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A Numerical Confirmation of a Fractional SEITR for Influenza Model Efficiency

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Abstract: The main idea of this study is to reduce the number of susceptible to infections so that ill patients can receive prompt hospitalization. Fractional SEITR was introduced for this purpose. Both endemic and disease-free equilibrium's' durability was examined. The fundamental reproduction number of the fractional SEITR model was determined using the next-generation matrix method. Our analytical results were supported by numerical models. Here, a graphical representation of the fractional order model is presented to validate the conclusion through numerical simulation. We have come to the conclusion that the fractional order model is more precise and provides more information about the true data of disease dynamics.

Keywords: Fractional SEITR model, Fractional Euler method, Stability analysis, Numerical simulation.

1 Introduction

At the beginning of the 20th century, Kermack and McKendrick [1]. A quantitative model, SIR, was presented for the first time. To describe how an outbreak spreads, the SEIR model was constructed by adding Exposed (E) as the fourth compartment to the SIR model [2]. Rafiqul Islam et al. [3] to analyze influenza in Bangladesh. ZhilanFeng (2007) [4] created an SEIR model for assessing various management approaches [5]. The SITR model, first proposed by Vinod kumar bais and Deepak kumar [6], emphasizes the classic importance of the dynamical condition in the spread of the H1N1 virus. Adding treatment T as a fifth compartment, Kumar and Venkatesh, A. (2023) [7] created a novel SEITR model. Seasonal influenza is a contagious respiratory virus that rapidly spreads from person to person through the nasal passages and oral cavities. Dengue, influenza, rabies, tuberculosis, and the COVID-19 pandemic all have latency and recovery phases, and the SEIR model has been applied to each [8,9,10,11,12,13,14]. Predicting influenza outbreaks in the United States, Long Zhou et al. [15] relied on the tried and true SEIR model. During the 2009 Italian influenza pandemic [16]. Various prevention and control measures were simulated using the SEIR model by Misse, closure of schools, and vaccinations are some of the measures taken to prevent disease. Influenza is a global health threat [17]. Religious mass meetings in Makkah and Al-Madinah, Saudi Arabia, often spread lung diseases, a global public health issue [18]. This could bring new, highly dangerous, and hardy viruses into Saudi Arabia, especially during the flu season. The Saudi Thoracic Society released influenza vaccination guidance for Hajj and Umrah [19]. These standards will require the Saudi Ministry of Hajj, its international counterparts, and public health bodies globally to implement. Evidence shows that visitors can bring the influenza back from Hajj [20]. Importantly, strain mismatch may explain why protected people get influenza [17,18]. Pilgrims from nations with year-round influenza or influenza seasons ahead of Saudi Arabia's September–March season could further exacerbate the situation. Therefore, Saudi Arabia should start and execute an active human influenza monitoring program, focusing on Hajj and Umrah seasons. To manage the disease, epidemic models must be studied, simulated, and compared with real data.

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Our primary focus is to reduce the number of susceptible contacts with infections to speed up hospitalization for critically ill patients. The graphics depicted the impact of environmental and social variables on epidemic populations. The five-partite framework of the Fractional SEITR epidemiological model and talks about its basic characteristics. Positivity and boundedness checks were carried out. For tiny values of $R_0 < 1$, it was shown that there is a disease-free equilibrium point, and that this point is both locally and universally asymptotically stable. Similarly, for big values of $R_0 > 1$, there must be a point where the endemic equilibrium is stable locally. The R_0 reproduction figure indicates that the epidemic has spread throughout the entire population. Therefore, increasing the rate of treatment is the only way to slow the spread of the epidemic.

2 Model Formation

To gain a better understanding of the dynamics of the influenza epidemic, we propose a fractional SEITR model that incorporates the treatment compartment (T) as the fifth component in the standard SEIR model. The population at time t, denoted as N(t), is divided into five sub-populations: susceptible (S(t)), exposed (E(t)), infected (I(t)), treated (T(t)), and recovering (R(t)). The susceptible population represents individuals who are at risk of contracting the virus, while the exposed population comprises individuals who are infected but not yet contagious. The infected population can transmit the disease to others, while the treated population consists of individuals receiving medical therapy in hospitals. The recovering population includes individuals who have shown improvement as a result of treatment.

Fractional differential equations have made significant advancements in recent decades. In related studies, Jagdev et al. [21] proposed a fractional fish farm model using Atangana-Baleanu derivatives to analyze the dynamic behavior of fish farms, and Jagdev Singh [22] presented a model for the fractional guava fruit memory effect. In this paper, we provide a concise overview of the formulation and analysis of the Fractional SEITR model. We investigate the model's stability on a global scale and examine the existence of endemic equilibrium. Through analytical and numerical approaches, we draw conclusive insights. Notably, we observe that as the treatment rate increases, the susceptible population increases while the infected, exposed, and treated populations decline.

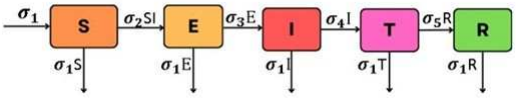

Fig. 1: SEITR Model Graphic Figure.

Figure 1 visually represents the SEITR model, providing a graphical illustration of the different compartments and their interconnections. It helps in comprehending the flow of individuals between the susceptible, exposed, infected, treated, and recovering populations, offering a visual representation of the model's structure and dynamics.

Table 1: The relative parameters are described.

Par.	Description	Val.	Sour.
$\wedge$	Rate of susceptible people	0.1	Constant
σ_1	Death rate	1.2	[23,24]
σ_2	Exposed rate of a susceptible population	0.2	[24]
σ_3	Infection rate of exposed people	0.4	[24]
σ_4	PInfected population therapy rate	0.1	[24]
σ_5	Treatment recovery rate	0.01	[25]

Table 1 provides an overview of the relative parameters utilized in the fractional SEITR model. These parameters play a crucial role in governing the dynamics of the model and determining the rates of various transitions within the compartments. The table presents the parameter name, its depiction, corresponding values, and the sources from which these values are derived.

3 Basic definitions and theorems

In this section, we provide an overview of the fundamental definitions and theorems concerning the Caputo fractional derivative and its applications. We begin by introducing the precise definitions of the Caputo fractional derivative and the Mittag-Leffler function. Additionally, we present two essential theorems: the local stability theorem and the global stability theorem. These theorems offer valuable insights into the stability properties of Caputo fractional systems. Finally, we illustrate the usage of Caputo fractional derivatives in computational models by discussing the SEITR model.[26,27,28,29,30]

Definition 1.*[31]*
The Caputo fractional derivative, denoted by ${}^{C}D^{\alpha} f(t)$*, is defined as follows:*

$$ {}^{C}D^{\alpha} f(t) = \frac{1}{\Gamma(n-\alpha)} \int_0^t (t-\tau)^{n-\alpha-1} f^{(n)}(\tau)\, d\tau. \qquad (1) $$

Definition 2.*[32] The Mittag-Leffler function, denoted by* $E_\alpha(t)$*, is given by the series representation:*

$$ E_\alpha(t) = \sum_{k=0}^{\infty} \frac{t^k}{\Gamma(\alpha k + 1)}. \qquad (2) $$

Theorem 1.*[33] For a Caputo fractional system described by the equilibrium equation*

$$^{C}D^{\alpha}x(t) = f(t,x), \tag{3}$$

if all eigenvalues λ_i, $i = 1,2,\ldots,n$, of the Jacobian matrix $\frac{\partial f_i}{\partial f_j}$, $j = 1,2,\ldots,n$, at the equilibrium x_e satisfy the condition:

$$|\arg(\lambda_i)| > \frac{\alpha\pi}{2}, \quad 0 < \alpha < 1. \tag{4}$$

then the system is locally asymptotically stable.

Theorem 2.*[34] Let Ω be a neighborhood containing the equilibrium solution x_e. Suppose $V : [0,\infty)\times\Omega \to \mathbb{R}$ is a continuous fractionally differentiable function that satisfies the following conditions:*

$$\begin{aligned} &\emptyset_1(x) \le V(t,x) \le \emptyset_2(x),\\ &^{C}D^{\alpha}V(t,x) \le -\emptyset_3, \end{aligned}$$

where $\emptyset_1$, $\emptyset_2$ and $\emptyset_3$ are continuous positive definite functions defined on Ω. If V is a Lyapunov function, then x^e is globally asymptotically stable.

The SEITR model represents a system of differential equations that captures the dynamics of susceptible (S), exposed (E), infected (I), treated (T), and recovered (R) individuals. It is described by the following equations:

$$\begin{aligned} \frac{dS}{dt} &= \wedge - \sigma_2 SI - \sigma_1 S,\\ \frac{dE}{dt} &= \sigma_2 SI - (\sigma_3+\sigma_1)E,\\ \frac{dI}{dt} &= \sigma_3 E - (\sigma_4+\sigma_1)I,\\ \frac{dT}{dt} &= \sigma_4 I - (\sigma_5+\sigma_1)T,\\ \frac{dR}{dt} &= \sigma_5 T - \sigma_1 R, \end{aligned} \tag{5}$$

where $S(0) \ge 0$, $E(0) \ge 0$, $I(0) \ge 0$, $T(0) \ge 0$ and $R(0) \ge 0$, and

$$N(t) = S(t) + E(t) + I(t) + T(t) + R(t).$$

Fractional-order models are often capable of handling variables within the unit interval, but adjustments can be made to accommodate data from other intervals. In our research, we utilize the Caputo fractional-order derivative operator to extend the canonical integer-order model to a fractional-order formulation as

$$\begin{aligned} {}^{C}_{0}D^{\alpha}_{t}S &= \wedge - \sigma_2 SI - \sigma_1 S,\\ {}^{C}_{0}D^{\alpha}_{t}E &= \sigma_2 SI - (\sigma_3+\sigma_1)E,\\ {}^{C}_{0}D^{\alpha}_{t}I &= \sigma_3 E - (\sigma_4+\sigma_1)I,\\ {}^{C}_{0}D^{\alpha}_{t}T &= \sigma_4 I - (\sigma_5+\sigma_1)T,\\ {}^{C}_{0}D^{\alpha}_{t}R &= \sigma_5 T - \sigma_1 R. \end{aligned} \tag{6}$$

4 Analysis of the fractional SEITR model

The section covers fractional SEITR-related topics such as positivity and boundedness of the solution, the basic reproduction number, and stability analysis.

4.1 Positivity and Boundedness

Theorem 3. *All the solutions $(S(t),E(t),I(t),T(t),R(t)) \in R^5_+$ of the system (6) with primary condition $S(t) \ge 0$, $E(t) \ge 0$, $I(t) \ge 0$, $T(t) \ge 0$, and $R(t) \ge 0$ are nonnegative and uniformly bounded for all $t \ge 0$.*

Proof. Assume that $(S(t),E(t),I(t),T(t),R(t)) \in R^5_+$ is a solution of (6) for $t \in [0,t_0)$, where $t_0 > 0$. Through 1st equation of system (6), we get

$$\begin{aligned} {}^{C}_{0}D^{\alpha}_{t}S &= \wedge - \sigma_2{}^{*}S^{*}I - \sigma_1{}^{*}S\\ &\ge \wedge - (\sigma_2{}^{*}I + \sigma_1)^{*}S, \end{aligned} \tag{7}$$

where $\phi(t) = \sigma_2{}^{*}I + \sigma_1$.
After integration, we get

$$\begin{aligned} S(t) &= S_0 \exp\left(-\int_0^t (\sigma_2{}^{*}I(s) + \sigma_1)\,ds\right)\\ &\quad + \wedge \exp\left(-\int_0^t (\sigma_2{}^{*}I(s) + \sigma_1)\,ds\right)\\ &\quad \int_0^t e^{\int_0^s (\sigma_2{}^{*}I(u)+\sigma_1)du}\,ds \ge 0,\\ &\Rightarrow S(t) \ge 0. \end{aligned} \tag{8}$$

From the 2nd equation of system (6), we develop

$$\begin{aligned} {}^{C}_{0}D^{\alpha}_{t}E &= \sigma_2 SI - (\sigma_3+\sigma_1)E\\ &\ge -(\sigma_3+\sigma_1)E. \end{aligned} \tag{9}$$

These leads

$$\begin{aligned} E(t) &= E_0 E_\alpha\left(-\int_0^t (\sigma_3+\sigma_1)\,ds\right) \ge 0,\\ &\Rightarrow E(t) \ge 0. \end{aligned} \tag{10}$$

From the 3rd equation of system (6), we acquire

$${}^{C}_{0}D^{\alpha}_{t}I = \sigma_3 E - (\sigma_4+\sigma_1) \ge -(\sigma_4+\sigma_1)I. \tag{11}$$

These leads

$$\begin{aligned} I(t) &= I_0 E_\alpha\left(-\int_0^t (\sigma_4+\sigma_1)\,ds\right) \ge 0,\\ &\Rightarrow I(t) \ge 0. \end{aligned} \tag{12}$$

From the 4th equation of system (6), we develop

$${}^{C}_{0}D^{\alpha}_{t}T = \sigma_4 I - (\sigma_5+\sigma_1)T \ge -(\sigma_5+\sigma_1)T, \tag{13}$$

leads to follow

$$T(t) = T_0 E_\alpha \left(- \int_0^t (\sigma_5 + \sigma_1) \right) ds \geq 0, \\ \Rightarrow T(t) \geq 0. \tag{14}$$

Similarly 5th equation of system (6), we acquire

$${}_0^C D_t^\alpha R = \sigma_5 T - \sigma_1 R \geq -\sigma_1 R, \tag{15}$$

leads to follow.

$$R(t) = R_0 E_\alpha \left(- \int_0^t \sigma_1 ds \right) \geq 0, \\ \Rightarrow R(t) \geq 0. \tag{16}$$

Hence, the results (S,E,I,T,R) of system (6) sustaining the primary conditions $S(t) \geq 0$, $E(t) \geq 0$, $I(t) \geq 0$, $T(t) \geq 0$, and $R(t) \geq 0$ for all $t \in [0, t_0)$ are nonnegative in the section $[0, t_0)$.

Now, we demonstrate that the boundedness of clarifications of system (6). The positivity of the solutions indicates that

$${}_0^C D_t^\alpha S \leq \wedge - \mu S. \tag{17}$$

From the beyond equation, we can write that $\lim_{t\to\infty} \leq \frac{\wedge}{\sigma_1}$ and $S \leq \frac{\Lambda}{\sigma_1}$.

Consider the total populations $N = S + E + I + T + R$. On differentiation gives ${}_0^C D_t^\alpha N \leq \wedge - \sigma_1 N$ which leads to $\lim_{t\to\infty} supN \leq \frac{(\wedge)}{(\sigma_1)}$. Then, we get $N \leq \frac{\Lambda}{\sigma_1}$

$$\Rightarrow S + E + I + T + R \leq \frac{\Lambda}{\sigma_1}. \tag{18}$$

Therefore, all the solution curves (S, E, I, T, R) sustaining by the primary conditions are consistently bounded in R_+^5 and in the section

$$\Omega = \left\{ (\mathrm{S}, \mathrm{E}, \mathrm{I}, \mathrm{T}, \mathrm{R}) \in R_+^5 \colon 0 \leq (\mathrm{S}, \mathrm{E}, \mathrm{I}, \mathrm{T}, \mathrm{R}) \leq \frac{\Lambda}{\sigma_1} \right\}. \tag{19}$$

4.2 Basic Reproduction Number

A crucial factor for communicable disease is the Basic Reproduction Number (R_0) which is distinct as the middling number of subordinate cases obtained by distinct primary case during the infectious dated in a susceptible populace. With R_0, the epidemic growth rate can be estimated, and the stability of the model will be analyzed [9]. R_0 Value can be determined through approach of next Generation Matrix method [35],

$$R_0 = \rho \left(F V^{-1} \right),$$

where

$$F = \begin{pmatrix} \sigma_2 + \sigma_1 \\ 0 \\ 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} (\sigma_3 + \sigma_1) E \\ \sigma_3 E - (\sigma_4 + \sigma_1) I \\ \sigma_4 I - (\sigma_5 + \sigma_1) T \end{pmatrix}.$$

The Jacobian of F and V are dual matrices F and V which determined at disinfection state $E = 0$, $I = 0$ and $T = 0$, we have

$$F = \begin{pmatrix} 0 & \sigma_2 & \sigma_1 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix}$$

and

$$V = \begin{pmatrix} (\sigma_3 + \sigma_1) & 0 & \\ \alpha & (\sigma_4 + \sigma_1) & 0 \\ 0 & -\sigma_4 & (\sigma_5 + \sigma_1) \end{pmatrix},$$

then

$$R_0 = \rho \left(F V^{-1} \right) = \frac{\sigma_2 \sigma_3}{(\sigma_3 + \sigma_1)(\sigma_4 + \sigma_1)} \\ + \frac{\sigma_3 \sigma_5 \sigma_1}{(\sigma_3 + \sigma_1)(\sigma_4 + \sigma_1)(\sigma_5 + \sigma_1)}. \tag{20}$$

4.3 Local Stability of Disease-Free Equilibrium

In this part, we utilized the method to investigate the local stability of the disease-free equilibrium point.

Theorem 4. *For $R_0 < 1$, the Disease-Free Equilibrium point $E_0 = \left(\frac{\wedge}{\sigma_1}, 0, 0, 0, 0 \right)$ was locally asymptotically stable and for $R_0 > 1$, it was unstable [36].*

Proof. The Jacobian matrix corresponding to the structure 1 at disease free equilibrium E_0 is

$$J(E_0) \\ = \begin{pmatrix} -\sigma_1 & 0 & -\sigma_2 & 0 & 0 \\ 0 & -(\sigma_1+\sigma_3) & \sigma_2 & 0 & 0 \\ 0 & \sigma_3 & -(\sigma_4+\sigma_1) & 0 & 0 \\ 0 & 0 & \sigma_4 & -(\sigma_5+\sigma_1) & 0 \\ 0 & 0 & 0 & \sigma & -\sigma_1 \end{pmatrix}. \tag{21}$$

The characteristic equation is

$$(\sigma_4 + \sigma_1)^2 (\sigma_4 + (\sigma_5 + \sigma_1)) \left({\sigma_4}^2 + a_1 \sigma_4 + a_2 \right) = 0, \tag{22}$$

where $a_1 = 2\sigma_1 + \sigma_3 + \sigma_4$ and $a_2 = (\sigma_1 + \sigma_3)(\sigma_4 + \sigma_1) - \sigma_3 \sigma_2$.

There are 5 Eigenvalues for the Jacobian matrix $J(E_0)$ of which first three are $-\sigma_1$, $-\sigma_1$, $(\sigma_5 + \sigma_1)$, and the remaining two Eigenvalues are roots of quadratic equation $(\lambda_2 + a_1 \lambda + a_2) = 0$, which are negative. Through Routh-Hurwitz criterion, all the roots of characteristic equation have destructive real part which revenues steady equilibrium if $a_1 > 0$ and $a_2 > 0$.

Since $\sigma_1 > 0$, $\alpha > 0$ and $\gamma > 0$, we have $2\sigma_1 + \alpha + \gamma > 0$ that is $a_1 > 0$.

Since $(\sigma_1+\alpha)(\gamma+\sigma_1)-\alpha\beta>0$ that is $a_2>0$.
If $R_0<1$, then

$$\frac{\sigma_1\sigma_2}{(\sigma_2+\sigma_1)(\sigma_4+\sigma_1)} + \frac{\sigma_2\sigma_5\sigma_1}{(\sigma_2+\sigma_1)(\sigma_4+\sigma_1)(\sigma_5+\sigma_1)}<1, \tag{23}$$

$\Rightarrow(\sigma_2+\sigma_3)(\sigma_4+\sigma_1)-\sigma_3\sigma_2>0$, that is $a_2>0$.
Therefore, $a_2>0$ if $R_0<1$.
Therefore, according to the Routh-Hurwitz criteria, the disease-free equilibrium point E_0 is locally asymptotically stable if $R_0<1$.

4.4 Global Stability of Disease-Free Equilibrium

In this part, we utilized the to investigate the global asymptotic stability of the disease-free equilibrium point.

Theorem 5. *The disease-free equilibrium points* $E_0=\left(\frac{\wedge}{\sigma_1},0,0,0,0\right)$ *of structure* 1 *was globally asymptotic stable if* $R_0<1$.

Proof. It can be detected that from the structure (6), the disease-free sections are S, R and the infected sections are E,I,T. The system of Equations (6) will be arranged as

$$\frac{dU}{dt}=Q(W,V),$$
$$\frac{dV}{dt}=F(W,V)$$
and
$$F(W,0)=0,$$

where W = $(S,R)\in R_+^2$, $V=(A,I,Q,J)\in R_+^3$.

By using the technique introduced by Casagrandi, Renato, et al [37], we derived global stability of the disease-free equilibrium point $E_0=\left(\frac{\Lambda}{\mu},0,0,0,0\right)$. For the worldwide asymptotic stability of E_0 the succeeding two conditions should be satisfied

1. $\frac{dW}{dt}=P(W,0)$ where X^* is worldwide asymptotically steady.
2. $F(W,V)=KV-\hat{F}(W,V)$, $\hat{F}(W,V)\geq 0$, where $K=D_VF(W^*,0)$ is the Metzler Matrix and $(X,Y)\in\omega$.

If the given system of equations (1) satisfies (2) then the equilibrium point E_0 is a global asymptotically stable for $R_0<1$.

Therefore, system (6) can be rewritten as

$$Q(W,0)=\begin{pmatrix}\wedge-\sigma_1S\\0\end{pmatrix},$$
$$K=\begin{pmatrix}(\sigma_3+\sigma_1)&0&0\\\alpha&(\sigma_4+\sigma_1)&0\\0&\sigma_4&(\sigma_5+\sigma_1)\end{pmatrix}$$
$$\hat{F}(W,V)=\begin{pmatrix}\sigma_2I(S_0-S)\\0\\0\end{pmatrix}.$$

Since $S_0>S$, by observation, $\hat{F}((W,V))\geq 0(W,V)\in\Omega$. We can say that the matrix K is M matrix by the definition of M and also, we able to find that $X^*=\left(\frac{\wedge}{\sigma_1},0\right)$ is globally asymptotic stable steady state of the limiting structure $\frac{dW}{dt}=Q(W,0)$.

Since the two conditions are fulfilled, the disease-free steady state $E_0=\left(\frac{\wedge}{\sigma_1},0,0,0,0\right)$ of structure of equations (6) is globally asymptotic stable if $R_0<1$.

4.5 Local Stability of the Endemic Equilibrium Point

We conclude the endemic steady state $X^*=(S^*E^*,I^*,T^*,R^*)$ with their possibility conditions are

$$S^*=\frac{\wedge}{\sigma_2I^*+\sigma_1},$$
$$E^*=\frac{\sigma_2S^*I^*}{(\sigma_3+\sigma_1)},$$
$$T^*=\frac{\sigma_4I^*}{(\sigma_3+\sigma_1)},$$
$$R^*=\frac{\sigma_5T^*}{\sigma_1},$$
$$I^*=\frac{(\wedge\sigma_3\sigma_2-\sigma_1(\sigma_4+\sigma_1))}{(\sigma_2(\sigma_4+\sigma_1(\sigma_5+\sigma_1)))}$$
$$=\frac{(\wedge(R_0-1)-\alpha\sigma_5\sigma_1)}{(\sigma_2(\sigma_4+\sigma_1)(\sigma+\sigma_1))}.$$

Theorem 6. *When* $R_0>1$, *then Endemic Equilibrium point* X^* *is locally asymptotically steady and unstable if* $R_0<1$.

Proof. The Jacobian matrix corresponding to the system (6) at endemic equilibrium point X^* is

$$J(X^*)=\begin{pmatrix}(-\sigma_2I^*+\sigma_1)&0&-\sigma_2S^*&0&0\\\sigma_2I^*&-(\sigma_1+\sigma_3)&\sigma_2S^*&0&0\\0&\sigma_3&-(\sigma_4+\sigma_1)&0&0\\0&0&\gamma&-(\sigma_5+\sigma_1)&0\\0&0&0&\sigma&-\sigma_1\end{pmatrix}. \tag{24}$$

The characteristic equation is

$$(\sigma_4+\sigma_1)(\sigma_4+(\sigma_5+\sigma_1))\left(\lambda^3+b_1\lambda^2+b_2\lambda+b_3\right)=0, \tag{25}$$

where

$$b_1=\sigma_2I^*+3\sigma_1+\sigma_3+\sigma_4,$$
$$b_2=(\sigma_3+\sigma_1)(\sigma_4+\sigma_1)-\alpha\sigma_2S^*+(\sigma_4+\sigma_1)(\sigma_2I^*+\sigma_1),$$

and

$$b_3=(\sigma_2I^*+\sigma_1)((\sigma_3+\sigma_1)(\sigma_4+\sigma_1)-\sigma_3\sigma_2S^*)-{\sigma_2}^2S^*I^*.$$

Therefore, the first two Eigen values are $-\sigma_1$, $-(\sigma_5+\sigma_1)$ and remaining three Eigenvalues are the roots of the $(\lambda^3+b_1\lambda^2+b_2\lambda+b_3)=0$.

Yet again if the constants of specific equation $a_1>0$, $a_2>0$, $a_3>0$ and $a_1a_2>a_3$ are true, formerly by Routh-Hurwitz criterion, altogether the roots of the specific equation have negative real portions and hence a stable equilibrium. Therefore, Endemic equilibrium at X^* is locally asymptotically stable if $R_0>1$.

5 Numerical Simulations

Here, we present some numerical models to illustrate potential behaviors of the hypothesized fractional-order flu. Taking various fractional-order values, we show several numerical simulations of susceptible, exposed, infected, treatment, and recovered individuals. All numerical simulations are performed in MATLAB for this research with the initial conditions of $S(0)=5$, $E(0)=2$, $I(0)=1$, $T(0)=1$, $R(0)=1$. Figure 2 shows the numerical solution of the flu model described by equation (9). It provides a comprehensive overview of the system's dynamics over time, illustrating the interactions between different population groups.

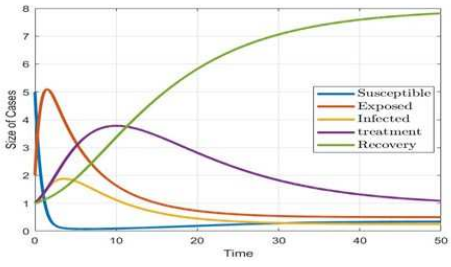

Fig. 2: Numerical solution of model (9).

Figure 3 illustrates the behavior of the susceptible population (S) as a function of time t. It showcases how the number of susceptible individuals changes over the course of the simulation, offering insights into the spread and containment of the flus.

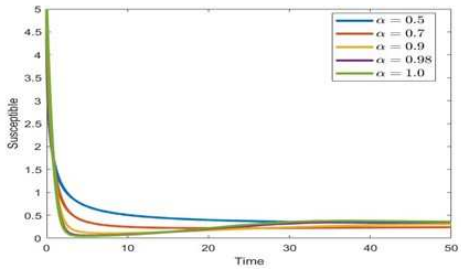

Fig. 3: Susceptible Population Over Time t.

Figure 4 displays the size of the exposed population (E) as a function of time t. It depicts the progression of individuals who have been exposed to the flu but are not yet infectious. This information is crucial for understanding the potential outbreak and transmission dynamics.

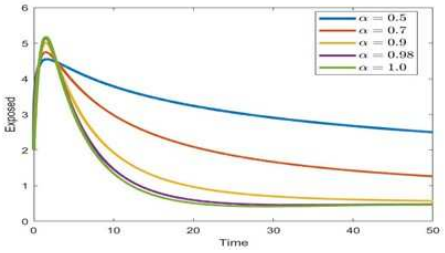

Fig. 4: Size of the exposed population over time t.

Figure 5 presents the size of the infected population (I) as a function of time t. It showcases the growth and decline of the infected individuals, providing valuable insights into the severity and progression of the flu outbreak.

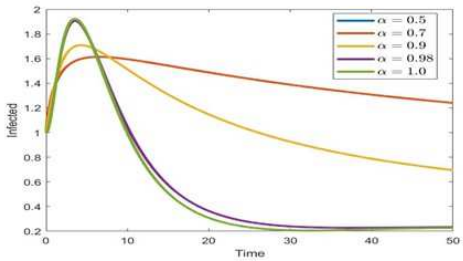

Fig. 5: Size of the infected population over time t.

Figure 6 illustrates the size of the treatment population (T) over time t. It depicts the number of individuals receiving medical treatment for the flu, providing insights into the healthcare system's demand and the effectiveness of treatment strategies.

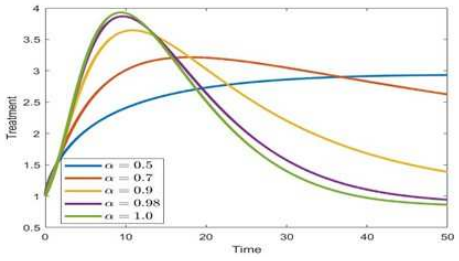

Fig. 6: Size of the treatment population over time t.

Figure 7 showcases the size of the recovered population (R) as a function of time t. It demonstrates the number of individuals who have successfully recovered from the flu, offering insights into the overall recovery rate and the duration of the outbreak.

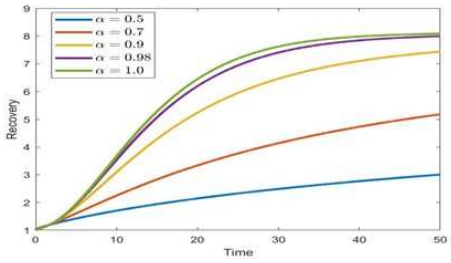

Fig. 7: Size of the recovered population over time t.

These figures collectively offer a comprehensive visual representation of the numerical simulations, enabling a deeper understanding of the dynamics and potential outcomes of the hypothesized fractional-order flu model.

6 Conclusion

In order to better comprehend the dynamics of the transmission of infectious diseases, epidemiological models have provided us with invaluable information. The paper presents the Fractional SEITR epidemiological model, which is a five-compartment framework, and discusses its fundamental properties. It was found to have a value of R_0 for the fundamental replication number. Verification of positivity and boundedness was carried out. It was proven that the disease-free equilibrium point E_0 exists and is locally and universally asymptotically stable for small values of $R_0 < 1$ similarly, the endemic equilibrium point X^* must exist and be locally asymptotically stable for large values of $R_0 > 1$. The reproduction number R_0 shows that the outbreak has reached epidemic proportions. As a result, the only way to decrease the spread of disease is to increase the rate of treatment. Furthermore, future studies can be performed to determine the most effective management strategies for the disease spread model, as well as the effects of medications and immunizations on the fractional SEITR model. As a future work, we advise the reader to study new models [38,39,40,41,42,43,44], with different kinds of fractional derivatives.

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