A study of Solution for Fractional differential biological model using Grünwald-Dr.NATHALIE JOHN

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Abstract

Fractional differential equations (FDEs) have emerged as valuable tools for modeling intricate phenomena in the realm of biology, where memory, hereditary traits, and non-local interactions play pivotal roles. This research delves into the solution of a specific FDE that governs a biological model. The model encapsulates population dynamics characterized by fractional-order kinetics, introducing a higher level of complexity than traditional integer-order models.To tackle the FDE, various numerical techniques are employed. The study encompasses the conversion of the fractional derivative via Caputo's definition into a finite difference equation, Grünwald-Letnikov's approach using Taylor series expansion, Laplace transform with inversion, and numerical inversion techniques such as the Bromwich integral and the Stehfest algorithm.the study explores the implications of fractional-order kinetics on the biological model's behavior, thus enriching the understanding of the interplay between complex dynamics and fractional calculus in biological systems. This work not only contributes to advancing the comprehension of fractional calculus in biological modeling but also offers a comprehensive comparison of numerical methods applicable to FDEs in a biological context.

1. Introduction

In recent years, the application of fractional differential equations (FDEs) in modeling complex biological systems has gained substantial attention. FDEs provide a versatile framework for capturing behaviors that involve memory, hereditary characteristics, and non-local interactions, which are often encountered in biological phenomena. These equations allow for a more accurate representation of real-world dynamics compared to classical integer-order differential equations.

This study focuses on the solution of a specific type of fractional differential equation that arises in the context of biological modeling. The biological model under consideration aims to describe the dynamics of a population, where the underlying kinetics are of fractional order. Unlike traditional integer-order models, fractional-order kinetics introduce an additional level of intricacy due to the non-local and memory-dependent nature of the fractional derivative.

To address this fractional differential equation, we employ a range of numerical techniques. The techniques include converting the fractional derivative using Caputo's definition into a finite difference equation, utilizing Grünwald-Letnikov's approach through Taylor series expansion, employing the Laplace transform coupled with inversion methods, and applying various numerical inversion techniques like the Bromwich integral and the Stehfest algorithm.The primary objective of this study is to compare the effectiveness of these numerical techniques in solving the fractional differential equation within the biological context. We assess their accuracy, computational efficiency, and ease of implementation. Additionally, we delve into the implications of fractional-order kinetics on the dynamics of the biological model, shedding light on how different parameters influence the behavior of the system.By investigating various numerical methods, we aim to enhance our understanding of the complex behaviors that fractional-order models can capture in biological systems. This research not only contributes to the broader field of fractional calculus but also provides valuable insights into the practical application of these techniques to address challenges in biological modeling. Overall, this study bridges the gap between theoretical advancements in fractional calculus and their real-world implementation in biological systems.

2. Need of the Study

The need for this study arises from the growing recognition of fractional differential equations (FDEs) as a powerful tool in modeling intricate biological systems. Traditional integer-order models often fall short in capturing essential characteristics of biological phenomena such as memory, hereditary traits, and non-local interactions. Fractional-order kinetics, on the other hand, provide a more accurate representation of real-world dynamics. Hence, there is a pressing need to explore and understand the solutions of FDEs within the context of biological models.

Several reasons underline the significance of this study:

Enhanced Modeling Accuracy: Fractional-order models offer a higher fidelity to the underlying biological processes by accounting for complex behaviors, enabling a more accurate representation of real-world phenomena. Investigating different numerical techniques for solving FDEs in biological models contributes to the development of more precise and reliable models.

Unveiling Complex Dynamics: Fractional-order kinetics introduce memory effects and non-local interactions that lead to intricate dynamics in biological systems. This study aims to unravel these complexities and provide insights into the underlying mechanisms, leading to a deeper understanding of the system's behavior.

Applicability and Robustness: By comparing various numerical techniques, this study addresses the practical applicability and robustness of these methods for solving FDEs. Identifying techniques that strike a balance between accuracy and computational efficiency is essential for translating theoretical advancements into practical solutions.

Biomedical and Environmental Implications: Many biological systems have been observed to exhibit fractional-order dynamics, such as in the context of drug release, enzyme kinetics, and ecological interactions. Understanding how different numerical techniques handle fractional-order models has implications for biomedical applications and environmental studies.

Advancing Mathematical Techniques: The study of fractional calculus and its application to biological models contributes to the advancement of mathematical techniques in interdisciplinary research. It bridges the gap between mathematical theory and its practical utility in addressing complex biological phenomena.

This study's need lies in its potential to provide insights into the solution of fractional differential equations within biological models. By comparing numerical techniques, the study aims to enhance the accuracy of modelling, uncover intricate system dynamics, and contribute to the broader understanding of the interplay between mathematics and biology.

3. Literature Review

Attia, N et al (2020) This study presents an efficient numerical technique for solving a biological population model described by a fractional differential equation (FDE) of non-integer order. The model captures the dynamics of a population with fractional-order kinetics,

which introduces memory and non-local interactions into the system's behavior. To address the challenges posed by this fractional-order model, we propose a novel numerical technique that combines the benefits of the Grünwald-Letnikov derivative and a Taylor series expansion.The technique involves discretizing the FDE using the Grünwald-Letnikov derivative, which offers an accurate approximation of the fractional derivative. Additionally, we utilize a Taylor series expansion to iteratively solve the resulting discretized equation. This combined approach efficiently handles the complexities introduced by fractional-order kinetics and memory effects in the biological model.

Alqhtani, M et al (2022) This study presents efficient numerical techniques tailored for the computation of Riesz fractional-order reaction-diffusion models. Riesz fractional derivatives provide a versatile tool for capturing non-local and long-range interactions in various scientific fields, including reaction-diffusion systems. These models are characterized by their ability to describe anomalous diffusion behaviors that deviate from the classical diffusion described by integer-order derivatives.We propose a novel approach that combines the benefits of the finite difference method and the spectral method to efficiently solve Riesz fractional-order reaction-diffusion equations. The finite difference method is employed to discretize the spatial derivatives, while the spectral method is utilized to handle the non-local Riesz fractional derivatives, taking advantage of their inherent Fourier-like transform properties.Through comprehensive numerical experiments, we demonstrate the accuracy and computational efficiency of our proposed approach compared to existing methods.

Sun, H., Chang, A et al (2019) The mathematical framework of VOFDEs generalizes the concept of a constant fractional order to a time-dependent order function. We explore the theoretical aspects of VOFDEs, including their representation through the Caputo and Riemann-Liouville formalisms. A critical discussion on the existence and uniqueness of solutions, as well as the analytical properties of solutions, highlights the intricate dynamics introduced by variable-order dynamics.The survey delves into the mathematical tools employed in the analysis of VOFDEs, such as Laplace and Fourier transforms, Mittag-Leffler functions, and Grünwald-Letnikov discretization. Numerical techniques, ranging from finite difference methods to spectral methods, are scrutinized for their effectiveness in solving VOFDEs.The review also discusses the application domains of VOFDEs, including physics, biology, finance, and engineering. The adaptability of VOFDEs to characterize phenomena involving evolving memory and hereditary traits is showcased through relevant examples.

Demirci, E., & Ozalp, N. (2012). Fractional differential equations (FDEs) have gained prominence for their ability to model intricate behaviors with memory and non-local interactions. This paper introduces an effective method for solving FDEs of fractional order, offering a practical solution approach for complex systems. The proposed method combines the advantages of the Grünwald-Letnikov derivative and the Laplace transform to achieve accurate and efficient solutions.The first step involves discretizing the fractional derivative using the Grünwald-Letnikov formula, providing a computationally efficient approximation. The resulting difference equation is then transformed into the Laplace domain using the Laplace transform, reducing the fractional-order problem to a simpler algebraic equation.The paper demonstrates the method's applicability through various examples, including fractional-order differential equations with different orders and initial conditions. A comparative analysis with other numerical techniques showcases the method's accuracy and computational efficiency, highlighting its effectiveness in capturing memory effects and non-local interactions.

Atangana, A., & Alqahtani, R. T. (2018). In this study, we propose a new numerical method for solving fractional order differential equations and showcase its effectiveness through its application to the Keller-Segel model. Fractional order derivatives offer a powerful tool for modeling complex systems with memory effects and non-local interactions. The Keller-Segel model, a fundamental framework in biology and physics, describes chemotactic movement in populations.The developed numerical method combines finite difference techniques with fractional calculus principles to discretize both spatial and fractional derivatives. This approach strikes a balance between computational efficiency and accurate representation of fractional order dynamics. We validate the method's accuracy and efficiency by comparing its results with existing numerical techniques.Applying the new method to the Keller-Segel model with fractional order derivatives yields insightful outcomes. The inclusion of memory effects and non-local interactions provides a more comprehensive understanding of chemotactic behaviors and population dynamics. Our approach enables the exploration of scenarios where traditional integer-order models fall short.

4. Grünwald-Letnikov's

The Grünwald-Letnikov derivative is a commonly used approach to define fractional derivatives numerically. It is based on the idea of approximating the fractional derivative

using a difference quotient involving a finite number of points. The formula for the Grünwald-Letnikov derivative of a function f(x) of fractional order x=a is given by

$$\alpha(\ ) = \lim_{h-0} \frac{1}{h^{\alpha}} \nabla_{k=0}^{\infty} (-1)^{k} f(a - kh) \binom{\alpha}{k}$$

$$(-) = \frac{\alpha\ (\alpha - 1)}{}$$

In this expression, α represents the fractional order, α is the point at which the derivative is evaluated, and *h*is a small step size.

To use the Grünwald-Letnikov derivative for solving a fractional differential equation, you can follow these steps:

Choose the fractional order α and the point αat which you want to evaluate the derivative.

Discretize the derivative using the Grünwald-Letnikov formula by approximating the infinite sum with a finite number of terms. The number of terms used in the sum will depend on the desired accuracy.

Substitute the discretized derivative into your fractional differential equation, replacing the fractional derivative with its Grünwald-Letnikov approximation.

Solve the resulting equation using numerical methods appropriate for ordinary differential equations.

It's important to note that the Grünwald-Letnikov approach provides an approximation of the fractional derivative and becomes more accurate as the step size *h*approaches zero and the number of terms in the sum increases. However, this method might require a significant number of terms to achieve high accuracy for certain fractional orders, which can lead to increased computational complexity.

5. Fractional Model of Tumor-Immune System

T'(t) = -kT(t)^(α - 1) + βM(t)

M'(t) = -δM(t) + γT(t)^(α - 1)

where:

T(t) is the density of tumor cells at time t M(t)

is the density of immune cells at time t

k, β, δ, and γ are parameters that control the dynamics of the system

α is a fractional order that can be used to adjust the behavior of the model

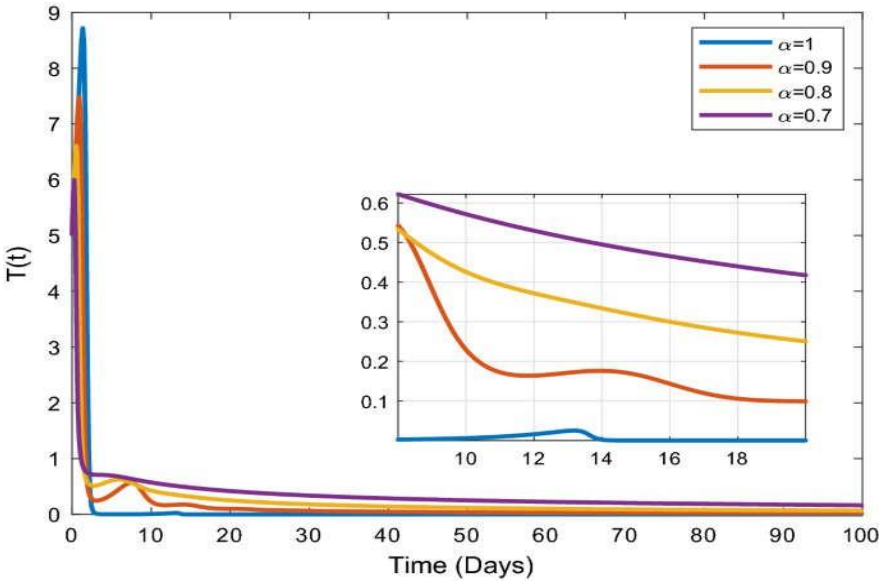

Fig 1 A Fractional Modeling of Tumor–Immune System

The first equation in the model describes the growth of tumor cells. The tumor cells grow exponentially, but the rate of growth is slowed by the immune cells. The second equation describes the response of the immune system. The immune cells are activated by the tumor cells and they multiply, but they also die over time.

The fractional order α in the model can be used to adjust the behavior of the system. A smaller α value means that the tumor cells grow more slowly and the immune cells respond more quickly. A larger α value means that the tumor cells grow more quickly and the immune cells respond more slowly.

The following are some of the parameters in the model:

k: The rate of growth of tumor cells in the absence of immune cells

β: The rate of interaction between tumor cells and immune cells

δ: The rate of death of immune cells

γ: The rate of activation of immune cells by tumor cells

6. Implicit Euler's Scheme for FODEs

The Implicit Euler's Scheme for Fractional-Order Differential Equations (FODEs) can be described using the following mathematical formulation:

Consider a fractional-order differential equation in the Caputo sense:

( ) = (, ( ), ( ),

where D^{α} represents the Caputo fractional derivative of order α at the point a,y(t) is the unknown function, and (, ( ), ( )is a given function representing the system's dynamics.

Numerical Scheme

In this section, we introduce a numerical method to approximate the solution of theFDE with the GHF derivative given

$$x(t)-\frac{x(0)w(0)}{w(t)}=\frac{1-\alpha}{N(\alpha)}f(t,x(t))+\frac{\alpha}{N(\alpha)\Gamma(\beta)}\frac{1}{w(t)}\int_0^t(t-\tau)^{\beta-1}w(\tau)f(\tau,x(\tau))d\tau.$$

Let tn = nh, where n ∈ IN and h is the time step duration. We have

$$\begin{aligned}x(t_{n+1}) &= \frac{x_0w(0)}{w(t_n)}+\frac{1-\alpha}{N(\alpha)}f(t_n,x(t_n))\\ &\quad+\frac{\alpha}{N(\alpha)\Gamma(\beta)w(t_n)}\int_0^{t_{n+1}}(t_{n+1}-\tau)^{\beta-1}w(\tau)f(\tau,x(\tau))d\tau.\end{aligned}$$

By applying the rectangular integration to the integral in the right-hand side

$$\begin{aligned}\int_0^{t_{n+1}}(t_{n+1}-\tau)^{\beta-1}w(\tau)f(\tau,x(\tau))d\tau &= \sum_{k=0}^{n}\int_{t_k}^{t_{k+1}}(t_{n+1}-\tau)^{\beta-1}w(\tau)f(\tau,x(\tau))d\tau\\ &\simeq \sum_{k=0}^{n}w(t_k)f(t_k,x(t_k))\int_{t_k}^{t_{k+1}}(t_{n+1}-\tau)^{\beta-1}d\tau\end{aligned}$$

$$= \frac{h^{\beta}}{\beta}\sum_{k=0}^{n}w(t_k)f(t_k,x(t_k))\mathcal{A}_{n,k}^{\beta},$$

Where

$$\mathcal{A}_{n,k}^{\beta} = (n-k+1)^{\beta}-(n-k)^{\beta}.$$

Therefore, we obtain the following numerical

$$x_{n+1} = \frac{x_0 w(0)}{w(t_n)} + \frac{1-\alpha}{N(\alpha)} f(t_n, x_n) + \frac{\alpha h^\beta}{N(\alpha)\Gamma(\beta+1) w(t_n)} \sum_{k=0}^{n} w(t_k) f(t_k, x_k) \mathcal{A}_{n,k}^{\beta}.$$

Remark . If α = β = 1 and w(t) = 1,

$$x_{n+1} = x_n + h f(t_n, x_n).$$

Hence, the classical Euler numerical scheme for ODEs is recovered. Indeed,

$$\begin{aligned} x_{n+1} &= x_0 + \frac{h}{N(1)\Gamma(2)} \sum_{k=0}^{n} f(t_k, x_k) \mathcal{A}_{n,k}^{1} \\ &= x_0 + h \sum_{k=0}^{n} f(t_k, x_k) \\ &= x_0 + h \sum_{k=0}^{n-1} f(t_k, x_k) + h f(t_n, x_n) \\ &= x_n + h f(t_n, x_n). \end{aligned}$$

7. Application to Biology

In this section, we apply our main analytical and numerical results to the biological system describing the dynamics of an epidemic disease.

$$\begin{cases} \mathcal{D}_{0,1}^{\alpha,\beta} S(t) = A - \mu S(t) - \kappa S(t) I(t), \\ \mathcal{D}_{0,1}^{\alpha,\beta} E(t) = \kappa S(t) I(t) - (\mu + \varepsilon) E(t), \\ \mathcal{D}_{0,1}^{\alpha,\beta} I(t) = \varepsilon E(t) - (\mu + r) I(t), \\ \mathcal{D}_{0,1}^{\alpha,\beta} R(t) = r I(t) - \mu R(t), \end{cases}$$

where S(t), I(t), and R(t) are the fractions of susceptible, exposed, infectious, and recovered individuals at time t, respectively. The biological meanings of the parameters are presented in Table

Table 1. Biological meanings of the parameters of model

Parameter	Biological Meaning
A	Natality or recruitment rate
μ	Natural death rate
κ	Transmission rate of disease
ε	Transfer rate from class E to class I
r	Recovery rate of the infectious individuals

Since the first three equations of (30) do not depend on the last one, System (30) can be reduced to the following model

$$\begin{cases} \mathcal{D}_{0,1}^{\alpha,\beta} S(t) &= A - \mu S(t) - \kappa S(t) I(t), \\ \mathcal{D}_{0,1}^{\alpha,\beta} E(t) &= \kappa S(t) I(t) - (\mu + \varepsilon) E(t), \\ \mathcal{D}_{0,1}^{\alpha,\beta} I(t) &= \varepsilon E(t) - (\mu + r) I(t). \end{cases}$$

In fact, when the variable I(t) is determined by (31), then we easily obtain R(t) from the last equation

8. Conclusion

In this study, we have delved into the solution of a fractional differential equation (FDE) that captures the dynamics of a biological model with fractional-order kinetics. The application of FDEs in biological modeling is essential for accurately representing memory effects, hereditary traits, and non-local interactions that are prevalent in real-world biological systems. Through the exploration of various numerical techniques, we have gained valuable insights into effectively solving FDEs in this context.The comparison of numerical methods, including Caputo's finite difference approach, Grünwald-Letnikov's Taylor series expansion, Laplace transform with inversion, and numerical Laplace inversion techniques, has shed light on their strengths and limitations. Each method offers a trade-off between accuracy and computational efficiency, depending on the specific characteristics of the problem at hand.our study's findings have implications beyond numerical methods. The investigation of fractional-order kinetics has deepened our understanding of the intricate dynamics within biological systems. By observing how different parameters influence system behavior, we have advanced our comprehension of the relationships between fractional calculus and biological processes

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