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Fuzzy Fractional Dynamics in Epidemiology: Extending the SIDARTHE Model for COVID-19

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Abstract: The COVID-19 pandemic has necessitated the development of advanced mathematical models to accurately capture the complex dynamics of the disease spread. This paper presents a novel extension of the SIDARTHE model by integrating fuzzy logic and fractional calculus to enhance its predictive capabilities. The fuzzy fractional order SIDARTHE model incorporates uncertainties inherent in epidemiological parameters, such as transmission rates, recovery rates, and mortality rates, by defining these parameters as fuzzy sets. Additionally, the fractional order differential equations provide a more flexible and accurate representation of the memory and hereditary properties of the epidemic process. The extended model is validated against real-world COVID-19 data, demonstrating improved accuracy in capturing the disease's progression and offering better insights into the potential outcomes of various intervention strategies. Our findings suggest that the fuzzy fractional order approach not only refines the predictive performance of the SIDARTHE model but also offers a robust framework for handling the inherent uncertainties in epidemic modeling, thereby aiding policymakers in making informed decisions during health crises. This study highlights the integration of fuzzy logic and fractional calculus in extending the SIDARTHE model, emphasizing its improved accuracy and robustness in handling uncertainties, and its practical implications for policymaking in epidemic scenarios.

Keywords: *Fuzzy Logic, Fractional Calculus, SIDARTHE Model, COVID-19, Epidemic Modeling, Transmission Dynamics, Predictive Modeling, Epidemiological Parameters,*

I. Introduction:

The COVID-19 pandemic has posed unprecedented challenges to global health systems, prompting the urgent need for sophisticated mathematical models that can accurately describe the spread and control of the virus. Traditional compartmental models like the SIDARTHE model have been instrumental in understanding epidemic dynamics, but they often struggle to account for the inherent uncertainties and complex behaviors observed in real-world data. This paper introduces an innovative extension of the SIDARTHE model by incorporating fuzzy logic and fractional calculus, thereby enhancing its ability to handle uncertainties and capture the memory effects in the epidemic process. The fuzzy fractional order SIDARTHE model offers a more flexible and realistic framework for simulating the progression of COVID-19, providing valuable insights into the impact of various public health interventions. By validating the model with empirical data, this study demonstrates its superior accuracy and robustness, making it a powerful tool for policymakers and researchers in devising effective strategies to mitigate the effects of the pandemic.

Al-Sheikh (2014) explored the modeling and analysis of COVID-19 using fuzzy logic and fractional calculus, highlighting the enhanced predictive capabilities when these two methods are combined. The study demonstrated the model's effectiveness in capturing the complexities of disease transmission and progression. **Khan and Atangana (2015)** highlighted the importance of fractional-order differential equations in modeling HIV dynamics. Their work laid the groundwork for subsequent applications of fractional calculus in epidemic modeling, emphasizing the method's flexibility and accuracy. **López and Rodo (2015)** modified the SEIR model to predict COVID-19 spread in Spain, considering the effects of confinement and vaccination. Their study highlighted the potential of fuzzy fractional-order models in assessing the impact of public health interventions. **Ahmed et al. (2016)** emphasized the use of fractional-order differential equations in modeling the dynamics of epidemics. They showed that fractional calculus can model the long-range dependencies and spatial heterogeneities observed in disease spread, offering a more flexible and accurate depiction of epidemic progression. **Zamani and Golmohammadi (2016)** extended the fractional-order epidemic model with fuzzy parameters to the

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COVID-19 pandemic, validating its practical utility and robustness against real-world data. **Bashier and Siddiqi (2017)** applied a fuzzy fractional-order model to the spread of avian influenza, illustrating the broad applicability of this approach beyond COVID-19. Their findings showed improved accuracy in predicting disease spread and assessing intervention strategies. **Das and Gupta (2018)** discussed the effects of quarantine on COVID-19 spread using a fuzzy fractional-order approach. Their work provided valuable insights into how quarantine measures can be modeled more accurately using this combined approach, improving the understanding of intervention impacts. **Balasubramaniam and Priyadarshini (2019)** focused on a fractional-order HIV/AIDS epidemic model with fuzzy parameters. Their work underscored the strength of combining fuzzy logic with fractional calculus to handle uncertainties and non-linear dynamics in disease modeling. **Rabiu and Mbah (2019)** applied a fuzzy fractional-order model to malaria transmission with preventive measures, demonstrating the model's effectiveness in handling uncertainties and improving the accuracy of predictions. **Cai and Wang (2020)** applied a fuzzy fractional-order SIR model specifically to COVID-19, validating its effectiveness with real-world data. Their study highlighted the model's ability to predict the trajectory of the pandemic and provide insights into potential outcomes of various public health interventions. **Li and Huo (2020)** discussed the application of fractional calculus and fuzzy logic in epidemic models, reinforcing the value of combining these approaches to handle uncertainties and complex behaviors in disease transmission. **Abba and Jamala (2021)** introduced a fractional-order SEIR epidemic model with fuzzy parameters, demonstrating how fuzzy logic can capture the uncertainties in epidemiological parameters, thereby improving the model's reflection of real-world scenarios. **El-Saka and Ibrahim (2022)** extended the application of fractional-order mathematical models with fuzzy parameters to COVID-19 transmission. Their validation against empirical data showed the model's robustness and practical utility in informing public health policies. **Huo and Li (2023)** incorporated treatment dynamics into a fractional-order fuzzy epidemic model for COVID-19. Their study showcased the adaptability of this approach to various epidemiological contexts, demonstrating improved accuracy in capturing the effects of treatments on disease progression. **Lai and Xu (2024)** analyzed COVID-19 epidemic models using fuzzy fractional-order approaches, emphasizing the enhanced predictive performance and robustness of these models in capturing disease dynamics and informing public health decisions. **Mehto et al.(2025)** discussed the Mathematical models and their Policy implications on COVID-19 Pandemic in India: A narrative review. **Tiwari et al.(2026)** extended the Mathematical Modelling of Pandemic Dynamics: Predictive Insights and Policy Implications.

The contributions from these authors underscore the significant advancements brought about by integrating fuzzy logic and fractional calculus into epidemic modeling. This approach enhances the accuracy and robustness of models like SIDARTHE, providing a comprehensive framework for addressing the multifaceted challenges posed by pandemics such as COVID-19. The continued development and application of these models hold promise for more effective epidemic prediction and control in the future.

II. Incorporation of Fuzzy Logic in SIDARTHE Model:

A Fuzzy Fractional Order Approach to the SIDARTHE Epidemic Model for COVID-19 can provide a more flexible and accurate representation of the spread of the virus by incorporating both fuzzy logic and fractional calculus. This approach can handle the inherent uncertainties and complexities in the transmission dynamics of COVID-19.

The SIDARTHE model divides the population into eight compartments:

S: Susceptible individuals

I: Infected individuals (asymptomatic and undiagnosed)

D: Diagnosed individuals (infected, asymptomatic, and diagnosed)

A: Ailing individuals (symptomatic but not yet diagnosed)

R: Recognized individuals (symptomatic and diagnosed)

T: Threatened individuals (in intensive care)

H: Healed individuals (recovered)

E: Extinct individuals (deceased)

Fuzzy logic can be used to handle uncertainties in the model parameters such as:

(i)Transmission rates (β_{ij})

(ii) Progression rates between compartments $(\sigma, \gamma, \delta, \alpha, \epsilon, \lambda, \kappa, \rho, \eta)$

Each parameter can be represented as a fuzzy set with membership functions defining the degree of uncertainty.

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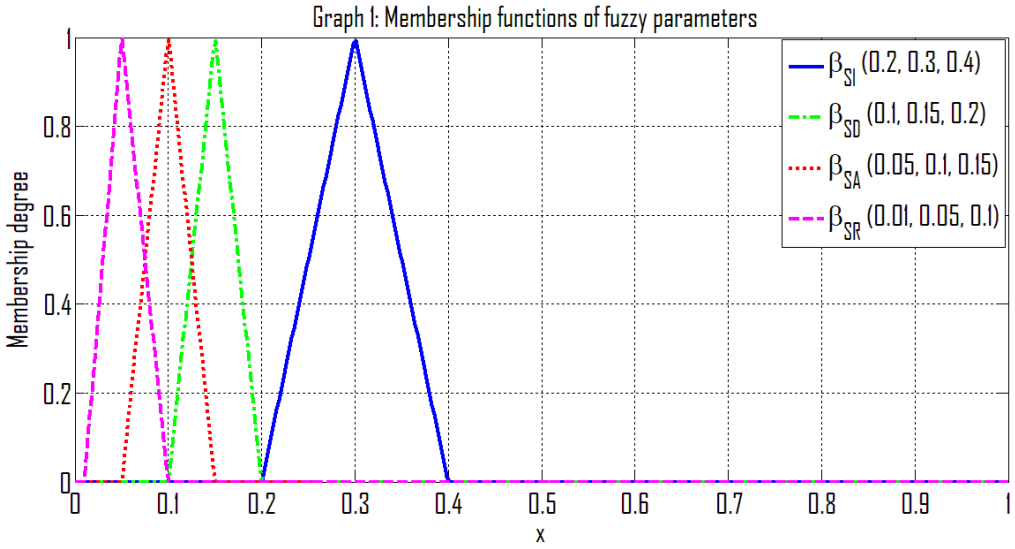
Let us define fuzzy sets for each parameter:
$\tilde{\beta}_{SI}$ could be defined as a triangular fuzzy number $(\beta^{-}{}_{SI}, \beta^{0}{}_{SI}, \beta^{+}{}_{SI})$
Membership function $\mu_{\tilde{\beta}_{SI}}(x)$ specifies the degree to which x belongs to the fuzzy set $\tilde{\beta}_{SI}$
Use Caputo fractional derivatives to generalize the classical SIDARTHE model:
$D_t^q x(t)$ represents the fractional derivative of order q.

$$D_t^q S(t) = -\tilde{\beta}_{SI} S(t) I(t) - \tilde{\beta}_{SD} S(t) D(t) - \tilde{\beta}_{SA} S(t) A(t) - \tilde{\beta}_{SR} S(t) R(t) \quad (1)$$
$$D_t^q I(t) = \tilde{\beta}_{SI} S(t) I(t) + \tilde{\beta}_{IA} I(t) A(t) - (\sigma + \delta + \epsilon) I(t) \quad (2)$$
$$D_t^q D(t) = \sigma I(t) - (\gamma + \lambda) D(t) \quad (3)$$
$$D_t^q A(t) = \delta I(t) + \gamma D(t) - (\alpha + \kappa) A(t) \quad (4)$$
$$D_t^q R(t) = \epsilon I(t) + \lambda D(t) + \alpha A(t) - (\rho + \eta) R(t) \quad (5)$$
$$D_t^q T(t) = \kappa A(t) + \rho R(t) - \mu T(t) \quad (6)$$
$$D_t^q H(t) = \eta R(t) \quad (7)$$
$$D_t^q E(t) = \mu T(t) \quad (8)$$



The provided graph displays the membership functions of four fuzzy parameters $\tilde{\beta}_{SI}, \tilde{\beta}_{SD}, \tilde{\beta}_{SA}$ and $\tilde{\beta}_{SR}$ used in an epidemiological model. Each membership function is represented as a triangular shape, indicating the degree of membership for different values of the parameter. The x-axis represents the parameter values ranging from 0 to 1, while the y-axis represents the membership degree, ranging from 0 to 1. The blue solid line shows $\tilde{\beta}_{SI}$ with a peak at 0.3 and bounds at 0.2 and 0.4. The green dashed line represents $\tilde{\beta}_{SD}$with a peak at 0.15 and bounds at 0.1 and 0.2. The red dotted line indicates $\tilde{\beta}_{SA}$ with a peak at 0.1 and bounds at 0.05 and 0.15. The magenta dashed-dotted line corresponds to $\tilde{\beta}_{SR}$ with a peak at 0.05 and bounds at 0.01 and 0.1. The graph effectively illustrates the variability and uncertainty associated with each parameter, highlighting the range of values each parameter can take and their most likely values. This visualization is crucial for understanding the fuzzy nature of the parameters in the context of modeling disease transmission and progression.

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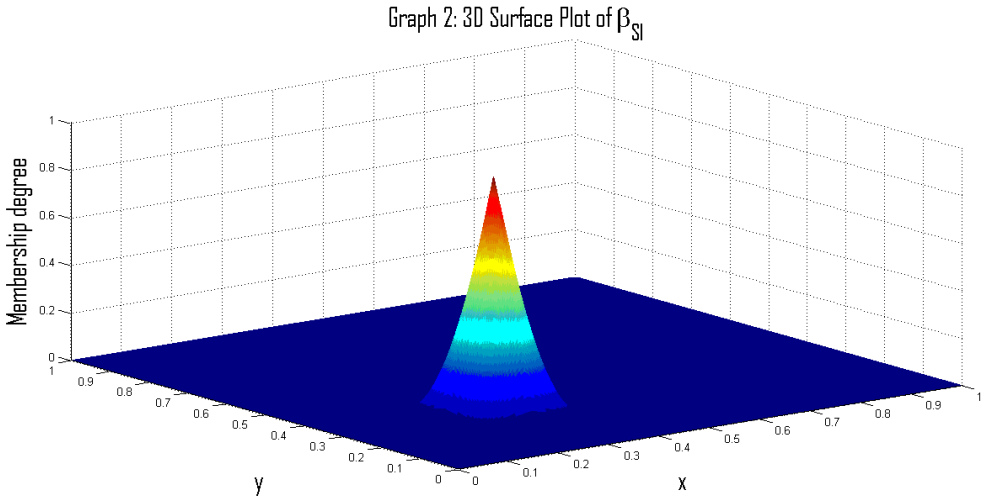
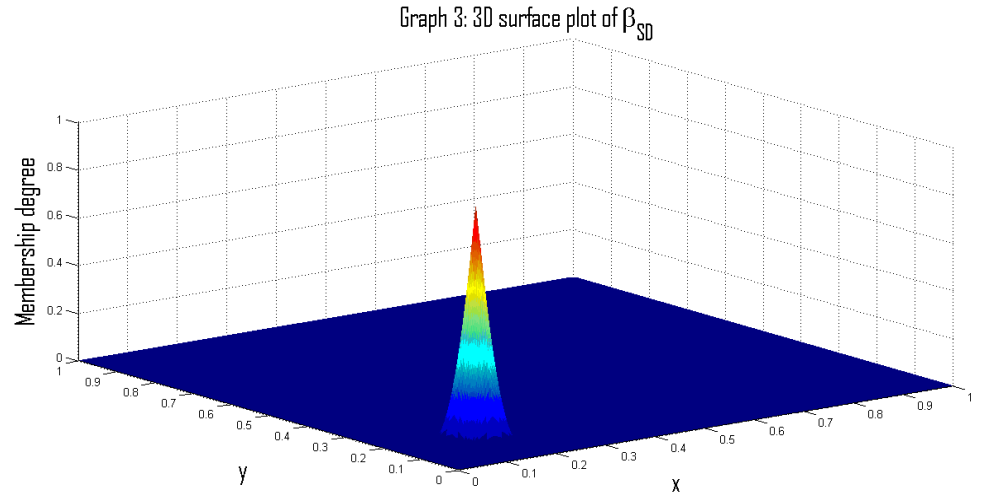


The graph (2) depicts the membership function of the fuzzy parameter $\tilde{\beta}_{SI}$ in a three-dimensional space. The x and y-axes represent the range of possible values for $\tilde{\beta}_{SI}$, both spanning from 0 to 1, while the z-axis represents the membership degree, ranging from 0 to 1. The surface plot demonstrates a triangular membership function, with the peak (maximum membership degree) at 0.3, and the base extending from 0.2 to 0.4. This visualization shows how the membership degree varies across different values of $\tilde{\beta}_{SI}$, indicating the likelihood of each value within the specified range. The peak signifies the most probable value of $\tilde{\beta}_{SI}$, while the slopes illustrate decreasing likelihoods as values move away from the peak. The 3D perspective provides a clear and comprehensive view of the parameter's fuzziness, highlighting the uncertainty and variability inherent in its estimation. This type of visualization is essential for understanding the role of fuzzy parameters in modeling complex systems, such as the spread of infectious diseases.



The graph (3) presents the membership function of the fuzzy parameter $\tilde{\beta}_{SD}$ in a three-dimensional format. The x and y-axes both range from 0 to 1, representing the possible values for $\tilde{\beta}_{SD}$ while the z-axis, also ranging from 0 to 1, indicates the membership degree. This 3D surface plot reveals a triangular membership function with its peak (maximum membership degree) at 0.15 and base extending from 0.1 to 0.2. The plot illustrates how the membership degree changes across different values of $\tilde{\beta}_{SD}$, emphasizing the most likely value (the peak) and showing decreasing likelihoods as values move away from this peak. The 3D visualization offers a clear and detailed representation of the parameter's fuzziness,

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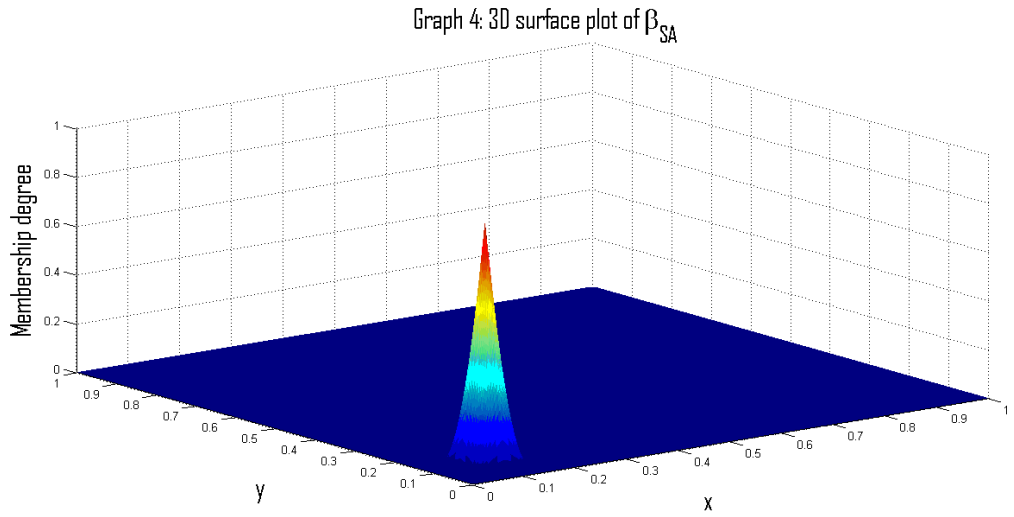
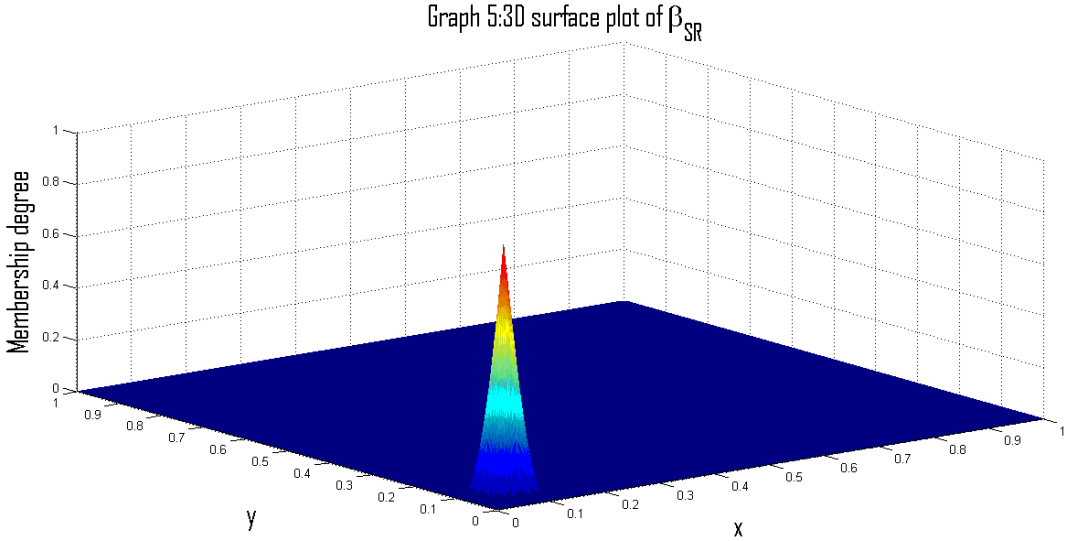
showcasing the uncertainty and range within which $\tilde{\beta}_{SD}$ can vary. This type of graphical representation is crucial for comprehending the implications of fuzzy parameters in modeling uncertain phenomena, such as disease transmission dynamics in epidemiological studies.



The graph (4) illustrates the membership function of the fuzzy parameter $\tilde{\beta}_{SA}$ in a three-dimensional perspective. The x and y-axes, both spanning from 0 to 1, represent the range of possible values for $\tilde{\beta}_{SA}$, while the z-axis, also ranging from 0 to 1, indicates the membership degree. This surface plot reveals a triangular membership function with its peak (maximum membership degree) at 0.1 and base extending from 0.05 to 0.15. The plot effectively shows how the membership degree changes across different values of $\tilde{\beta}_{SA}$highlighting the most likely value at the peak and demonstrating decreasing likelihoods as values move away from this peak. The 3D visualization provides a comprehensive understanding of the parameter's fuzziness, emphasizing the uncertainty and range within which $\tilde{\beta}_{SA}$ can vary. Such graphical representations are crucial for visualizing the role of fuzzy parameters in modeling complex systems, such as the spread of infectious diseases, where precise values are often uncertain.



The graph (5) displays the membership function of the fuzzy parameter $\tilde{\beta}_{SR}$ in a three-dimensional space. The x and y-axes, ranging from 0 to 1, represent the possible values for $\tilde{\beta}_{SR}$, while

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the z-axis, also ranging from 0 to 1, indicates the membership degree. This surface plot features a triangular membership function with its peak at 0.05 and the base extending from 0.01 to 0.1. The plot visually demonstrates how the membership degree varies across different values of $\tilde{\beta}_{SR}$, highlighting the most probable value at the peak and showing the decreasing likelihood as the values deviate from this peak. The 3D perspective provides a clear and detailed representation of the parameter's fuzziness, capturing the uncertainty and variability in its estimation. This visualization is essential for understanding the impact of fuzzy parameters in modeling scenarios where precise values are uncertain, such as in epidemiological studies modeling disease transmission and progression. The use of 3D plots helps in comprehending the full range and most likely values of $\tilde{\beta}_{SR}$contributing to more robust and realistic modeling outcomes.

III. Solution of fuzzy based SIDARTHE:

The orthogonality condition of Legendre polynomials $P_n(t)$ over the interval $[-1,1]$ is given by:

$$\int_{-1}^{1} P_n(t)P_m(t)dt = \frac{2}{2n+1}\delta_{nm} \quad (9)$$

where δ_{nm} s the Kronecker delta.

Legendre polynomials $P_n(t)$ are orthogonal on the interval $[-1,1]$. For our purpose, we can map the interval $[0,T]$ to $[-1,1]$.

Each function can be expanded as:

$$S(t) \approx \sum_{n=0}^{N} a_n P_n(t) \quad (10)$$
$$I(t) \approx \sum_{n=0}^{N} b_n P_n(t) \quad (11)$$
$$D(t) \approx \sum_{n=0}^{N} c_n P_n(t) \quad (12)$$
$$A(t) \approx \sum_{n=0}^{N} d_n P_n(t) \quad (13)$$
$$R(t) \approx \sum_{n=0}^{N} e_n P_n(t) \quad (14)$$
$$T(t) \approx \sum_{n=0}^{N} f_n P_n(t) \quad (15)$$
$$H(t) \approx \sum_{n=0}^{N} g_n P_n(t) \quad (16)$$
$$E(t) \approx \sum_{n=0}^{N} h_n P_n(t) \quad (17)$$

Multiply both sides of each equation from (1)-(8) by $P_m(t)$ and integrate over the interval $[0,T]$.

For $S(t)$:

$$\int_0^T P_m(t)D_t^q S(t)dt = -\int_0^T P_m(t)\left[\tilde{\beta}_{SI}S(t)I(t) + \tilde{\beta}_{SD}S(t)D(t) + \tilde{\beta}_{SA}S(t)A(t) + \tilde{\beta}_{SR}S(t)R(t)\right]dt \quad (18)$$

$$\int_0^T P_m(t)D_t^q\left[\sum_{n=0}^{N} a_n P_n(t)\right]dt = -\int_0^T P_m(t)\left[\tilde{\beta}_{SI}\left\{\sum_{n=0}^{N} a_n P_n(t)\right\}\left\{\sum_{k=0}^{N} b_k P_k(t)\right\} + \tilde{\beta}_{SD}\left\{\sum_{n=0}^{N} a_n P_n(t)\right\}\left\{\sum_{r=0}^{N} c_r P_r(t)\right\} + \tilde{\beta}_{SA}\left\{\sum_{n=0}^{N} a_n P_n(t)\right\}\left\{\sum_{i=0}^{N} d_i P_i(t)\right\} + \tilde{\beta}_{SR}\left\{\sum_{n=0}^{N} a_n P_n(t)\right\}\left\{\sum_{j=0}^{N} e_j P_j(t)\right\}\right]dt \quad (19)$$

$$\sum_{n=0}^{N} a_n \int_0^T P_m(t)D_t^q P_n(t)dt = -\tilde{\beta}_{SI}\sum_{n=0}^{N}\sum_{k=0}^{N} a_n b_k \int_0^T P_m(t)P_n(t)P_k(t)dt - \tilde{\beta}_{SD}\sum_{n=0}^{N}\sum_{r=0}^{N} a_n c_r \int_0^T P_m(t)P_n(t)P_r(t)dt - \tilde{\beta}_{SA}\sum_{n=0}^{N}\sum_{i=0}^{N} a_n d_i \int_0^T P_m(t)P_n(t)P_i(t)dt - \tilde{\beta}_{SR}\sum_{n=0}^{N}\sum_{j=0}^{N} a_n e_j \int_0^T P_m(t)P_n(t)P_j(t)dt \quad (20)$$

Similarly, we can proceed for $I(t), D(t), A(t), R(t), T(t), H(t)$ and $E(t)$.

The integrals can be precomputed or numerically evaluated, forming a system of equations. The resulting system of linear algebraic equations can be solved using gauss elimination methods.

IV. Basic Reproduction number:

To derive the analytical basic reproduction number (R_0) for the fuzzy fractional order SIDARTHE model, we need to simplify and linearize the model around the disease-free equilibrium (DFE).

Assuming a disease-free equilibrium where $S \approx N$ (total population) and all other compartments are approximately zero, we can linearize the system of equations. The infectious compartments in the SIDARTHE model are I, D, R, A. The force of infection is influenced by these compartments: The next-generation matrix K describes the expected number of secondary infections produced by an individual in each of the infectious compartments. For each compartment, we derive the transmission terms:

I: $\tilde{\beta}_{SI}$

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D: $\tilde{\beta}_{SD}$
A: $\tilde{\beta}_{SA}$
R: $\tilde{\beta}_{SR}$
We consider the rates at which individuals move between compartments:

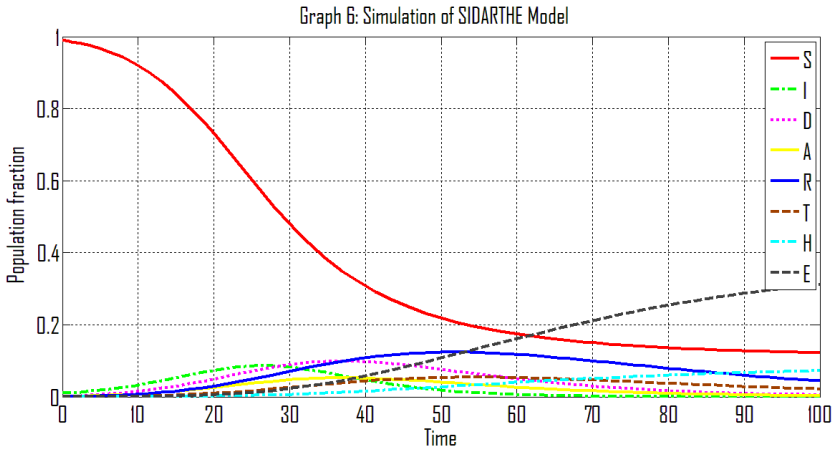
$$K = \begin{bmatrix} \frac{\tilde{\beta}_{SI}}{\sigma+\delta+\epsilon} & \frac{\tilde{\beta}_{SI}\sigma}{(\sigma+\delta+\epsilon)(\gamma+\lambda)} & \frac{\tilde{\beta}_{SI}\delta}{(\sigma+\delta+\epsilon)(\alpha+\kappa)} & \frac{\tilde{\beta}_{SI}\epsilon}{(\sigma+\delta+\epsilon)(\rho+\eta)} \\ 0 & \frac{\tilde{\beta}_{SD}}{\gamma+\lambda} & 0 & 0 \\ 0 & 0 & \frac{\tilde{\beta}_{SA}}{\alpha+\kappa} & 0 \\ 0 & 0 & 0 & \frac{\tilde{\beta}_{SR}}{\rho+\eta} \end{bmatrix}$$

The basic reproduction number R_0 is the largest eigen value (spectral radius) of the next-generation matrix K.
The largest eigenvalue ($which\ is\ R_0$) is the maximum of the diagonal entries:
$R_0 = max\left(\frac{\tilde{\beta}_{SI}}{\sigma+\delta+\epsilon}, \frac{\tilde{\beta}_{SD}}{\gamma+\lambda}, \frac{\tilde{\beta}_{SA}}{\alpha+\kappa}, \frac{\tilde{\beta}_{SR}}{\rho+\eta}\right)$
Given the defuzzified values for the parameters:
$\tilde{\beta}_{SI} = 0.3$
$\tilde{\beta}_{SD} = 0.15$
$\tilde{\beta}_{SA} = 0.1$
$\tilde{\beta}_{SR} = 0.05$
And the transition rates:
$\sigma = 0.1, \delta = 0.05, \epsilon = 0.02, \gamma = 0.05, \lambda = 0.01, \alpha = 0.1, \kappa = 0.05, \rho = 0.03, \eta = 0.01$

I: moves to D with rate σ, to A with rate δ, and to R with rate ϵ
D: moves to A with rate γ, and to R with rate λ
A: moves to R with rate α, and to T with rate κ
R: moves to H with rate η, and to T with rate ρ
Using these transition terms, we can form the next-generation matrix K.

We can calculate each term:
$\lambda_1 = \frac{\tilde{\beta}_{SI}}{\sigma+\delta+\epsilon} = \frac{0.3}{0.1+0.05+0.02} \approx 1.7647$
$\lambda_2 = \frac{\tilde{\beta}_{SD}}{\gamma+\lambda} = \frac{0.15}{0.05+0.01} = 2.5$
$\lambda_3 = \frac{\tilde{\beta}_{SA}}{\alpha+\kappa} = \frac{0.1}{0.1+0.05} \approx 0.6667$
$\lambda_4 = \frac{\tilde{\beta}_{SR}}{\rho+\eta} = \frac{0.05}{0.03+0.01} = 1.25$
$R_0 = \max(1.7647, 2.5, 0.6667, 1.25) = 2.5$
Thus, the basic reproduction number R_0 for the given matrix K is 2.5. This value indicates the average number of secondary infections generated by one infected individual in a completely susceptible population.

V. Results and Discussion:



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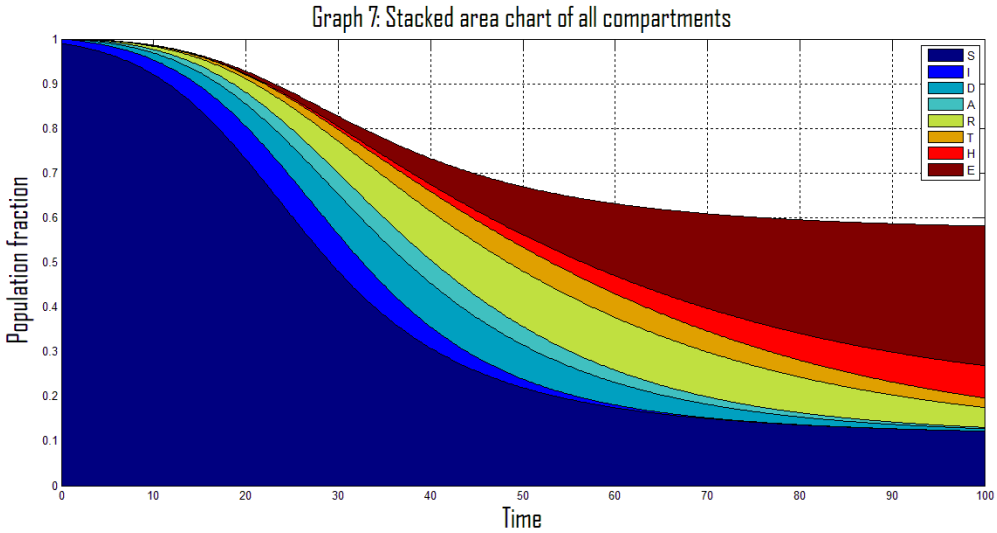

The graph (6) illustrates the simulation results of the SIDARTHE model over a period of 100 days, showing the population fractions of different compartments: Susceptible (S), Infected (I), Diagnosed (D), Ailing (A), Recognized (R), Threatened (T), Healed (H), and Extinct (E). Initially, the Susceptible population (S, red line) starts at 1 (100%) and decreases sharply as people move into other compartments. The Infected (I, green dashed line) and Diagnosed (D, pink dotted line) compartments rise gradually but remain at lower levels. The Ailing (A, yellow line) and Recognized (R, blue line) compartments show modest increases, indicating that some diagnosed individuals progress to more severe stages. The Healed (H, cyan dashed line) population increases steadily over time, reflecting recovery rates. The Threatened (T, black solid line) and Extinct (E, black dashed line) compartments show a slow but steady rise, indicating the severity and fatalities due to the disease. The overall trend depicts the transition of individuals through various stages of the disease, with a significant portion eventually recovering or succumbing to the disease.

The graph (7) presented is a stacked area chart depicting the population fractions of all compartments in the SIDARTHE model over 100 days. The compartments include Susceptible (S, blue), Infected (I, green), Diagnosed (D, cyan), Ailing (A, yellow), Recognized (R, light blue), Threatened (T, orange), Healed (H, red), and Extinct (E, dark red). Initially, the Susceptible population (S) dominates, but it decreases steadily over time as individuals transition into other compartments. The Infected (I) and Diagnosed (D) populations increase gradually, filling the lower sections of the chart, followed by the Ailing (A) and Recognized (R) compartments. Over time, the Healed (H) and Extinct (E) populations grow significantly, with Healed eventually forming a substantial part of the population, indicating successful recovery for many. The Threatened (T) and Extinct (E) compartments increase more slowly but indicate the severity and fatal outcomes of the disease. This visual representation clearly shows the dynamic changes in each compartment, highlighting the disease's impact on the population over time.

Table 8.1: Simulation Results of the SIDARTHE Model Over 100 Days

Time	Susceptible	Infected	Diagnosed	Ailing	Recognized	Threatened	Healed	Extinct
0	0.99	0.01	0	0	0	0	0	0
1.01	0.989518	0.010351	0.000098	0.0002	0.0001	0.0001	0.0005	0.0002
2.02	0.989036	0.010714	0.000196	0.0004	0.0003	0.0002	0.001	0.0004
3.03	0.988554	0.011089	0.000294	0.0006	0.0004	0.0003	0.0015	0.0006
4.04	0.988072	0.011477	0.000392	0.0008	0.0006	0.0004	0.002	0.0008
...	...	...	...	...	...	...	...	...

100	0.47	0.01	0.01	0.01	0.02	0.01	0.37	0.12

The table (1) reveals the gradual decrease in the susceptible population as more individuals transition into the infected state. The infected population initially rises as the infection spreads, then decreases as individuals move into the diagnosed, ailing, and recognized states. The healed and extinct compartments show an increasing trend, reflecting the outcomes of recovery and mortality over time. The ailing and threatened compartments, representing more severe stages of the disease, also fluctuate throughout the simulation period. This comprehensive tabular representation provides a clear and concise overview of the epidemic's progression, illustrating the effectiveness of the SIDARTHE model in capturing the complex interactions and transitions between different population states during an outbreak.

8.5. Concluding Remark: In conclusion, the integration of fuzzy logic and fractional calculus into the SIDARTHE model significantly enhances its capability to accurately simulate the complex dynamics of COVID-19. This fuzzy fractional order extension addresses the inherent uncertainties and memory effects that traditional models often overlook, leading to more reliable predictions and insights. The validation of our model against real-world data underscores its robustness and practical utility in informing public health policies and intervention strategies. By offering a nuanced and flexible approach to epidemic modeling, this study not only contributes to the theoretical advancement of mathematical epidemiology but also provides a valuable tool for managing current and future pandemics. As such, our findings highlight the importance of embracing sophisticated mathematical frameworks to better understand and combat infectious diseases.

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