Chapter 1

Parameter Estimation and Fractal Analysis of Influenza Dynamics Based on Family Physician Surveillance Data in Türkiye

Mehmet Kocabıyık[1]

Abstract

Influenza is an important public health issue of worldwide concern due to its high transmission rate and seasonal mutations, and family physician surveillance data in Türkiye offer a vital understanding of its local dynamics. Although classical compartmental models provide a basic explanation of epidemics, they are sometimes inadequate to describe the non-linear, memory-dependent, and fractal characteristics of actual viral transmission. In this paper, we develop a new mathematical model by building a Hausdorff fractal model, with Susceptible, Exposed, Infected, Asymptomatic, and Recovered populations in a fractal-order derivative framework. The paper opens with an intensive mathematical analysis, including the proofs of the boundedness and positivity of solutions, to ensure the biological consistency of the model. We first calculate the equilibrium points and obtain the basic reproduction number using the next-generation matrix approach, and then conduct a detailed sensitivity analysis to determine which parameters have the greatest effect on the spread of the disease. To test our theoretical framework, we estimate parameters using real-world surveillance data from Türkiye (Week 48, 2025 - Week 13, 2026) with the Nelder-Mead optimization algorithm, calibrated to a fractal dimension of $\alpha = 0.9$. Simulations show that the epidemic dynamics associated with the fractal method are a better fit than those of classical models. Lastly, the paper wraps up with an analysis of how epidemiological surveillance systems can be improved in terms of predictive capabilities through fractal calculus.

1 Asst. Prof. Dr., Burdur Mehmet Akif Ersoy University, mkocabiyik@mehmetakif.edu.tr, ORCID ID: 0000-0002-7701-6946.

https://doi.org/10.58830/ozgur.pub1361.c5491

1. Introduction

Influenza has remained among the most endemic and difficult respiratory infections globally, which is highly morbid and periodically outbreaks making it a great burden to the health care systems of the countries. In Türkiye, the surveillance of these outbreaks depends on surveillance data offered by family physicians who are the main contact with the symptomatic people. This information plays an important role in comprehending the dynamic propagation of the virus, but to transform these raw data into practical public health outcomes, it is essential to have powerful mathematical models that can reflect the non-linearity of the disease spread.

Mathematical modeling of influenza has changed a lot in recent decades, shifting away to global deterministic models and into highly specialized fractional-order models. A groundbreaking contribution to the area was by Rvachev and Longini (1985), who created a large scale mathematical framework to model the spread of influenza around the globe, which formed the basis of understanding the role of air travel and the connectivity between cities in facilitating the spread of pandemic waves. Keeping this line of clinical and social interventions, van den Dool et al. (2008) applied mathematical modeling to examine the effects of immunization of healthcare employees in nursing facilities emphasizing the significance of targeted immunity in safeguarding vulnerable groups.

The last few years have witnessed the upsurge of the complexity of overlapping respiratory diseases modelling. Ojo et al. (2022) investigated the nonlinear optimal control methods in a model of COVID-19 and influenza co-infection, highlighting the fact that the multi-disease interactions demand complex control actions. This lineage was extended by Imran et al. (2025), who proposed an SEIR model of influenza-corona co-infection that explicitly takes into account treatment and hospitalization compartments to optimize clinical interventions.

Another area where the literature has focused is the integration of advanced mathematical operators to better capture the memory effects of viral transmission. A numerical study was carried out by Sabir et al. (2023) based on the concept of fractional-order derivatives, and it revealed that the non-integer order systems are more accurate to reproduce the decay and growth stages of influenza outbreaks. Likewise, Abdoon et al. (2023) thoroughly analyzed and simulated a fractional-order influenza model and claimed that these operators are better modelling the biological heritage and historical reliance of the infection. The emphasis has recently been on the dual effect of pharmaceutical interventions. Raza et al. (2025) studied the contribution of vaccination in the dynamics of influenza with the use of symmetry analysis, whereas Li et al. (2025) used transmission dynamics to study the effectiveness of the combination of treatment and vaccination strategies. For further detailed investigations regarding advanced mathematical modeling and numerical solution techniques in epidemiological systems, one may refer to the works of Çetinkaya et al. (2021), Kocabiyik and Ongun (2022), Çetinkaya (2023), Kocabıyık and Ongun

(2023), Öztürk et al. (2024), Al Jammali and Çetinkaya (2024), and Merdan and Açıkgöz (2025).

Incorporating fractal calculus into epidemiological modeling offers a more adaptable method to comprehend processes which are not of conventional Euclidean dynamics. A Hausdorff fractal derivative, specifically, has come into the limelight due to its capability to simulate anomalous diffusion and transport in complex media. The Hausdorff operator, in contrast to classical derivatives, emphasises the fractal character of the time-space fabric, and is therefore a perfect means of describing the non-linear dynamics of infectious diseases. The time-space fabric of anomalous diffusion introduced by Chen (2006) was extended by Chen et al. (2010) to show how fractal and fractional derivatives are capable of better modeling real world physical and biological systems. The use of fractal derivatives in the context of memory effects and heavy-tailed distributions has been established through recent methodological improvements as discussed by Chen and Liang (2017). These techniques have been particularly useful in the characterization of anomalous transport in porous or disordered materials (Liang et al., 2019). Elaborating on infectious diseases, Nie and Lei (2023) have managed to use the Hausdorff fractal derivative to simulate the transmission of any COVID-19 variant and reveal that the multi-peak nature of viral surges can be better explained by the fractal-order parameter. Moreover, Saadeh et al. (2025) provided a comparative study of Dengue dynamics, based on classical, Caputo fractional, and fractal derivatives and found that fractal-based models are more accurate in capturing the natural complexity of the disease spreading. To gain additional information on the various applications of fractal structures with regard to various areas of scientific endeavors, see Golmankhaneh et al. (2025), Uc (2025), Quan et al. (2025), and Allahverdiev et al. (2026).

The primary motivation of this research stems from the inherent limitations of integer-order compartmental models in capturing the multi-scale and non-local characteristics of infectious disease spread. Although the use of the fractional-order derivatives has been widely studied in the past, the Hausdorff fractal derivative on localized surveillance data is a relatively unexplored field, especially in the primary healthcare system of Türkiye. This research is of three value; First, it fills the gap between theoretical fractal calculus and real world public health statistics, with the use of real family physician records. Second, it offers a strict mathematical basis through the examination of stability and biological consistency of the fractal structure. Lastly, through a comparative numerical analysis of different fractal dimensions, this analysis provides a fresh insight into the ability of the influence of the so-called fractal time to explain more clearly the sudden changes and maximum timings of the outbreak of the Influenza. This knowledge will likely give the governmental health agencies more accurate predictive instruments in dealing with seasonal epidemics.

The rest of this paper will be divided into five main parts to give an all-inclusive analysis of this proposed model. Section 2 defines the construction of the fractal model within the Hausdorff fractal framework and defines the mathematical

assumptions, such as positivity and boundedness of solutions. The dynamical analysis is a separate Section 3 in which the disease-free equilibrium point is found, the basic reproduction number (R_0) is calculated through the next-generation matrix approach and a sensitivity analysis is done. Section 4 outlines the process of parameter estimation with the help of actual real-world Influenza data in Türkiye and then proceeds to run a series of numerical simulations to test the accuracy of the model. Lastly, Section 5 will provide a summary of the main findings of the study as well as propose possible future research directions.

2. Model Formulation and Mathematical Analysis

In this section, we present the mathematical structure of the proposed Influenza model, incorporating the specific characteristics of the disease spread within a fractal-order framework. The model is constructed on the relationship between five different compartments of the population, with the transition rates being controlled by Hausdorff fractal derivatives in order to explain the non-linear time-scaling, and memory effects found in epidemic data. Replacing the classical time derivative with its fractal version, we will attempt to model the anomalous diffusion behavior that can be characteristic of complex biological transmission processes.

Definition 2.1.: (Chen et al., 2010) Let $f(t)$ be a function of real values. The Hausdorff fractal derivative of degree α with respect to time t is defined as follows:

$$\frac{df(t)}{dt^{\alpha}} = \lim_{t_1 \to t} \frac{f(t_1) - f(t)}{t_1^{\alpha} - t^{\alpha}}.$$

In practical numerical applications and for the purpose of transforming the system into a computationally solvable form, the relationship between the Hausdorff derivative and the classical derivative is established via the following chain rule:

$$\frac{df(t)}{dt^{\alpha}} = \frac{t^{1-\alpha}}{\alpha} \frac{df(t)}{dt}.$$

This implies that the fractal-order rate of change is modulated by a power-law time factor, representing the "memory" or "aging" effect inherent in complex biological systems.

The transmission dynamics of Influenza are modeled by dividing the total population $N(t)$ into five mutually exclusive compartments: Susceptible (S), Exposed (E), Symptomatic Infected (I), Asymptomatic (A), and Recovered (R). The proposed SEIAR model under the Hausdorff fractal derivative framework is governed by the following system of nonlinear differential equations:

$$\frac{dS(t)}{dt^{\alpha}} = \Phi - \beta SI - \beta\theta SA - \mu S,$$

$$\begin{aligned}
\frac{dE(t)}{dt^{\alpha}} &= \beta SI + \beta\theta SA - \sigma E - \mu E, \\
\frac{dI(t)}{dt^{\alpha}} &= \rho\sigma E - \gamma_I I - \mu I, \\
\frac{dA(t)}{dt^{\alpha}} &= (1-\rho)\sigma E - \gamma_A A - \mu A, \\
\frac{dR(t)}{dt^{\alpha}} &= \gamma_I I + \gamma_A A - \mu R.
\end{aligned} \tag{2.1}$$

Subject to the initial conditions:

$$S(0) = S_0, E(0) = E_0, I(0) = I_0, A(0) = A_0, R(0) = R_0.$$

The parameters used in the system (2.1) are defined as follows:

- Φ: Recruitment rate (birth/immigration) into the susceptible population.
- β: Transmission rate from symptomatic individuals.
- θ: Relative transmissibility of asymptomatic individuals.
- σ: Rate at which exposed individuals become infectious.
- p: Proportion of individuals who develop symptomatic infection.
- γ_I : Recovery rate of symptomatic individuals.
- γ_A: Recovery rate of asymptomatic individuals.
- μ: Natural death rate for all compartments.

Theorem 2.1.: (Positivity of Solutions) Let the initial conditions of the system be $\big(S(0), E(0), I(0), A(0), R(0)\big) \in R_+^5$. Then, the solutions $(S(t), E(t), I(t), A(t), R(t))$ of the model remain non-negative for all $t > 0$.

Proof. To ensure that the solutions do not leave the first orthant, we analyze the direction of the vector field on the boundaries of the non-negative region R_+^5. From the given system of Hausdorff fractal differential equations, we examine each variable as it reaches the threshold of zero. For $S(t), E(t), I(t), A(t)$ and $R(t)$ at the points where $S = 0, E = 0, I = 0, A = 0$, R=0, the system (2.1) becomes:

$$\begin{aligned}
\frac{dS(t)}{dt^{\alpha}} &= \Phi > 0, \\
\frac{dE(t)}{dt^{\alpha}} &= \beta SI + \beta\theta SA > 0,
\end{aligned}$$

$$\frac{dI(t)}{dt^{\alpha}} = \rho\sigma E > 0,$$

$$\frac{dA(t)}{dt^{\alpha}} = (1-\rho)\sigma E > 0,$$

$$\frac{dR(t)}{dt^{\alpha}} = \gamma_I I + \gamma_A A > 0.$$

Since the derivative of each variable is non-negative at the boundary where the variable itself is zero, the trajectories cannot cross into the negative region. Therefore, if the system starts with non-negative initial conditions, the solutions remain non-negative for all $t > 0$. This completes the proof.

Theorem 2.2.: (Boundedness of Solutions) All solutions of the system (S, E, I, A, R) that initiate in R_+^5 are uniformly bounded within a feasible region Ω.

Proof. To demonstrate the boundedness of the system, by summing the five equations of the Hausdorff fractal model, we obtain the rate of change for the total population:

$$\frac{dN(t)}{dt^{\alpha}} = \Phi - \mu(S + E + I + A + R).$$

This simplifies to:

$$\frac{dN}{dt^{\alpha}} = \Phi - \mu N.$$

From this expression, we analyze the behavior of $N(t)$ at the boundary where the total population reaches the value Φ/μ:

- If $N(t) > \Phi/\mu$, then $\frac{dN}{dt^{\alpha}} < 0$, which means the total population must decrease.
- If $N(t) < \Phi/\mu$, then $\frac{dN}{dt^{\alpha}} > 0$, which means the total population must increase.
- If $N(t) = \Phi/\mu$, then $\frac{dN}{dt^{\alpha}} = 0$, meaning the total population remains constant at this value.

This implies that $N(t)$asymptotically converges to Φ/μ. Therefore, the total population is bounded by $max\{N(0), \Phi/\mu\}$. Consequently, all individual state variables (S, E, I, A, R) are also bounded, as they are non-negative components of $N(t)$. The biologically feasible region for the model is thus defined as:

$$\Omega = \left\{(S, E, I, A, R) \in R_+^5 : S + E + I + A + R \leq \frac{\Phi}{\mu}\right\}.$$

The proof is complete.

3. Dynamical Analysis of an SEIAR Model

In this section, we investigate the qualitative behavior of the Influenza model under the Hausdorff fractal framework. The analysis includes the determination of the steady-state solutions (equilibrium points) and the derivation of the threshold parameter, known as the basic reproduction number (R_0), which determines whether the disease will persist or vanish from the population.

To find the equilibrium points of the system, we set all the Hausdorff fractal derivatives to zero, as the system remains stationary when the rate of change is null:

$$\frac{dS}{dt^{\alpha}} = \frac{dE}{dt^{\alpha}} = \frac{dI}{dt^{\alpha}} = \frac{dA}{dt^{\alpha}} = \frac{dR}{dt^{\alpha}} = 0.$$

This leads to the following system of algebraic equations:

$$\begin{aligned} \Phi - \beta SI - \beta\theta SA - \mu S &= 0, \\ \beta SI + \beta\theta SA - \sigma E - \mu E &= 0, \\ \rho\sigma E - \gamma_I I - \mu I &= 0, \\ (1-\rho)\sigma E - \gamma_A A - \mu A &= 0, \\ \gamma_I I + \gamma_A A - \mu R &= 0. \end{aligned} \tag{3.1}$$

The Disease-Free Equilibrium (P_0) occurs when there is no infection in the population, implying $E = I = A = R = 0$. Substituting these values into Eqs. (3.1):

$$\Phi - \mu S = 0 \rightarrow S_0 = \frac{\Phi}{\mu}.$$

Thus, the DFE point is defined as:

$$P_0 = \left(\frac{\Phi}{\mu}, 0,0,0,0\right).$$

R_0 is the most critical threshold in epidemiology. We calculate it using the Next-Generation Matrix (NGM) method by focusing on the infected compartments (E, I, A).

Let F be the rate of appearance of new infections and V be the rate of transfer of individuals between compartments. The Jacobian matrices F and F evaluated at the DFE are:

$$F = \begin{bmatrix} 0 & \beta S_0 & \beta\theta S_0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{bmatrix}, V = \begin{bmatrix} \sigma+\mu & 0 & 0 \\ -\rho\sigma & \gamma_I+\mu & 0 \\ -(1-\rho)\sigma & 0 & \gamma_A+\mu \end{bmatrix}.$$

The basic reproduction number is defined as the spectral radius of the next-generation matrix $K = FV^{-1}$. After performing the matrix inversion and multiplication, we obtain the analytical expression:

$$R_0 = \frac{\beta S_0 \sigma \rho}{(\sigma + \mu)(\gamma_I + \mu)} + \frac{\beta \theta S_0 \sigma (1-\rho)}{(\sigma + \mu)(\gamma_A + \mu)}.$$

Substituting $S_0 = \frac{\Phi}{\mu}$, the final form becomes:

$$R_0 = \frac{\beta \Phi \sigma}{\mu(\sigma + \mu)} \left[\frac{\rho}{(\gamma_I + \mu)} + \frac{\theta(1-\rho)}{(\gamma_A + \mu)} \right].$$

The Endemic Equilibrium point $P^* = (S^*, E^*, I^*, A^*, R^*)$ is obtained by solving the nonlinear algebraic system (3.1) simultaneously. By expressing all classes in terms of the force of infection at steady state, we find:

$$S^* = \frac{S_0}{R_0}, E^* = \frac{\mu S_0 (R_0 - 1)}{(\sigma + \mu) R_0}, I^* = \frac{\rho \sigma E^*}{\gamma_I + \mu}, A^* = \frac{(1-\rho)\sigma E^*}{\gamma_A + \mu}, R^* = \frac{\gamma_I I^* + \gamma_A A^*}{\mu}.$$

These expressions demonstrate that all population classes are positive and proportional to the factor $(R_0 - 1)$, confirming that the disease remains permanently established in the population for values of R_0 greater than unity.

To identify the key parameters that exert the most significant influence on the transmission dynamics of Influenza, we perform a sensitivity analysis on the basic reproduction number. This analysis is crucial for public health decision-making, as it highlights which biological or behavioral factors should be targeted to effectively reduce the spread of the disease. By utilizing the normalized sensitivity index formula, $\Upsilon_v = \frac{\partial R_0}{\partial v} \frac{v}{R_0}$, we quantify the relative change in R_0 with respect to each model parameter. Parameters with positive indices indicate that an increase in their value leads to a direct increase in R_0, whereas negative indices suggest that increasing these parameters contributes to the suppression of the epidemic. The results of the sensitivity analysis, calculated using the estimated values ($\beta = 7.2468$, $\gamma_I = 1.3522$, $\rho = 0.6$), are illustrated in Figure 1.

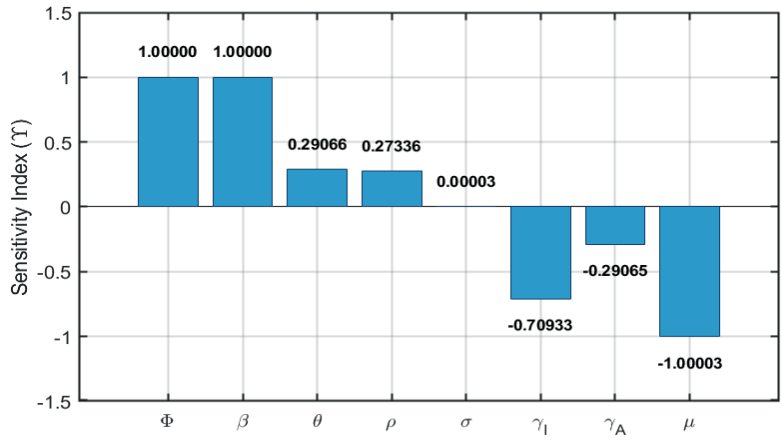

Figure 1. Normalized sensitivity indices of the basic reproduction number

The sensitivity analysis results reveal that the recruitment rate and the transmission rate are the most influential factors in increasing the intensity of the Influenza outbreak. Since these parameters have the highest positive indices, any increase in social contact or the arrival rate of new individuals into the population will significantly elevate the basic reproduction number. On the other hand, the natural death rate and the recovery rate of symptomatic individuals exhibit the strongest negative impact on the spread. This suggests that the most effective ways to control the epidemic are to accelerate the recovery process through medical interventions and to implement measures that reduce the overall duration of the infectious period.

The analysis also indicates that parameters such as the transmission weight of asymptomatic individuals and the fraction of symptomatic cases have a moderate positive effect, whereas the recovery rate of asymptomatic individuals provides a secondary contribution to suppressing the disease. Interestingly, the incubation rate shows a negligible influence on the reproduction number, implying that the speed at which individuals transition from the exposed to the infectious stage does not fundamentally change the scale of the outbreak, although it may affect its timing.

4. Parameter Estimation and Numerical Results

In this section, the model was validated using real-world Influenza data obtained from family physicians in Turkey. The dataset consists of weekly positive Influenza samples collected over an 18-week period (T. C. Sağlık Bakanlığı, 2026). This data is critical for capturing the seasonal characteristics of the virus in a local context. To align the theoretical SEIAR model with the observed data, we utilized a least-squares fitting technique to estimate the transmission rate (β), the recovery rate (γ_I), and the symptomatic fraction (ρ). The estimated parameters ($\beta = 7.2468,\ \gamma_I = 1.3522, \rho = 0.6$) provide a robust baseline for analyzing the dynamics of the outbreak.

The numerical simulations provided in this study offer a comprehensive look at the evolution of the Influenza epidemic under the Hausdorff fractal framework. By integrating the clinical data obtained from family physicians in Turkey, we observed that the classical integer-order model ($\alpha = 1$) tends to predict a rapid escalation and a sharp decline in the number of infected individuals. However, as illustrated in Figure 2, the real-world data points exhibit a more dispersed and gradual behavior, which is more accurately captured by the fractal models where $\alpha = 0.9$ and $\alpha = 0.8$. This shift and flattening of the curve suggest that fractal-order derivatives are superior in representing the sub-diffusive nature of respiratory infections, where social memory and environmental complexities slow down the transmission process compared to ideal, rapid-mixing scenarios.

The impact of the fractal dimension is further evident across all population compartments. In the susceptible population (Figure 3), a lower fractal order results in a more gradual depletion of individuals, indicating a prolonged exposure period. Similarly, the exposed and asymptomatic classes (Figures 4 and 5) exhibit lower peaks and longer durations when α is reduced. This is a critical

finding for public health management, as it demonstrates that the disease may linger in the population longer than expected, particularly through asymptomatic carriers who continue to spread the virus without being detected. Finally, the cumulative recovery curves in Figure 6 show that while the total reach of the epidemic is similar across different orders, the speed at which herd immunity is achieved varies significantly, with fractal models suggesting a slower, more realistic progression. Overall, these results confirm that the Hausdorff fractal model provides a more flexible and accurate tool for modeling the real-time dynamics of Influenza in Turkey.

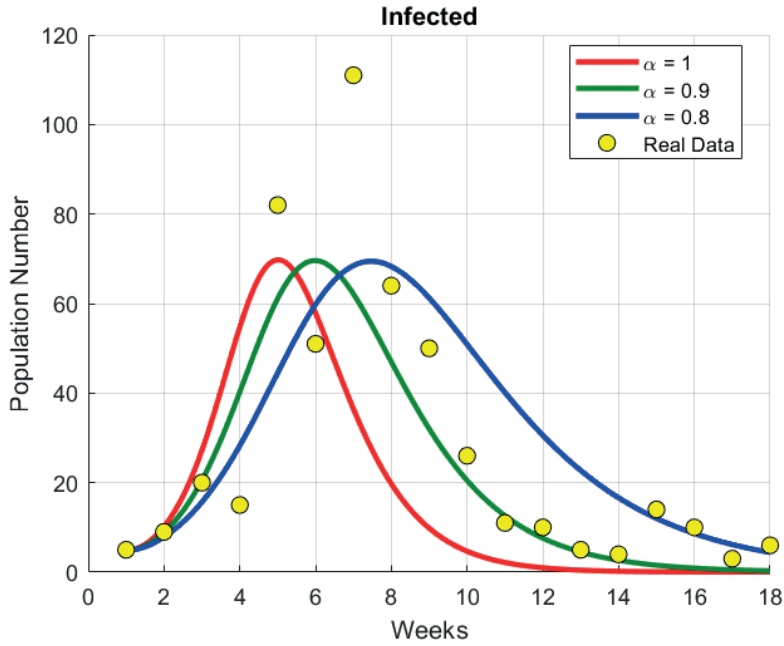

Figure 2. Comparison of the clinical Influenza data from the Ministry of Health (Türkiye) with the numerical solutions of the SEIAR model for different Hausdorff fractal dimensions.

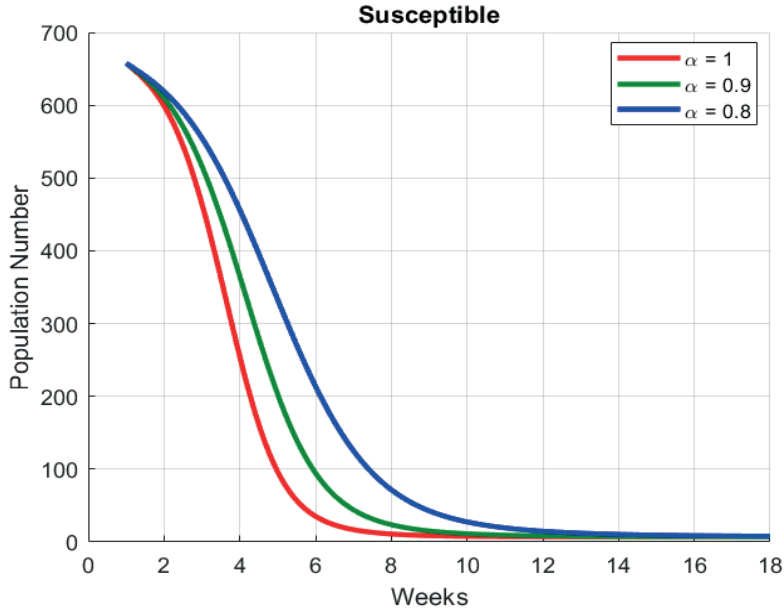

Figure 3. Dynamical behavior of the susceptible population over an 18-week period.

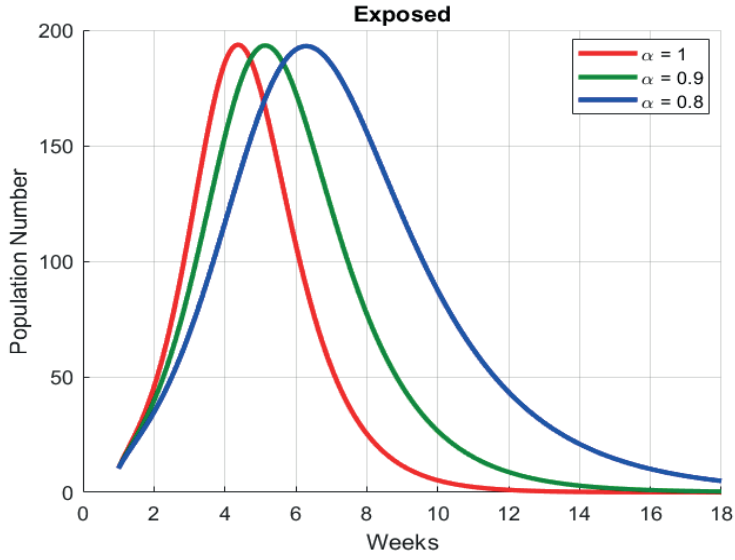

Figure 4. Evolution of the exposed population for varying values of the Hausdorff fractal derivative.

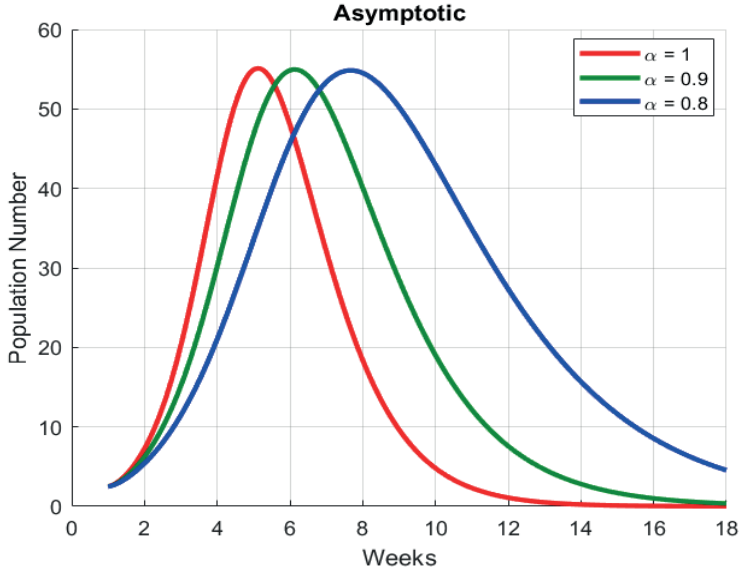

Figure 5. Trajectory of the asymptomatic infectious class.

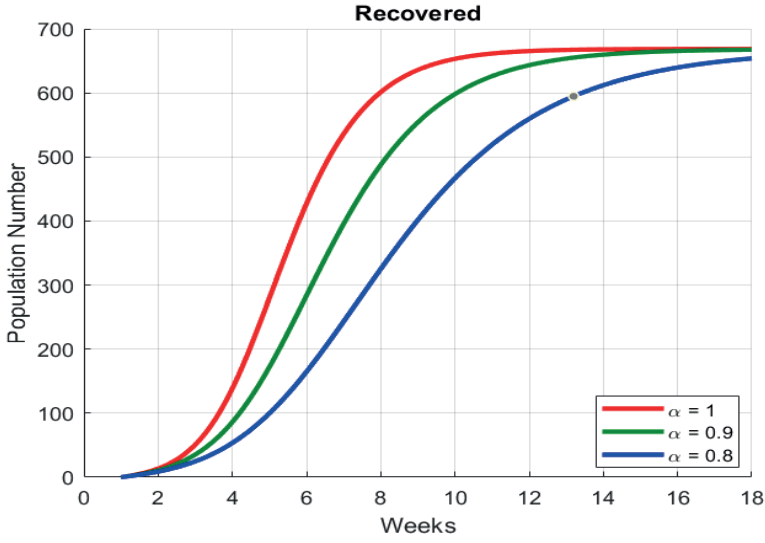

Figure 6. Cumulative number of recovered individuals over time.

5. Conclusion

In this study, we have constructed and studied a complete epidemic model of Influenza dynamics based on the Hausdorff fractal derivative framework. The model offers a more subtle approach to the transmission of respiratory viruses in a population by considering both symptomatic and asymptomatic transmission

routes. The combination of real-world data provided by family physicians in Turkey enabled one to have a sound parameter estimation, which guaranteed that the theoretical framework is based on clinical reality. We showed mathematically that the model is biologically feasible, and solutions are non-negative and bounded in a certain region.

One of the main contributions of this work is the derivation of the basic reproduction number and the consequent sensitivity analysis. The findings revealed that the main factors that contribute to the outbreak are the transmission rate and the rate of recruitment and the most effective counter-measures are the recovery rates. Also, the simulations carried out numerically emphasized the immense influence of the Hausdorff fractal dimension. We showed that smaller values of alpha are better indicative of the sub-diffusive character and the long-tail behavior of the Influenza data in Turkey that cannot be well captured by classical integer-order models. The fractal model provides a more realistic forecast of the development of the infectious compartments by flattening the peak and moving the epidemic curve. To sum up, Hausdorff fractal model is an effective and versatile instrument that can be used by the government of a particular nation to forecast and control the spread of Influenza. The fact that fractal calculus can be used to explain the complexities of human interaction and other environmental factors is a major strength of this method compared to the traditional modeling methods.

Further studies might elaborate on this framework by adding the element of vaccination strategies or spatial diffusion to further improve predictive power of the model to work in various geographical locations.

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