Lambda^{\alpha} - \beta^{\alpha} S I - \eta^{\alpha} S - \mu^{\alpha} S, \\
\mathbf{T}^{\alpha} E(t) &= \beta^{\alpha} S I + (\sigma\beta)^{\alpha} V I - (\gamma^{\alpha} + \mu^{\alpha}) E, \\
\mathbf{T}^{\alpha} I(t) &= \gamma^{\alpha} E - (\delta^{\alpha} + \mu^{\alpha}) I, \\
\mathbf{T}^{\alpha} H(t) &= \delta^{\alpha} I - ((1-\kappa^{\alpha})\lambda^{\alpha} + (\kappa\rho)^{\alpha} + \mu^{\alpha}) H, \\
\mathbf{T}^{\alpha} R(t) &= (1-\kappa^{\alpha})\lambda^{\alpha} H - \mu^{\alpha} R, \\
\mathbf{T}^{\alpha} D(t) &= (\kappa\rho)^{\alpha} H, \\
\mathbf{T}^{\alpha} V(t) &= \eta^{\alpha} S - (\sigma\beta)^{\alpha} V I - \mu^{\alpha} V
\end{aligned} \tag{1}$$

under the conditions

$$S(0) = S_0 \geq 0, \quad E(0) = E_0 \geq 0, \quad I(0) = I_0 \geq 0, \quad H(0) = H_0 \geq 0, \quad R(0) = R_0 \geq 0,$$
$$D(0) = D_0 \geq 0, \quad V(0) = V_0 \geq 0$$

and $N(t) = S(t) + E(t) + I(t) + H(t) + R(t) + D(t) + V(t)$.

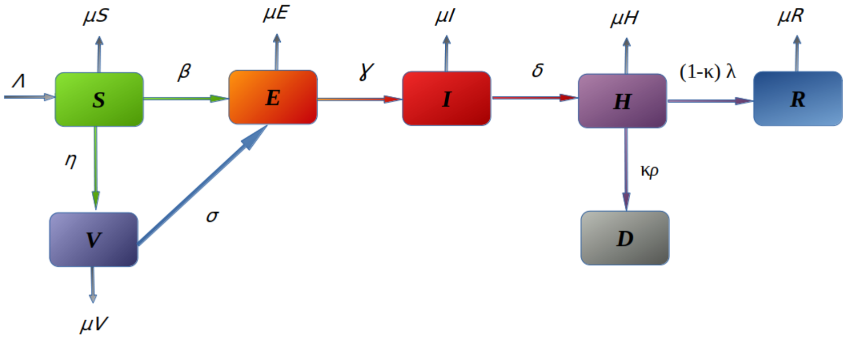


Figure 1: Compartmental diagram for the transmission dynamics of COVID-19.

In the following two sections, the analysis of the nonlinear epidemiological model is carried out under certain constraints on the parameters of the model to ensure the biological acceptability as well as its mathematical structure, the positive populations, plausible and sequential disease case rates. These characteristics are particularly important for describing the long-term development of an infectious disease process, including its retention or extinction. In terms of systems theory, the stability of these nonlinear models is of great importance in terms of the equilibrium point and its robustness against perturbations that revolve around the fundamental concepts of nonlinear dynamics.

3 Non-Negativity and Boundedness of Solutions

The objective of this section is to analyze and demonstrate the positivity and boundness of the system's solutions by introducing a new innovative integral technique named the Sumudu transform to solve differential systems.

Proposition 3.1 *The region* $\Omega = \{(S, E, I, H, R, D, V) \in \mathbb{R}^7 : 0 < N \leq \left(\frac{\Lambda}{\mu}\right)^{\alpha}\}$ *is non-negative invariant for the model (1) for* $t \geq 0$*.*

Proof. We have

$$\mathbf{T}^{\alpha}(S+E+I+H+R+D+V)(t) = \Lambda^{\alpha} - \mu^{\alpha}(S+E+I+H+R+D+V)(t).$$

$$\Longrightarrow \quad \mathbf{T}^{\alpha}N(t) = \Lambda^{\alpha} - \mu^{\alpha}N(t)$$
$$\Longrightarrow \quad \mathbf{T}^{\alpha}N(t) + \mu^{\alpha}N(t) = \Lambda^{\alpha}.$$

Taking the Sumudu transform, we have

$$\begin{aligned} \frac{1}{v}\left[\mathcal{S}_{\alpha}[N(t)](v) - N(0)\right] + \mu^{\alpha}\mathcal{S}_{\alpha}[N(t)](v) &= \Lambda^{\alpha} \\ \Longrightarrow \quad \mathcal{S}_{\alpha}[N(t)](v) + v\mu^{\alpha}\mathcal{S}_{\alpha}[N(t)](v) &= N(0) + v\Lambda^{\alpha} \\ \Longrightarrow \quad \mathcal{S}_{\alpha}[N(t)](v) &= \frac{N(0)+v\Lambda^{\alpha}}{1+v\mu^{\alpha}} \\ \Longrightarrow \quad \mathcal{S}_{\alpha}[N(t)](v) &= \frac{N(0)}{1+v\mu^{\alpha}} - \frac{\Lambda^{\alpha}}{\mu^{\alpha}(1+v\mu^{\alpha})} + \frac{\Lambda^{\alpha}}{\mu^{\alpha}}. \end{aligned}$$

Applying the inverse Sumudu transform, we get

$$N(t) = \frac{\Lambda^{\alpha}}{\mu^{\alpha}} + \left(N(0) - \frac{\Lambda^{\alpha}}{\mu^{\alpha}}\right) e^{\frac{-\mu^{\alpha}t^{\alpha}}{\alpha}}.$$

Thus

$$\lim_{t\to\infty} SupN(t) \leq \left(\frac{\Lambda}{\mu}\right)^{\alpha}.$$

As a result, the functions S, E, I, H, R, D and V are all non-negative.

4 Equilibrium Points and Basic Reproduction Number of the Model

The primary objective of this section is to determine two essential equilibrium states: the Disease-Free Equilibrium and the Endemic Equilibrium. Additionally, we aim to determine the Basic Reproduction Number $\mathcal{R}_0$.

Based on [12], Basic Reproduction Number $\mathcal{R}_0$ and the Disease-Free Equilibrium point (DFE) of the model (1) are given as follows:

$$\mathcal{R}_0 = \frac{(\beta\gamma\Lambda)^{\alpha}\epsilon_5}{\mu^{\alpha}\epsilon_1\epsilon_2\epsilon_3}, \quad X^0 = \left(\frac{\Lambda^{\alpha}}{\epsilon_1}, \quad 0, \quad 0, \quad 0, \quad 0, \quad \frac{(\eta\Lambda)^{\alpha}}{\mu^{\alpha}\epsilon_1}\right),$$

and the Endemic Equilibrium point (DEE) is given by

$$X^1 = \left(\frac{\Lambda^{\alpha}}{\beta^{\alpha}I^1+\epsilon_1}, \quad \frac{\epsilon_3}{\gamma^{\alpha}}I^1, \quad \frac{\sqrt{M_1}+M_2}{M_3}, \quad \frac{\delta^{\alpha}}{\epsilon_4}I^1,\right.$$
$$\left.\frac{(1-\kappa^{\alpha})(\lambda\delta)^{\alpha}}{\mu^{\alpha}\epsilon_4}I^1, \quad \frac{(\eta\Lambda)^{\alpha}}{(\beta^{\alpha}I^1+\epsilon_1)((\sigma\beta)^{\alpha}I^1+\mu^{\alpha})},\right),$$

where

$$\begin{gathered}\epsilon_1 = \mu^\alpha + \eta^\alpha, \quad \epsilon_2 = \mu^\alpha + \gamma^\alpha, \quad \epsilon_3 = \mu^\alpha + \delta^\alpha,\\ \epsilon_4 = \mu^\alpha + \lambda^\alpha(1-\kappa^\alpha) + (\kappa\rho)^\alpha, \quad \epsilon_5 = \mu^\alpha + (\eta\sigma)^\alpha\end{gathered}$$

and

$$\begin{aligned}M_1 =& (\epsilon_2\epsilon_3\mu^\alpha)^2 + (\Lambda\beta\gamma\sigma)^{2\alpha} + (\epsilon_1\epsilon_2\epsilon_3\sigma^\alpha)^2 - 2(\sigma\mu)^\alpha\epsilon_1\epsilon_2^2\epsilon_3^2\\ &+ 4\mathcal{R}_0(\sigma\mu)^\alpha\epsilon_1\epsilon_2^2\epsilon_3^2 - 2(\Lambda\beta\sigma\gamma\mu)^\alpha\epsilon_2\epsilon_3 - 2(\beta\sigma^2\gamma\Lambda)^\alpha\epsilon_1,\\ M_2 =& (\beta\sigma\gamma\Lambda)^\alpha - \sigma^\alpha\epsilon_1\epsilon_2\epsilon_3 - \mu^\alpha\epsilon_2\epsilon_3, \quad M_3 = 2(\beta\sigma)^\alpha\epsilon_2\epsilon_3\epsilon_2\epsilon_3. \end{aligned} \tag{2}$$

5 Stability Analysis

In this section, our objective is to investigate the Local Asymptotic Stability (LAS) and to study also the Global Asymptotic Stability (GAS) of the Equilibrium points (DFE) X^0 and (DEE) X^1 for the model (1).

5.1 Local stability of the equilibrium points

By the use of the basic reproduction number $\mathcal{R}_0$ [12], we can present the theorem that establishes the local stability of the Disease-Free Equilibrium (DFE), which is defined as follows.

Theorem 5.1 *The disease-free equilibrium X^0 is locally asymptotically stable if $\mathcal{R}_0 < 1$ and unstable if $\mathcal{R}_0 > 1$.*

Proof. The Jacobian matrix at the DFE point X^0 is given by

$$J(X^0) = \begin{pmatrix} -\epsilon_1 & 0 & -\dfrac{\mathcal{R}_0\mu^\alpha\epsilon_2\epsilon_3}{\epsilon_5\gamma^\alpha} & 0 & 0 & 0\\ 0 & -\epsilon_2 & \dfrac{\epsilon_2\epsilon_3\mathcal{R}_0}{\gamma^\alpha} & 0 & 0 & 0\\ 0 & \gamma^\alpha & -\epsilon_3 & 0 & 0 & 0\\ 0 & 0 & \delta^\alpha & -\epsilon_4 & 0 & 0\\ 0 & 0 & 0 & (1-\kappa^\alpha)\lambda^\alpha & -\mu^\alpha & 0\\ \eta^\alpha & 0 & -\dfrac{\mathcal{R}_0(\sigma\eta)^\alpha\epsilon_2\epsilon_3}{\gamma^\alpha\epsilon_5} & 0 & 0 & -\mu^\alpha \end{pmatrix}.$$

The roots of the characteristic equation are defined as follows:

$$\begin{aligned} s_1 &= -\epsilon_1 < 0, \quad s_2 = -\epsilon_4 < 0, \quad s_3 = -\mu^\alpha < 0, \quad s_4 = -\mu^\alpha < 0,\\ s_5 &= -\frac{1}{2}\left(\epsilon_2 + \epsilon_3 + \sqrt{(\epsilon_2-\epsilon_3)^2 + 4\mathcal{R}_0\epsilon_2\epsilon_3}\right) < 0,\\ s_6 &= -\frac{1}{2}\left(\epsilon_2 + \epsilon_3 - \sqrt{(\epsilon_2-\epsilon_3)^2 + 4\mathcal{R}_0\epsilon_2\epsilon_3}\right) < 0 \quad \text{iff} \quad \mathcal{R}_0 < 1. \end{aligned}$$

The disease-free equilibrium X^0 is locally asymptotically stable or unstable according to $\mathcal{R}_0 < 1$ or $\mathcal{R}_0 > 1$.

5.2 Global stability of the equilibrium points

The theorems that establish the global stability of the Equilibrium points (DFE) and (DEE) are formulated as follows.

Theorem 5.2 *The disease-free equilibrium* X^0 *is global asymptotically stable in* $\Omega = \{(S, E, I, H, R, D, V) \in \mathbb{R}^7_+ / S+E+I+H+R+D+V \leq N, \quad S(0) > 0, E(0) > 0, I(0) > 0, H(0) > 0, R(0) > 0, D(0) > 0, V(0) > 0\}$ *if* $\mathcal{R}_0 \leq 1$*, otherwise unstable.*

Proof. Following [10], let us consider the Lyapunov function

$$\mathcal{V}(E, I) \quad = \quad E + \frac{\gamma + \mu}{\gamma} I.$$

The conformal derivative of the Lyapunov function, denoted by $\mathbf{T}^\alpha \mathcal{V}(E, I)$, is given by

$$\begin{aligned}
\mathbf{T}^\alpha \mathcal{V}(E, I) &= \mathbf{T}^\alpha E(t) + \mathbf{T}^\alpha I(t) \left(\frac{\epsilon_2}{\gamma^\alpha} \right), \\
&= \beta^\alpha SI + (\sigma\beta)^\alpha VI - \epsilon_2 E + \frac{\epsilon_2}{\gamma^\alpha} (\gamma^\alpha E - \epsilon_3 I), \\
&= \beta^\alpha (S + \sigma^\alpha V) - \frac{\epsilon_2 \epsilon_3}{\gamma^\alpha}, \\
&= \frac{\epsilon_2 \epsilon_3}{\gamma^\alpha} \left[\frac{\epsilon_1 \mu^\alpha \mathcal{R}_0 (S + \sigma^\alpha V)}{\Lambda^\alpha \epsilon_5} - 1 \right] I \quad \leq \quad \frac{\epsilon_2 \epsilon_3}{\gamma^\alpha} (\mathcal{R}_0 - 1) I.
\end{aligned}$$

Thus, $\mathbf{T}^\alpha \mathcal{V}(E, I) < 0$ if $\mathcal{R}_0 < 1$, and $\mathbf{T}^\alpha \mathcal{V}(E, I) = 0$ if $I(t) = 0$ and $\mathcal{R}_0 = 1$. Therefore, the largest invariant set contained in this set is

$$L = \{(S, E, I, H, R, D, V) \in \Omega / \mathbf{T}^\alpha \mathcal{V}(E, I) = 0\},$$

which is reduced to DFE. Hence, by LaSalle's Invariance Principle, it follows that the disease-free equilibrium point is Globally Asymptotically Stable in Ω whenever $\mathcal{R}_0 < 1$.

Theorem 5.3 *If* $\mathcal{R}_0 > 1$*, then the endemic equilibrium of the model (1) given by* X^1 *is globally asymptotically stable in* Ω.

Proof. The non-linear Lyapunov function of the Goh-Volterra form [8] is as follows:

$$\begin{aligned}
\mathcal{V}(S, E, I, H, V) \quad &= \quad \big(S - S^1 ln(S)\big) + \big(E - E^1 ln(E)\big) + \frac{\beta^\alpha S^1 I^1}{\gamma^\alpha E^1} \big(I - I^1 ln(I)\big) \\
&\quad + \frac{\beta^\alpha S^1}{\delta^\alpha} \big(H - H^1 ln(H)\big) + \big(V - V^1 ln(V)\big),
\end{aligned}$$

the conformable derivative of the Lyapunov function, $\mathbf{T}^\alpha \mathcal{V}(S, E, I, H, V)$, is expressed as

$$\begin{aligned}
\mathbf{T}^\alpha \mathcal{V}(S, E, I, H, V) = &\left(1 - \frac{S^1}{S}\right) \mathbf{T}^\alpha S(t) + \left(1 - \frac{E^1}{E}\right) \mathbf{T}^\alpha E(t) \\
&+ \frac{\beta^\alpha S^1 I^1}{\gamma^\alpha E^1} \left(1 - \frac{I^1}{I}\right) \mathbf{T}^\alpha I(t) \\
&+ \frac{\beta^\alpha S^1}{\delta^\alpha} \left(1 - \frac{H^1}{H}\right) \mathbf{T}^\alpha H(t) + \left(1 - \frac{V^1}{V}\right) \mathbf{T}^\alpha V(t).
\end{aligned}$$

Furthermore, we have

$$\mathbf{T}^\alpha S(t) \leq \Lambda^\alpha - \beta^\alpha SI, \quad \mathbf{T}^\alpha E(t) \leq \beta^\alpha SI + (\sigma\beta)^\alpha VI, \quad \mathbf{T}^\alpha I(t) \leq \gamma^\alpha E$$

$$\mathbf{T}^\alpha H(t) \leq \delta^\alpha I, \quad \mathbf{T}^\alpha V(t) \leq \eta^\alpha S - (\sigma\beta)^\alpha VI.$$

Therefore,

$$\begin{aligned}\mathbf{T}^\alpha \mathcal{V}(S,E,I,H,V) < {} & \Lambda^\alpha \left(1 - \frac{S^1}{S}\right) + \eta^\alpha S^1 \left(\frac{S}{S^1} - \frac{V^1 S}{V S^1}\right) \\ & + (\sigma\beta)^\alpha V^1 I^1 \left(\frac{I}{I^1} - \frac{E^1 V I}{E V^1 I^1}\right) \\ & + \beta^\alpha S^1 I^1 \left(\frac{E}{E^1} + 2\frac{I}{I^1} - \frac{E^1 S I}{E S^1 I^1} - \frac{I^1 E}{I E^1} - \frac{H^1 I}{H I^1}\right) \\ < {} & 0\end{aligned}$$

so that the following inequalities hold:

$$1 - \frac{S^1}{S} \leq 0, \quad \frac{S}{S^1} - \frac{V^1 S}{V S^1} \leq 0, \quad \frac{I}{I^1} - \frac{E^1 V I}{E V^1 I^1} \leq 0$$

and

$$\frac{E}{E^1} + 2\frac{I}{I^1} - \frac{E^1 S I}{E S^1 I^1} - \frac{I^1 E}{I E^1} - \frac{H^1 I}{H I^1} \leq 0.$$

Thus $\mathbf{T}^\alpha \mathcal{V}(t) \leq 0$ for $\mathcal{R}_0 > 1$. The point X^1 is globally asymptotically stable if $\mathcal{R}_0 > 1$.

6 Numerical Results and Discussion

In this section, we present a numerical study that simulates the SEIHRDV model with a conformable fractional derivative applied to the spread of COVID-19 in Algeria. The parameters are determined using real-time data on COVID-19 cases in Algeria provided by the World Health Organization (WHO) and the Algerian Ministry of Health. The primary objective of this simulation is to assess the impact of the vaccination campaign on disease transmission. We employ the Runge-Kutta 4th order (RK4) method in MATLAB for this study.

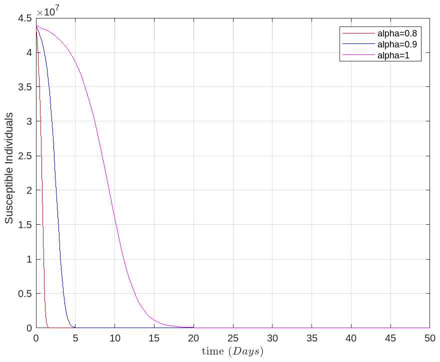
The baseline parameters and the initial values for our proposed model are shown in Tables 1 and 2.

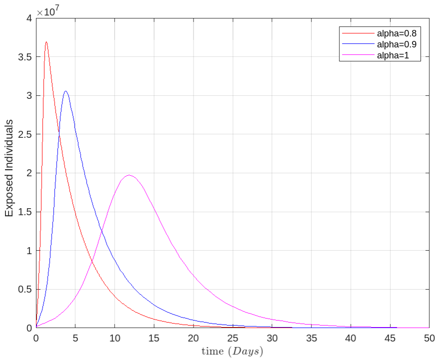
Parameter	Interpretation	Initial Value	Reference
μ	Natural birth and death rate	3×10^{-5} person/day	Estimated
Λ	New births	1350 person/day	[14]
$\gamma^{-}1$	Incubation period	5.5 days	[4]
$\delta^{-}1$	Infection time	3.8 days	[4]
$\lambda^{-}1$	Recovery time	10 days	[4]
$\rho^{-}1$	Time until death	15 days	[4]
η	Vaccination rate (rate of people who are vaccinated)	4×10^{-4} day^{-1}	Estimated
σ	Vaccine inefficacy	0.05 day^{-1}	[11]
β	Transmission rate divided by N	5.7×10^{-8} day^{-1}	Estimated
κ	Case fatality rate	0.028	[15]

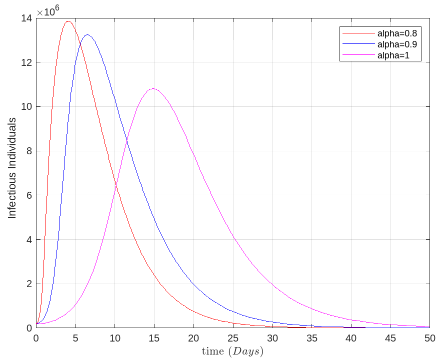
Table 1: Initial model parameters.

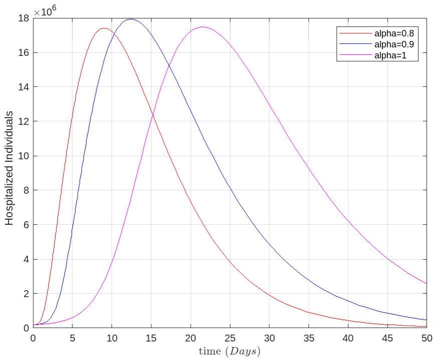
Variable	N	I_0	E_0	H_0	R_0	D_0	V_0	S_0
Initial Value	44,600,000	202,122	150,000	180,000	138,362	5,739	0	44,457,156
Reference	[13]	[15]	Estimated	Estimated	[15]	[15]	[15]	Estimated

Table 2: The initial values for the model variables.









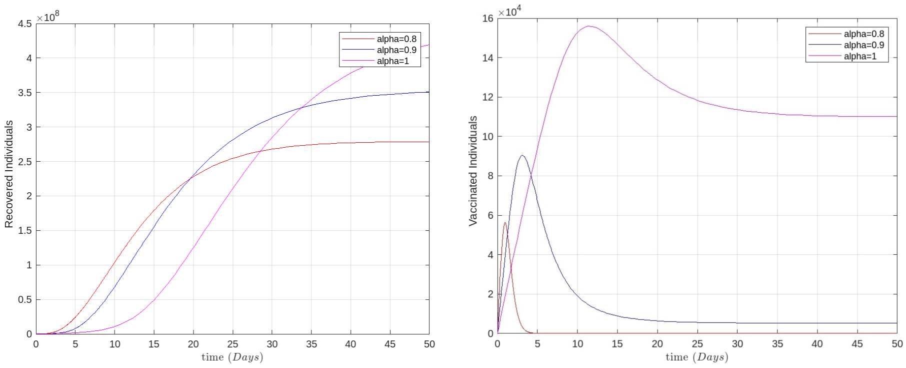


Figure 2: Plots of S(t), E(t), I(t), H(t), R(t) and V(t) for different values of $\alpha = 0.6, 0.8, 1.0$ with respect to time (days).

The graphs highlight the dynamics of disease spread and the impact of the α parameter. Over time, the number of susceptible individuals decreases as more people become exposed and infected, with lower α values resulting in fewer susceptibles. Exposed individuals peak and decline more quickly with lower α values, showing a faster transition to the infectious stage. Infectious individuals exhibit a distinct peak and subsequent decline, with lower α values leading to an earlier and higher peak, indicating a more rapid and intense spread. Hospitalized individuals peak and then decline, with lower α values causing a later and lower peak, suggesting a reduced burden on the healthcare system. The number of recovered individuals increases over time, with the lowest recovery rates at $\alpha = 1$. Vaccinated individuals rise rapidly at first and then stabilize, with lower α values leading to faster vaccination rates but reaching this stabilization sooner.

7 Conclusion

In this paper, we analyze fractional order derivatives utilizing the confomable derivatives with an order of $0 < \alpha \leq 1$ within the SEIHRDV nonlinear epidemiological models with vaccination. To this end, COVID-19 case data from Algeria at the beginning of vaccine implementation (September, 2021) are used. To prove the positivity of the system's solutions, we introduce the Sumudu transform (an integral technique for solving differential systems) as a new innovative approach. After that, we establish the local stability of the equilibrium points by calculating the Jacobian matrix and proving that its eigenvalues are negative. To demonstrate the global stability of the equilibrium points, we construct a Lyapunov function. Our study shows that a lower value of α is associated with a more effective response to the disease. However, it is important to note that α is not the only factor that determines the effectiveness of a response. Other factors such as the effectiveness of the vaccine and the availability of healthcare resources, also play a role in the analysis of Covid-19 epidemiological models.

References

[1] Z. Al-Zhour, F. Alrawajeh, N. Al-Mutairi and R. Alkhasawneh. New results on the conformable fractional Sumudu transform: theories and applications. *International Journal of Analysis and Applications* **17** (6) (2019) 1019–1033.

[2] K. Benyettou, D. Bouagada and M. A. Ghezzar. Solution of 2D State Space Continuous-Time Conformable Fractional Linear System Using Laplace and Sumudu Transform. *Computational Mathematics and Modeling* **32** (2021) 94–109.

[3] M. C. Benkara Mostefa and N. E. Hamri. Stability and Hopf Bifurcation of a Generalized Differential-Algebraic Biological Economic System with the Hybrid Functional Response and Predator Harvesting. *Nonlinear Dynamics and Systems Theory* **23** (4) (2023) 398–409.

[4] G. Evensen et al. An international assessment of the COVID-19 pandemic using ensemble data assimilation. *medRxiv* `https://doi.org/10.1101/2020.06.11.20128777`

[5] R. Ghostine et al. An extended SEIR model with vaccination for forecasting the COVID-19 pandemic in Saudi Arabia using an ensemble Kalman filter. *Mathematics* **9** (2021) 636, `https://doi.org/10.3390/math9060636.`

[6] W. O. Kermack and A. G McKendrick. A Contribution to the Mathematical Theory of Epidemics. In: *Proceedings of the Royal Society of London. Series A*, London **115** (1927) 700–721.

[7] R. Khalil et al. A new definition of fractional derivative. *Journal of computational and applied mathematics* **264** (2014) 65–70.

[8] A. Korobeinikov. Lyapunov functions and global properties for SEIR and SEIS epidemic models. *Mathematical medicine and biology: a journal of the IMA* **21** (2) (2004) 75–83.

[9] K. Mesbah and N.E. Hamri. Adaptive Control for the Stabilization, Synchronization and Anti-Synchronization of New Chaotic System with a Line Equilibrium. *Nonlinear Dynamics and Systems Theory* **24** (3) (2024) 298–308.

[10] M. Y. Li and J. S. Muldowney. Global stability for the SEIR model in epidemiology.*Mathematical biosciences* **125** (2) (1995) 155–164.

[11] F. P. Polack et al. Safety and efficacy of the BNT162b2 mRNA Covid-19 vaccine. *England journal of medicine* **383** (27) (2020) 2603–2615.

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

[13] *Article on the total population in Algeria.* `https://www.aps.dz/societe/134560-demographie-44-6-millions-d-habitants-en-algerie-en-janvier-2021.` www.aps.dz/societe.

[14] *The parameter* Λ. `https://countrymeters.info/fr/Algeria`. Accessed: 31-03-2022.

[15] *Situation report on the COVID-19 outbreak in Algeria 2021.* `https://reliefweb.int/report/algeria/alg-rie-rapport-de-situation-sur-l-pid-mie-du-covid-19-544-du-23-septembre-2021`, reliefweb.int/report 2021.