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Numerical Simulation of an Influenza Epidemic: Prediction with Fractional SEIR and the ARIMA Model

Salem Mubarak Alzahrani[1], *Rania Saadeh*[2,*], *Mohamed A.Abdoon*[3,4], *Ahmad Qazza*[2], *Fathelrhman EL Guma* [5,6], *and Mohammed Berir*[4,5]

[1]Department of Mathematics, Faculty of Science and Arts, Al-Baha University, Almandaq 1988, Saudi Arabia
[2]Department of Mathematics, Faculty of Science, Zarqa University, Zarqa 13110, Jordan
[3]Department of Basic Sciences (Mathematics), Deanship of Common First Year, Shaqra University, Riyadh 15342, Saudi Arabia
[4]Department of Mathematics, Faculty of Science, Bakht Al-Ruda University, Duwaym 28812, Sudan
[5]Department of Mathematics, Faculty of Science and Arts, Al-Baha university, Baljurashi 1988, Saudi Arabia
[6]Department of Statistical Study, Alsalam University, Alfula ,54411, Sudan

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Abstract: This article offers a condensed analysis of a fractional SEIR model used to track and forecast influenza spread. In addition, the seasonal evolution of influenza epidemics is predicted using the ARIMA model. The Atangana-Baleanu-Caputo (ABC) fractional derivative operator, which offers a more precise explanation of influenza dynamics than conventional integer operators, is the subject of the study. The study shows that the fractional order model outperforms the ARIMA model and agrees with actual data. The results emphasize the significance of using fractional models to health risk management and creating numerical methods with accurate parameter values. Graphical illustrations of several fractional orders are included in the article. Graphical illustrations of various fractional order and fractal dimension levels are included in the article. These findings have significance for creating pandemic mathematical models that are more accurate and devising realistic influenza control methods.

Keywords: Influenza, fractional SEIR, numerical simulation, ARIMA model, sensitivity analysis.

1 Introduction

During flu season, the highly contagious virus influenza, which spreads quickly through human contact, poses a serious threat to the public's health. This respiratory condition, which has symptoms ranging from mild to severe, affects people of all ages. While certain influenza strains can spread from humans to animals and vice versa, others are only contagious between people. The annual winter influenza epidemic is caused by influenza A and B, and the disease burden is also influenced by influenza C and D viruses [1,2,3,4]. It's crucial to comprehend the mechanics of the illness and create efficient management plans if you want to effectively stop and manage influenza epidemics. These objectives can be accomplished in large part by using mathematical modeling techniques, which also help researchers assess and forecast disease outbreaks.

Significant study has been put into mathematical modeling of the flu in recent years to help us better understand how it spreads and to enable effective preventative measures. In specifically, Abdoon et al. [5] created the fractional-order ABC derivation operator model, which enables the investigation of disease-free equilibrium stability, the study of endemic equilibrium points, and the examination of solutions that are positive for the influenza virus. Through numerical comparisons, this model based on fractions has produced promising results. Sabir et al. completed a big contribution as well. In 2023, [6] used stochastic neural networks to present the Mathematical Influenza Disease Model (MIDM). With lower mean square error values during training, validation, and testing than integer-order models, the MIDM subcategory demonstrated enhanced accuracy. The possibility for a revolution due to these improvements in modeling methodologies. These advances in modeling techniques have the potential to revolutionize the field of influenza research.

* Corresponding author e-mail: rsaadeh@zu.edu.jo

The use of numerous mathematical models has allowed for a thorough study of influenza virus propagation patterns. This research is essential because it enables us to comprehend the course of an influenza pandemic and create efficient defense and management measures. We can greatly influence public health outcomes by establishing early surveillance and prompt warnings of influenza epidemics [7,8,9,10,11]. Several techniques exist right now for forecasting the onset of infectious disease outbreaks. The neural network prediction model [12,13,14], the SEIR model [2,15,16], and ARIMA [17, 18,19] are notable examples, each with unique benefits and drawbacks. The best model must be chosen in order to increase prediction accuracy, which necessitates a thorough study of the particular disease and the data that are available. The vast majority of current research on modeling influenza is centered on traditional mathematical models that do not take into consideration memory effects, which are crucial to many biological processes.

Recent research, however, has demonstrated that non-local operators are more effective at capturing memory features than conventional local differential and integral operators [20,21,22,23,24,25,26,27,28]. Our study intends to construct a unique mathematical model that uses the operator-based derivation of the fractional-order ABC operator in order to overcome this restriction and enhance the realism of influenza modeling. We anticipate that our model will offer a more thorough understanding of influenza transmission dynamics by taking memory effects into account through fractional leads [19,29,30].

We contrast the outcomes of our suggested fractional model with those of the ARIMA model, a popular strategy in epidemic modeling, to see how effective it is. Through this comparison, we can assess the fractional model's benefits for capturing memory-related phenomena and its potential to surpass established techniques for predicting and controlling influenza outbreaks [31,32,33,34].

Our investigation's major goal is to increase the understanding of the flu pandemic through the creation and evaluation of fractional SEIR and ARIMA models [35,36]. Our goal is to produce precise and dependable predictions of influenza dynamics in Saudi Arabia by meticulous parameter estimate and careful consideration of population infectivity levels.

It is crucial to remember that conventional models that disregard memory effects might not adequately capture the intricacy of actual epidemics. In order to ensure that our results are consistent with the actual epidemiological situation and to increase the practical relevance and applicability of our results, we incorporate non-local operators and validate our models' using data from reliable sources, such as the World Health Organization and medical literature [37,38].

The key findings of our study will provide insight into the improvements in influenza modeling made possible by the application of fractional SEIR and ARIMA models. We seek to provide useful insights into the dynamics of influenza transmission and the possible advantages of adopting these novel modeling tools by completely presenting the results and giving detailed analysis.

Our research has the potential to considerably contribute to the development of more efficient influenza surveillance, outbreak prediction, and response tactics by fusing cutting-edge mathematical modeling methods with actual data and thorough analysis. The findings of this study may not only have positive effects on Saudi Arabia's public health, but they may also have wider ramifications for the investigation of other infectious diseases and intricate biological systems. This interdisciplinary approach brings up fresh research opportunities and creative modeling strategies, improving epidemic preparedness and response globally.

This document is divided into the following sections: Section 2 presents the materials and methods used in our study; Section 3 performs a thorough analysis of the proposed model; Section 4 presents the application of the ARIMA model; Section 5 presents numerical simulations for validating our models; Section 6 presents influenza predictions derived from the ARIMA model; Section 7 assesses the performance of both models; and Section 8 discusses the findings.

2 Materials and Methods

We give the background material required for our study in the following section.

2.1 Atangana-Baleanu derivatives

We define the innovative fractional derivatives developed by Atangana and Baleanu [39,40] in this subsection.

Definition 1.*[39] As a function $f(t)$, the Atangana-Baleanu fractional integral with nonlocal kernel is defined as*

$$
\begin{aligned}
&{}^{AB}_{a}I^{\alpha}_{t}[f(t)] \\
&\quad = \frac{1-\alpha}{B(\alpha)}f(t) + \frac{\alpha}{B(\alpha)\Gamma(\alpha)}\int_{a}^{t} f(j)(t-j)^{\alpha-1}dj,
\end{aligned}
\tag{1}
$$

where $\Gamma(\alpha)$is the Gama function and $(B(\alpha) = 1-\alpha+\frac{\alpha}{\Gamma(\alpha)}$.

Note that when $\alpha = 0$, the initial function is recovered, and $\alpha = 1$ gives the ordinary integral.

Definition 2.*Let $f \in H^1(a,b)$, $b > a$, and H^1 the space of the square-integrable functions such that*

$$
H^1(a,b) = \left\{\psi(s) \in L^2(a,b) \,|\, \psi'(s) \in L^2(a,b)\right\}. \tag{2}
$$

Then, the Atangana-Baleanu fractional derivative in the Riemann-Liouville sense [39] for $f(t)$ is given by

$$ {}^{ABR}_{a}D^{\alpha}_{t}\left(f\left(t\right)\right)=\frac{B\left(\alpha\right)}{1-\alpha}\frac{d}{dt}\int_{a}^{t}f\left(x\right)E_{a}\left[-\alpha\frac{\left(t-x\right)^{\alpha}}{1-\alpha}\right]dx, \tag{3} $$

and the Atangana-Baleanu fractional derivative in the Caputo sense [41]for $f(t)$ is given by

$$ {}^{ABC}_{a}D^{\alpha}_{t}\left(f\left(t\right)\right)=\frac{B\left(\alpha\right)}{1-\alpha}\int_{a}^{t}f^{'}\left(x\right)E_{\alpha}\left[-\alpha\frac{\left(t-x\right)^{\alpha}}{1-\alpha}\right]dx, \tag{4} $$

where $\alpha\in[0,1]$, $B\left(\alpha\right)=1-\alpha+\frac{\alpha}{\Gamma(\alpha)}$ and E_{α} is the Mittag-Leffler function.

According to the argument, $B(\alpha)$ has the same characteristics as in the Caputo and Fabrizio situations. These definitions have practical applications and are advantageous when applying the Laplace transform to resolve specific physical issues.

Definition 3.*A continuous function's Laplace transform is given by*

$$ \mathcal{L}\left[f\left(t\right)\right]=F\left(s\right)=\int_{0}^{\infty}e^{-st}f\left(t\right)dt,Re\left(s\right)>0. $$

The Laplace transform of the Atangana-Baleanu fractional derivative in the sense of Riemann-Liouville (3) and Caputo (4) respectively, are given by [41]

1.
$$ \mathcal{L}\left[{}^{ABR}_{0}D^{\alpha}_{t}\left(f\left(t\right)\right)\right]=\frac{B\left(\alpha\right)}{1-\alpha}\frac{s^{\alpha}F\left(s\right)}{s^{\alpha}+\frac{\alpha}{1-\alpha}}, \tag{5} $$

2.
$$ \mathcal{L}\left[{}^{ABC}_{0}D^{\alpha}_{t}\left(f\left(t\right)\right)\right]=\frac{B\left(\alpha\right)}{1-\alpha}\frac{F\left(s\right)s^{\alpha}-s^{\alpha-1}f\left(0\right)}{s^{\alpha}+\frac{\alpha}{1-\alpha}}. \tag{6} $$

2.2 The fractional model

The SIR model, first presented by [42], quantifies the spread of an outbreak. The SEIR model was created by incorporating an exposed (E) compartment into the SIR model in order to account for the disease's latent period [43]. This model has been used by researchers like Zhilan Feng [44] and Rafiqul Islam et al. [11] to examine influenza epidemics in Bangladesh and assess various management approaches, respectively.
The SEIR model is a commonly used segmented epidemiological model for characterizing epidemic disease outbreaks. It considers the susceptible population and the dynamics of disease transmission. During the incubation period, individuals may be infected but not display symptoms. Additionally, the SEIR model can be modified to include a compartment solely for individuals who are sick but not actively transmitting the virus [45, 46].

In the SEIR model, individuals in the susceptible (S) compartment transition to the exposed (E) compartment through effective contact transmission from infected individuals (I) at a rate of α_2. Other model parameters include the infection rate (α_3) and the recovery rate (α_4). Assuming a constant population size, we obtain the population-scaled SEIR classical model [10,47,48] described by the following equations:

$$ \begin{aligned} \frac{dS\left(t\right)}{dt}&=-\frac{\alpha_2}{N}I\left(t\right)S\left(t\right)+\alpha_0N-\alpha_1S\left(t\right),\\ \frac{dS\left(t\right)}{dt}&=-\frac{\alpha_2}{N}I\left(t\right)S\left(t\right)+\alpha_0N-\alpha_1S\left(t\right),\\ \frac{dE\left(t\right)}{dt}&=-\left(\alpha_1+\alpha_3\right)E\left(t\right)+\frac{\alpha_2}{N}I\left(t\right)S\left(t\right),\\ \frac{dI\left(t\right)}{dt}&=-\left(\alpha_1+\alpha_4\right)I\left(t\right)+\alpha_3E\left(t\right),\\ \frac{dR(t)}{dt}&=-\alpha_1R\left(t\right)+\alpha_4I\left(t\right). \end{aligned} \tag{7} $$

These equations capture the dynamics of susceptible (S), exposed (E), infected (I), and recovered (R) individuals in the population.
The Atangana-Baleanu-Caputo fractional order derivatives provide more realistic solutions for the fractional-order mathematical influenza disease model, as fractional derivatives inherently involve memory. By replacing the time derivatives in the SEIR model (1) with ABC operators, more accurate results can be obtained. Thus, the fractional nonlinear system SEIR model in the sense of ABC derivative is given by

$$ \begin{aligned} D^{ABC}S\left(t\right)&=-\frac{\alpha_2}{N}I\left(t\right)S\left(t\right)+\alpha_0N-\alpha_1S\left(t\right),\\ D^{ABC}E\left(t\right)&=-\left(\alpha_1+\alpha_3\right)E\left(t\right)+\frac{\alpha_2}{N}I\left(t\right)S\left(t\right),\\ D^{ABC}I\left(t\right)&=-\left(\alpha_1+\alpha_4\right)I\left(t\right)+\alpha_3E\left(t\right),\\ D^{ABC}R(t)&=-\alpha_1R\left(t\right)+\alpha_4I\left(t\right). \end{aligned} \tag{8} $$

The entire population is divided into four distinct categories under the fractional epidemiological model: vulnerable, incubating, infected, and recovering. Additionally, it is presumptive that people leave the system at the natural death rate and that the population is exposed at the natural birth rate. The pace of transfers fluctuates because the virus spreads efficiently across people. While preserving a fixed population size, the model also takes into account the rates of infection, infection of latent people, and recovery [39]. The fractional-order mathematical influenza disease model is solved using a novel mathematical model for influenza in which the normal derivative operator is swapped out for the Atangana-Baleanu-Caputo (ABC) fractional-order derivative operator.

2.3 Estimation of Parameter Values

We use numerical techniques to incorporate real influenza infection data into the system (8) in order to accurately anticipate the spread of the disease. We use the method outlined in [18,49,50,51] to estimate the parameters and numerically solve the system. Table 1 contains the estimated and modified parameter values. Notably, the key threshold value, the fundamental reproduction number, is expected to be around 0.17.
For the initial conditions, we initialize the system as follows: $N = 48,000,000$, $S(0) = 47,999,990$, $E(0) = 3$, $I(0) = 7$, and $R(0) = 0$.
To estimate the values of $\alpha_0, \alpha_1, \alpha_2, \alpha_3$ and α_4, we utilize a fitting procedure that employs a non-linear least squares algorithm. The resulting parameter values obtained from the fitting procedure are presented in Table 1.
The values of $\alpha_0, \alpha_1, \alpha_2, \alpha_3$, and α_4 are estimated using a fitting technique that makes use of the non-linear least squares algorithm. The final parameter values determined through the fitting process are listed in Table 1.

Table 1: Parameter values

Variable	Description	Value	Source
α_0	Natural birth rate	0.001	Fitted
α_1	The natural death rate	0.001	Fitted
α_2	The transmission rate	0.98	Fitted
α_3	The incubation rate	0.78	Fitted
α_4	Recovery rate	0.62	Fitted

3 Analysis of the Model

In this section, the stability and equilibrium points of the fractional order model (8) presented in the work are discussed. Two different types of equilibrium points are studied: endemic equilibrium (EE) and disease-free equilibrium (DFE). The EE point is derived by solving the system of equations and assuming a non-zero infected individual, while the DFE point is obtained by assuming there are no infected individuals. The dynamics of the disease are illustrated by the equations for S, E, I and R at the EE point. The fundamental reproduction number R_0, which serves as a stability indicator, is derived from the equilibrium points. A sensitivity study that assesses how model parameters affect R_0 is also provided.

3.1 The Equilibrium Points of the Model

To analyze the fractional-order model (8) and understand its equilibrium points, we distinguish between two main categories: the DFE and EE.
For the DFE point, we assume $I = 0$ and set the right-hand side of all equations in system (8) to 0. Thus, the DFE point of the system is given by

$$T_{def} = (N, 0, 0, 0). \tag{9}$$

On the other hand, if one considers $I \neq 0$, the (EE) solution satisfies the following conditions

$$\frac{\alpha_2}{N} IS + \alpha_0 N - \alpha_1 S(t) = 0, \tag{10}$$

$$-(\alpha_1 + \alpha_3) E + \frac{\alpha_2}{N} IS = 0, \tag{11}$$

$$-(\alpha_1 + \alpha_4) I + \alpha_3 E = 0, \tag{12}$$

$$-\alpha_1 R + \alpha_4 I = 0. \tag{13}$$

From equation (12), we can express E as

$$E = \frac{\alpha_1 + \alpha_4}{\alpha_3} I. \tag{14}$$

Substituting (14) into [52] and dividing by I, we obtain an expression for S

$$S = \frac{N(\alpha_1 + \alpha_3)(\alpha_1 + \alpha_4)}{\alpha_2 \alpha_3}. \tag{15}$$

Substituting in [5] and setting $\alpha_0 = \alpha_1$, we can solve for I

$$I = \frac{\alpha_1 N(\alpha_1 \alpha_3 - (\alpha_1 + \alpha_3)(\alpha_1 + \alpha_4))}{\alpha_2 (\alpha_1 + \alpha_3)(\alpha_1 + \alpha_4)}. \tag{16}$$

From (14), an expression for E is obtained as

$$E = \frac{\alpha_1 N(\alpha_1 \alpha_3 - (\alpha_1 + \alpha_3)(\alpha_1 + \alpha_4))}{\alpha_2 \alpha_3 (\alpha_1 \alpha_3)}. \tag{17}$$

Finally, using (13) and (16), we can express R as

$$R = \frac{\alpha_4 N[\alpha_1 \alpha_3 - (\alpha_1 + \alpha_3)(\alpha_1 + \alpha_4)]}{\alpha_2 (\alpha_1 + \alpha_3)(\alpha_1 + \alpha_4)}. \tag{18}$$

Based on the above discussion, the EE point can be represented as follows

$$T_{EE} = (S_0, E_0, I_0, R_0), \tag{19}$$

where

$$\begin{aligned} S_0 &= \frac{N(\alpha_1 + \alpha_3)(\alpha_1 + \alpha_4)}{\alpha_2 \alpha_3}, \\ E_0 &= \frac{\alpha_1 N(\alpha_1 \alpha_3 - (\alpha_1 + \alpha_3)(\alpha_1 + \alpha_4))}{\alpha_2 \alpha_3 (\alpha_1 \alpha_3)}, \\ I_0 &= \frac{\alpha_1 N(\alpha_1 \alpha_3 - (\alpha_1 + \alpha_3)(\alpha_1 + \alpha_4))}{\alpha_2 (\alpha_1 + \alpha_3)(\alpha_1 + \alpha_4)}, \\ R_0 &= \frac{\alpha_4 N(\alpha_1 \alpha_3 - (\alpha_1 + \alpha_3)(\alpha_1 + \alpha_4))}{\alpha_2 (\alpha_1 + \alpha_3)(\alpha_1 + \alpha_4)}. \end{aligned} \tag{20}$$

The equilibrium points of the fractional-order model (8) are crucial for various stability conclusions related to the fundamental reproductive number R_0, which will be discussed in the next subsection.

3.2 The basic reproduction numbers

The computation of basic reproduction numbers plays a crucial role in understanding the dynamics of infectious diseases. In the context of Equation (8), it is evident that the classes $I(t)$ and $E(t)$ are the ones primarily affected. To analyze the system holistically, we can represent the fractional-order differential operator as

$$D^{\alpha}\varnothing(t) = F(\varnothing(t)) - V(\varnothing(t)). \tag{21}$$

Considering the combined class $\varnothing = [E.I]$, we define the vectors f and v as follows:

$$f = \begin{bmatrix} \frac{\alpha_2 SI}{N} \\ 0 \end{bmatrix}, v = \begin{bmatrix} (\alpha_1+\alpha_3)E(t) \\ (\alpha_1+\alpha_4)I(t) + \alpha_3 E(t) \end{bmatrix}. \tag{22}$$

The Jacobian matrices F and V are obtained by differentiating f and v with respect to $\varnothing$, respectively:

$$F = \begin{bmatrix} 0 & \frac{\alpha_2 S}{N} \\ 0 & 0 \end{bmatrix}, V = \begin{bmatrix} \alpha_1+\alpha_3 & 0 \\ \alpha_3 & \alpha_1+\alpha_4 \end{bmatrix}. \tag{23}$$

To calculate the basic reproduction number, we need the inverse of matrix V:

$$V^{-1} = \begin{bmatrix} \frac{1}{\alpha_1+\alpha_3} & 0 \\ \frac{\alpha_3}{(\alpha_1+\alpha_3)(\alpha_1+\alpha_4)} & \frac{1}{\alpha_1+\alpha_4} \end{bmatrix}. \tag{24}$$

The product of matrices F and V^{-1}, denoted as FV^{-1}, provides us with the expression for the basic reproduction number R_0:

$$FV^{-1} = \alpha_1 \begin{bmatrix} \frac{\alpha_0\alpha_2\alpha_3}{(\alpha_1+\alpha_3)(\alpha_1+\alpha_4)} & \frac{\alpha_0\alpha_2}{\alpha_1(\alpha_1+\alpha_4)} \\ 0 & 0 \end{bmatrix}. \tag{25}$$

Hence, the basic reproduction number R_0 is given by the spectral radius of FV^{-1}, which can be computed as follows:

$$R_0 = \rho\left(FV^{-1}\right) = \frac{\alpha_0\alpha_2\alpha_3}{\alpha_1(\alpha_1+\alpha_3)(\alpha_1+\alpha_4)}. \tag{26}$$

For determining the disease's potential for epidemic spread, it is essential to comprehend the value of R_0. If R_0 is less than 1, it means that there won't likely be a significant outbreak of the illness. On the other hand, if R_0 is higher than 1, it may indicate that the disease has a high chance of populating a large area.

It is important to remember that the calculation of R_0 in Equation (26) relies on the precise parameter values shown in Table 1.

According to Section 2.3, a fitting approach was used to estimate these values. Sensitivity analysis is another method that may be used to assess how each parameter affects the value of R_0.

This analysis provides insights into which parameters have a more significant influence on the disease's reproductive potential.

3.3 Local Stability of Disease-Free Equilibrium

In this subsection, we analyze the stability properties of the system around the disease-free equilibrium to determine whether it is stable or unstable.

Theorem 1.*The system described by Equation (8) exhibits local stability at the disease-free equilibrium point, denoted as E_{def}, if the basic reproduction number $R_0 < 1$ is less than 1. Conversely, it is unstable if R_0 is greater than 1.*

Proof: To begin, we compute the Jacobian matrix for the system given by Equation (8):

$$J = \begin{bmatrix} \frac{-\alpha_2}{N}I - \alpha_1 & 0 & \frac{-\alpha_2 S}{N} & 0 \\ \frac{\alpha_2 I}{N} & -(\alpha_1+\alpha_3) & \frac{\alpha_2 S}{N} & 0 \\ 0 & \alpha_3 & -(\alpha_1+\alpha_4) & 0 \\ 0 & 0 & \alpha_4 & -\alpha_1 \end{bmatrix}. \tag{27}$$

At the disease-free equilibrium point E_{def}, the Jacobian matrix simplifies to:

$$J(E_{\text{def}}) = \begin{bmatrix} -\alpha_1 & 0 & \frac{-\alpha_2\alpha_0}{\alpha_1} & 0 \\ 0 & -(\alpha_1+\alpha_3) & \frac{\alpha_2\alpha_0}{\alpha_1} & 0 \\ 0 & \alpha_3 & -(\alpha_1+\alpha_4) & 0 \\ 0 & 0 & \alpha_4 & -\alpha_1 \end{bmatrix}. \tag{28}$$

By analyzing the eigenvalues, we have

$$\begin{aligned} \lambda_1 &= -\alpha_1, \\ \lambda_2 &= -\alpha_1, \\ \lambda_3 &= \frac{-\left(2\alpha_1^2+\alpha_1\alpha_3+\alpha_1\alpha_4\right)-K}{2\alpha_1}, \\ \lambda_4 &= \frac{-\left(2\alpha_1^2+\alpha_1\alpha_3+\alpha_1\alpha_4\right)+K}{2\alpha_1}, \end{aligned} \tag{29}$$

where

$$k = \sqrt{4\alpha_0\alpha_1\alpha_2\alpha_3 + \alpha_1^2\alpha_3^2 - 2\alpha_1^2\alpha_3\alpha_4 + \alpha_1^2\alpha_4^2}. \tag{30}$$

If $2\alpha_1^2 + \alpha_1\alpha_3 + \alpha_1\alpha_4 > k$, and $\lambda_3 < 0$, then $R_0 < 1$. When $R_0 < 1$, it fulfills this requirement, proving that the system in Equation (8) is locally asymptotically stable. Contrarily, if $2\alpha_1^2 + \alpha_1\alpha_3 + \alpha_1\alpha_4 > k$, then $\lambda_3 > 0$, and we draw the conclusion that $R_0 > 1$. For $R_0 > 1$, the system given by Equation (8) is hence unstable.

Note that the stability analysis in Theorem 1 offers vital insights into how the system behaves close to the disease-free equilibrium. However, the analysis makes some assumptions about parameter values, which are detailed in Section 2.3. To determine how particular factors affect the stability of the system, sensitivity analysis should be carried out.

3.4 Sensitivity Analysis

To determine the effect of various parameters on the fundamental reproduction number, R_0, we conduct a sensitivity analysis in this subsection.
The sensitivity analysis offers useful insights into how changes in a parameter can affect the system dynamics.

Definition 4.*[47] The basic reproduction number, R_0, is sensitive to a particular parameter, k, as measured by the normalized sensitivity index, abbreviated as C_K^R. In order to compute it, use the equation:*

$$C_k^{R_0} = \frac{\partial R_0}{\partial k} \times \frac{k}{R_0}.$$

By applying the formulation given in Equation (13) and utilizing the parameter values from Table 1, we can compute the sensitivity indices for each parameter in R_0. The resulting sensitivity indices are presented in Table 2, highlighting the sensitivity of each parameter.

Table 2: Fitted parameter values for influenza cases and their corresponding sensitivity indices.

Variable	Value	Sensitivity Index
α_0	0.001	1
α_1	0.009	-1.0284489
α_2	0.98	+0.99999
α_3	0.78	+0.0126399
α_4	0.62	-0.9841909

The sensitivity indices provide insights into the relationship between parameter variations and the resulting changes in R_0. Positive sensitivity indices for parameters α_0, α_2 and α_3 indicate that increasing or decreasing these parameters while holding the others constant will result in a corresponding increase or decrease in R_0. This suggests that an increase of R_0 is detrimental to the population. Conversely, negative sensitivity indices for parameters α_1 and α_4 suggest that altering the values of these parameters in either direction, while keeping the others constant, will lead to changes in R_0 in the opposite direction.
It is important to consider the sensitivity analysis results when making decisions or implementing interventions related to the control and prevention of influenza outbreaks. By understanding the influence of individual parameters on R_0, policymakers and public health officials can prioritize interventions targeting the most sensitive parameters, thereby maximizing the effectiveness of disease control measures.

4 Autoregressive integrated moving average (ARIMA)

The ARIMA model is a well-established linear model widely used for time series forecasting. Despite its long-standing presence, ARIMA has been creatively employed in forecasting tasks. In this research, ARIMA was utilized with the aid of *R*programming. ARIMA processes offer a significant advantage in simulating time series that exhibit trends, seasonal patterns, and short-term correlations, even when working with limited data. Before applying ARIMA for time series analysis [10,40], the following steps need to be performed:

- Model identification: The appropriate ARIMA model parameters need to be identified, which include autoregressive terms, moving average terms, and the number of differences required for achieving stationarity.
- Parameter estimation: The model parameters are estimated using various techniques such as maximum likelihood estimation.
- Diagnostics through residual testing: The residuals obtained from the fitted ARIMA model are examined for any patterns or deviations from randomness. Diagnostic tests help assess the adequacy of the model and identify any further improvements needed.
- Future prediction: Once the ARIMA model is validated and deemed satisfactory, it can be used for making future predictions and forecasting the behavior of the time series.

ARIMA models assume linearity and adherence to a statistical distribution in the time series being analyzed. They encompass different popular forms such as autoregressive models, moving average models, and seasonal ARIMA (SARIMA) models [34-35]. By utilizing the lag operator, we can represent the ARIMA $(\Lambda_1, \Lambda_2, \Lambda_3)$ model as follows

$$\Psi(I)(1-I)^2 x_t = \Phi(I)\xi_t. \tag{31}$$

Here, Λ_1 represents the number of autoregressive terms, Λ_2 denotes the number of moving average terms, and Λ_3 indicates the number of differencing operations required to achieve stationarity. These parameters are nonnegative integers. The coefficients Ψ and Φ correspond to the model's autoregressive and moving average terms, respectively.

5 Numerical Simulations

This section contains a series of numerical simulations performed with the influenza model to show how fractional order influenza is expected to behave. Using the ABC operator with a fractional order of $\alpha = 0.95$, our proposed model is presented visually. Furthermore, we use numerical simulations to study the dynamics of

vulnerable, exposed, infected, and recovered individuals across different fractional-order values. Using the starting values and parameter values listed in Table 1, all simulations are performed in MATLAB.

The Saudi Ministry of Health provided a dataset for the simulations, covering 305 weeks from the first week of January 2017 to the 47th week of 2022. The Saudi Arabian Ministry of Health provided accurate data used to calculate the parameter values in Table 1. The number of confirmed influenza cases over a 200-week period is shown in Figure 1 to give viewers a visual understanding of the cases in Saudi Arabia -to mediate Arabia.

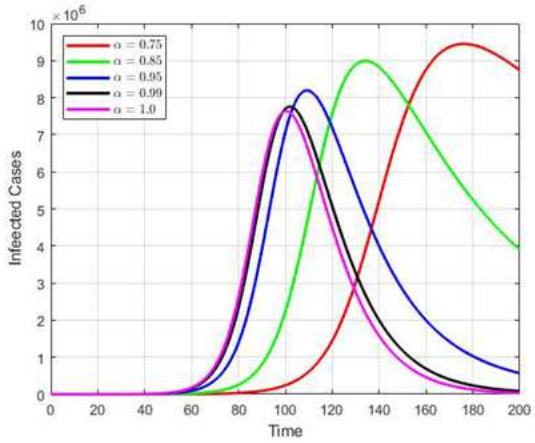

Fig. 1: Number of influenza cases confirmed in Saudi Arabia over time.

These simulations allow us to see how the influenza model dynamically responds to different fractional order scenarios and provide us with important information on how the virus spread and what impact it had in Saudi Arabia.

6 Forecasting influenza using ARIMA

This section presents the results of applying ARIMA models to weekly data reflecting the number of influenza cases from week 1 of 2017 to week 42 of 2022. The right ARIMA model was found, its parameters estimated, and its performance evaluated using R and Python software. The dataset used provides a comprehensive overview of influenza incidence over time and spans a six-year period. Figure 2 shows the development of influenza cases between 2017 and 2022. The two years with the highest infection rates were 2020 and 2023, while the years with the mildest outbreaks were 2019 and 2018. In contrast, fewer cases were recorded in the first year of 2017, the year of records, as well as in the COVID lockdown years of 2021 and 2022.

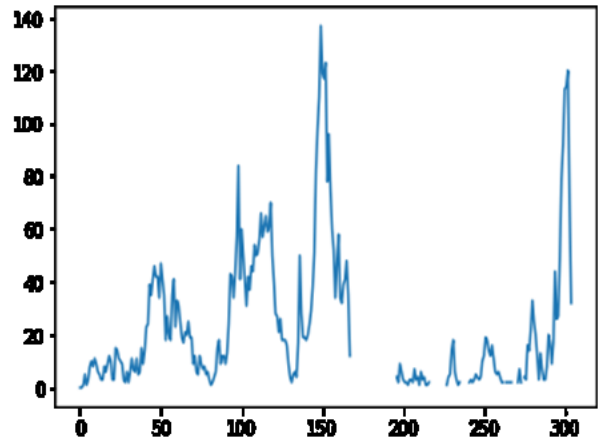

Fig. 2: Weekly influenza cases in Saudi Arabia, from winter 2016/7 to winter 2022/3.

To evaluate the stationarity of the influenza case series, an Augmented Dickey-Fuller test was performed, and the results are presented in Table 3. The Augmented Dickey-Fuller value of 3.6829 with a probability value of 0.02548 indicates that the series is stationary, supporting the suitability of applying ARIMA models.

Table 3: Augmented Dickey-Fuller Test

Value of Dickey Fuller	Lag order	p-value
3.6829	6	0.02548

Additionally, the correlogram, auto correlation function (ACF), and partial auto correlation function (PACF) plots (Figure 3) were analyzed for the confirmed influenza cases. The empirical findings suggest a gradual decay of the ACF towards zero, while the PACF shows a significant positive peak at one lag. These observations align with the established hypotheses and provide further support for the chosen models.

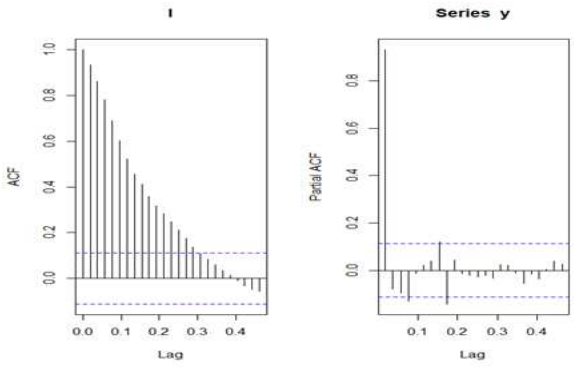

Fig. 3: ACF and PACF of the weekly influenza cases in Saudi Arabia.

Utilizing the ARIMA library in R programming, the ARIMA $(2,0,1)$ model with a nonzero mean was identified as the appropriate model for modeling the confirmed influenza case data based on established model selection criteria. Once the models are identified and the parameters are estimated, the next step involves validating the models by examining the residuals. Figure 3 indicates that the residuals follow a normal distribution and exhibit independence, resembling white noise. The majority of residuals align with the straight line, indicating normality, with only a few falling outside the line. These findings support the conclusion that there are no significant correlations among the residuals in the series.
To further assess the distribution of errors, histograms and normal probability plots (Figure 4) were employed. A straight line on the normal probability plot suggests that the residuals follow a normal distribution, with slight deviations indicating the best-fit line. Figure 4 shows the residuals of the ARIMA (2,0,1) model with a non-zero mean for weekly influenza cases in Saudi Arabia.

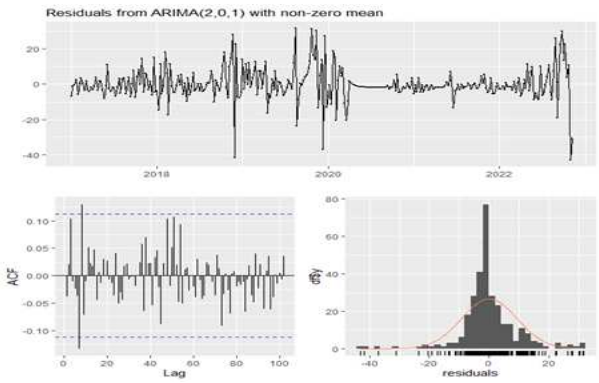

Fig. 4: Weekly influenza cases in Saudi Arabia, residual values of ARIMA (2,0,1) with non-zero mean.

The main goal of ARIMA modeling is to predict a variable using the information already available. Figure 5 shows a 30-week forecast generated using the ARIMA $(2,0,1)$ model with a non-zero mean to provide information about the expected future behavior of influenza cases.

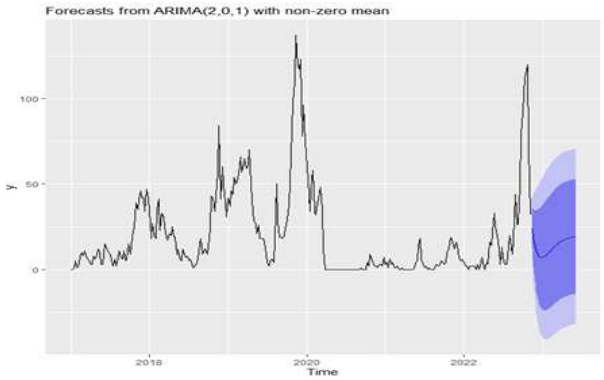

Fig. 5: 30-week forecast generated using ARIMA $(2,0,1)$ with non-zero mean.

These results demonstrate how accurately ARIMA models predict influenza cases and provide relevant data for public health planning and interventions.

7 Evaluation of the Precision of Fractional SEIR and ARIMA Methods

This section evaluates the ability of the fractional SEIR and ARIMA models to predict and account for confirmed influenza cases. We use absolute mean error (MAE) and root mean square error (RMSE) metrics [39] to assess the effectiveness of these models. Below is the formula for calculating the MAE:

$$MAE = \frac{\sum_{j=1}^{n} |y_t - \delta_t|}{n}. \tag{32}$$

The RMSE is calculated as follows:

$$RMSE = \sqrt{\frac{\sum_{j=1}^{n} (y_t - \delta_t)^2}{n}}. \tag{33}$$

In this case, represents the total number of time series points, y_t the value observed at the point in time t, and δ_t the value predicted by the fitted model that considered the 30-week projection.
Using the degrees of fit of the fractional SEIR and ARIMA models, we assess the prevalence of influenza in Saudi Arabia. To assess the effectiveness of each model, its performance is measured against a number of criteria. It is important to remember that the particular data set being examined will determine that one model is more effective than another.
The fractional SEIR model implemented with the ABC operator fits the observed data better than the ARIMA model results, as shown by the results in Table 4. Therefore, in these circumstances, the fractional SEIR model would be a good choice to mimic influenza cases.

Table 4: Performance comparison of the fractional SEIR and ARIMA models.

Method	MAE	RMSE
Fractional SEIR	4.26814	0.3625
ARIMA (2,0,1) with non-zero mean	4.26814	2.788

These results underscore the increased accuracy of the fractional SEIR model in detecting and predicting influenza cases and demonstrate its potential to strengthen influenza surveillance and control initiatives.

8 Conclusion

The purpose of this study was to simulate, model and predict the spread of the influenza virus in Saudi Arabia.

We used both the fractional SEIR model and the ARIMA model to analyze reported influenza cases from the first week of 2017 to the thirty-first week of 2022. While the ARIMA model was used to predict the seasonal trends of the influenza epidemic, the fractional SEIR model was used to simulate the confirmed cases. Through sensitivity analyses, we uncovered important factors that have a major impact on the dynamics of influenza transmission in Saudi Arabia. We found that higher influenza prevalence can be caused by increases in natural birth rate, transmission rate and incubation rate. These sensitive parameters must be estimated precisely, as even small changes can have a significant impact on the quantitative results. Insensitive parameters, on the other hand, do not require an exact estimate, since minor fluctuations in these parameters do not have a significant impact on the target variable. In terms of accuracy in predicting influenza outbreak dynamics, the proposed fractional SEIR model performed better than the ARIMA (2,0,1) model with a non-zero mean. According to these results, the fractional SEIR model could be an effective method for predicting confirmed influenza cases.

ARIMA models, being a prevalent choice in time series forecasting, are subject to certain limitations that can impact their accuracy. These limitations are inherent to various statistical forecasting methodologies.

The limitation of ARIMA models lies in their assumption of linearity in variable relationships, thereby constraining their capacity to effectively capture intricate non-linear relationships.

Future studies should investigate disease prevention methods and drug effects in the context of fractional SEIR models [53,54,55,56]. To better understand influenza dynamics and increase forecast accuracy, additional models such as those mentioned in references [57,58,59] can be further investigated. Overall, this study advances influenza modeling and sheds light on influenza transmission dynamics in Saudi Arabia. The conclusions impact public health preparedness and can help design successful influenza control and prevention programs. In the future, we intend to solve new models with new fractional operators.

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Salem Mubarak Alzahrani Salem Mubarak Alzahrani holds the position of Associate Professor in Operations Research and Applied Statistics at the Faculty of Science, AL-BAHA University. In 2016, he obtained a Doctor of Philosophy degree from the University of Salford, Britain, in Operations Research and Applied Statistics. In 2011, he obtained a master's degree from the University of Salford, Britain, in Operations Research and Applied Statistics. In 2009, he obtained a Diploma in English Language from the University of Manchester Institute for one year. In 2007, he obtained a bachelor's degree at Al Baha University, majoring in mathematics. The primary area of his research centers around the study of operations research applied statistics, and statistical production methodologies. He engages in collaborative research efforts with fellow scholars within a research collective. His research findings have been disseminated through several esteemed worldwide publications and scientific conferences. He serves as a supervisor for graduate students pursuing master's degrees and doctorates in the field of statistics.

Rania Saadeh is Associate Professor in mathematics at faculty of Science, Zarqa University. She earned her PhD in mathematics from the University of Jordan in 2016. Her research focuses on fractional differential equations and mathematical physics. She collaborates with other researchers in a research group. Her work has been published in many international journals and scientific conferences. She was one of the organization committee members of the conferences in mathematics that held in Zarqa University starting from 2006, she is also a Chairman of the preparatory committee of the 6th International Arab Conference on Mathematics and Computations (IACMC 2019). She is a supervisor for many of master degree students.

Mohamed A.Abdoon Mohamed A. Abdoon is an assistant Professor of mathematics at Shaqra University in Saudi Arabia. He received the B.Sc. and M.Sc. degrees in mathematics and science from the Sudan University of Science and Technology in 2008 and 2013, respectively. and a Ph.D. in mathematics from the Omdurman Islamic University in 2016. With over 14 years of experience in teaching mathematics and research. He has had several research papers published in reputed international journals and conferences. My current research interests include applied and computational mathematics, numerical solutions, modelling, simulation, and biomathematicss.

Ahmad Qazza received the B.Sc. and Ph.D degrees in Differential Equations from Kazan State University, Russia, in 1996 and 2000 respectively. He is an Associate Professor of Mathematics in Zarqa University since 2017 and Vice Dean of the Faculty of Science at Zarqa University. He has several research papers published in reputed international journals and conferences. Among his research interests are boundary value problems for PDEs of mathematical physics, boundary integral equation methods, boundary value

problems for analytic complex functions, fractional differential equations and numerical methods.

Fath Elrhman EL Guma Fath Elrhman EL Guma holds the position of Associate Professor in Applied Statistics at the Faculty of Art and Science inside Baljursi, AL-BAHA University. In 2012, he obtained a Doctor of Philosophy degree in applied statistics from the University of Sudan University of Science and Technology. The primary area of his research centers around the study of epidemiological modeling and statistical production methodologies. He engages in collaborative research efforts with fellow scholars within a research collective. His research findings have been disseminated through several esteemed worldwide publications and scientific conferences. He serves as a supervisor for graduate students pursuing master's degrees and doctorates in the field of statistics.

Mohammed Berir Mohammed Berir I received my BSc degree in mathematics in 2006 from the University of Sudan, Sudan; my M.Sc degree in applied mathematics in 2009 from the University of Khartoum, Sudan; and my PhD in mathematics science in 2015 from the University of Omdurman, Sudan. He has been an Assistant professor of Mathematics at Al Baha University since 2015 and head of the department of mathematics. He has had several research papers published in reputed international journals and conferences. Among his research interests are functional analysis, fractional differential equations, and numerical methods.