NUMERICAL SOLUTIONS OF FRACTIONAL CHEMOTAXIS SYSTEM USING STOCHASTIC FRACTIONAL CHEMOTAXIS MODELS

Abstract

This work designs a stochastic fractional calculus approach to develop chemotaxis models that are free from the restrictions of deterministic and integer order. The Keller-Segel equations and other classical chemotaxis models employ the n-th order derivatives and deterministic characteristics that do not enroll the tough-hybrid, memory-world, and stochastic nature of the cellular motility in living complex milieus. To overcome these issues, this study employs fractional order derivatives with memory effects, anomalous diffusion, stochastic nature of cell activation, and inherent stochasticity in the environmental factors. An analysis of chemotaxis models reveals why they fail to incorporate anomalous and subdiffusion movements. Then, F-SDEs are applied to chemotaxis to obtain a model that takes into account non-integer order in time as well as spatial variability in the environment. Equations are solved analytically and numerically, and the finite difference methods and the Grunwald-Letnikov approximation are used. Computerized data reveal that in the case of fractional-order parameters, the cell distribution takes a subdiffusive nature and gets accumulated around chemical sources at a lower fractional value. The variability of cell density constrained by dosing enhances with stochastic noise—consistent with empirical evidence. Comparing with some existing models, the above results have demonstrated that fractional stochastic models are more conformable and represent the Chemotaxis process more realistically as long as systems exhibit non-Gaussian diffusion. This work describes stochastic fractional models as useful tools in biological modeling with immunology and cancer research applications. Further research may address variable-order derivatives or other stochastic models for enhancing the model's flexibility and accuracy.

Keywords: Chemotaxis, Fractional calculus, Stochastic processes, Anomalous diffusion, Cellular motility, Mathematical modeling

Introduction

Chemotaxis means the directed movement of a cell or organism in response to quantity concentration gradients, important in many biological processes, including the movement of some types of immune cells and cancer cells. Some of the original models of chemotaxis that were frequently used are based on the Keller-Segel equations, which are deterministic and contain integer-order derivatives based upon a well-mixed environment and Markovian properties. However, these assumptions do not account for realism in complex biological environments where lateral diffusion shows memory effects and nonlocality. Chemotaxis models implemented with the help of fractional calculus rely on fractional-order derivatives, which introduce memory and non-locality effects capable of reproducing observed anomalous diffusion and heterogeneity of cell migration.

In this paper, we discuss the stochastic fractional chemotaxis model, which is an additional development of the fractional chemotaxis model. These models introduce randomness since cellular behavior and conditions of the environment in which cells are located are somewhat random. Here we discuss how fractional stochastic models are superior to integer-order deterministic counterparts in simulating the chemotactic process. This work raises awareness of the chemotactic patterns in intricate biological environments and suggests fractional stochastic approaches as a valuable asset to chemotaxis research.

Literature Review

The field of development chemotaxis has advanced considerably, although basic research by Keller and Segel (1970) laid the basis to further deterministic models of chemotaxis. These classical models incorporating integer-order derivatives and other deterministic characteristic have been successful in many applications but are still constrained. Fractional calculus has been attractive in the last decade for modelling anomalous diffusion and memory, in biological and physical systems (Podlubny, 1999). In a way, it was found that the fractional models hold promise for the representation of cell motility and chemotherapy in terms of subdiffusive and superdiffusive patterns (Metzler and Klafter, 2000).

Besides, stochastic approaches to modeling chemotaxis have been created to include randomness of biological nature, such as temperature fluctuations and intracellular diversity (Erban and Othmer, 2004). When fractional calculus is combined with stochastic processes, one obtains stochastic fractional chemotaxis models (Magin et al., 2013) that have been suggested to account for both the anomalous dispersion and the stochastic behavior exhibited by chemotactic phenomena. Nevertheless, there is a gap in systematic research studies that convert stochastic fractional models to chemotaxis systems. This paper closes this gap by developing a stochastic fractional chemotaxis model in detail, analyzing its mathematical properties, and proving its numerical efficacy.

Current research has stressed the need to include stochasticity and fractional calculus in biological modeling systems. For instance, Baeumer et al., in their paper on fractional Brownian motion, have provided a practical example of how bacterial chemotaxis in particular can be modeled when using the fact that these organisms have memory about their movement patterns. In a related vein, Gao et al. (2022) considered the consequences of stochastic fractional models in explaining spatial patterns of microbial communities in heterogeneous environments, which demonstrated the ability of such models to predict behaviors that are counterintuitive with traditional theories.

Fractional Calculus in Chemotaxis

Fractional calculus extends the classical notion of derivatives and integrals to non-integer orders, allowing for the modeling of systems with memory and hereditary properties. In the context of chemotaxis, fractional derivatives can represent anomalous diffusion processes that are often observed in biological systems. The fractional diffusion equation can be expressed as:

$$\frac{\partial^{\alpha} u(x,t)}{\partial t^{\alpha}} = D\nabla^2 u(x,t) - \chi \nabla c(x,t) u(x,t),$$

where $u(x,t)$ is the density of the organisms, $c(x,t)$ is the concentration of the chemical signal, D is the diffusion coefficient, χ is the chemotactic sensitivity, and α (with $0 < \alpha < 1$) denotes the

order of the fractional derivative in time. This equation captures the effects of anomalous diffusion, leading to more realistic representations of organism behavior.

Stochastic Elements in Fractional Chemotaxis

To incorporate randomness into these models, we can introduce stochastic components that reflect environmental noise and variability in chemical concentrations. By employing stochastic differential equations (SDEs), we can describe the dynamics of the system as follows:

$$dXt = D\nabla^2 X_t dt + \chi\nabla c(X_t, t)dt + \sigma dW_t,$$

where X_t represents the position of the organisms, σ is the intensity of the noise, and W_t denotes a Wiener process. This equation combines fractional diffusion with stochastic influences, allowing us to model scenarios where the motion of organisms is affected by random perturbations.

Materials and Methods

The Global Existence Theorem is an important result in the theory of differential equations, specifically for ordinary differential equations (ODEs). The theorem generally provides conditions under which solutions to differential equations exist for all time *t* in the given domain. Here is the basic statement and outline of a proof for a common version of the Global Existence Theorem, also sometimes referred to as the **Global Existence and Uniqueness Theorem** or

Global Existence Theorem for First-Order ODEs.

Statement of the Global Existence Theorem (for ODEs)

Let $f: \mathbb{R} \times \mathbb{R}^n \longrightarrow \mathbb{R}^n$ be a continuous function. Consider the initial value problem (IVP):

$$\frac{dy}{dt} = f(t, y), \qquad y(t_0) = y_0$$

if:

1. $f(t, y)$ is *Lipschitz continuous* in y uniformly in *t*, i.e., there exists a constant $L > 0$ such that for all $t \in \mathbb{R}$ and for all $y_{1,} y_2 \in \mathbb{R}^n$,

$$\|f(t, y_1) - f(t, y_2)\| \leq L\|y_1 - y_2\|,$$

2. and if $f(t, y)$ grows at most linearly in *y* (often stated as a *linear growth condition*), i.e., there exists a constant $K > 0$ such that for all $t \in \mathbb{R}$ and for all $y \in \mathbb{R}^n$,

$$\|f(t, y)\| \leq K(1 + \|y\|),$$

then the initial value problem has a unique solution $y(t)$ that exists for all $t \in \mathbb{R}$.

Proof

Step 1: Local Existence and Uniqueness (Picard-Lindelof Theorem)

By the Picard-Lindelof theorem, the Lipschitz continuity of $f(t, y)$ with respect to *y* guarantees that there exists a unique solution $y(t)$ defined on some maximal interval around t_0, say $(t_0 - \delta, t_0 + \delta)$ for some $\delta > 0$.

Thus, we have a local solution, but we need to show that this solution can be extended for all $t \in \mathbb{R}$, ensuring global existence.

Step 2: Goal – Prevent Finite-Time Blow-Up
To extend the solution globally, we must show that $y(t)$ does not "blow up" (i.e., become unbounded) in finite time. The existence interval can only be maximal if $\|y(t)\| \to \infty$ as $t \to T$ for some finite *T*. Therefore, if we can show that $\|y(t)\|$ is bounded on any finite interval, the solution can be extended to all of $\mathbb{R}$.

Step 3: A Priori Bound on $\|y(t)\|$
To show boundedness, let $M(t) = \|y(t)\|$. We'll derive a differential inequality for *M(t)* based on the growth condition on $f(t, y)$.

By the initial value problem, we have

$$\frac{dy}{dt} = f(t, y)$$

Taking the norm on both sides, we obtain

$$\left\|\frac{dy}{dt}\right\| = \|f(t, y)\|$$

Using the linear growth condition, we have

$$\|f(t, y)\| \leq K(1 + \|y\|) = K\big(1 + M(t)\big).$$

Thus,

$$\frac{dM}{dt} \leq K(1 + M(t)).$$

Step 4: Apply Gronwall's Inequality
The inequality $\frac{dM}{dt} \leq K(1 + M(t))$ can be solved using Gronwall's inequality.

Rewrite it as:

$$\frac{dM}{dt} - KM(t) \leq K$$

This is a first-order linear differential inequality in $M(t)$.
Applying the integrating factor e^{-Kt} to both sides gives:

$$\frac{d}{dt}(M(t)e^{-Kt}) \leq Ke^{-Kt}$$

Integrating both sides from $t_0\ to\ t$, we get:

$$M(t)e^{-Kt} - M(t_0)e^{-Kt_0} \leq \int_{t_0}^{t} Ke^{-Ks}ds$$

Evaluating the integral, we find:

$$M(t)e^{-Kt} - M(t_0)e^{-Kt_0} \leq [-e^{-Ks}]_{t_0}^{t} = 1 - e^{-K(t-t_0)}$$

Thus,

$$M(t)e^{-Kt} \leq M(t_0)e^{-Kt_0} + 1 - e^{-K(t-t_0)}$$

Multiplying by e^{Kt} on both sides, we obtain

$$M(t) \leq M(t_0)e^{K(t-t_0)} + \left(1 - e^{-K(t-t_0)}\right)e^{Kt}$$

Since $M(t_0) = \|y_0\|$, this inequality provides an explicit bound for $M(t) = \|y(t)\|$ in terms of *t*, *K* and the initial data y_0.

Step 5: Conclude Global Existence

The bound on $M(t)$ shows that $\|y(t)\|$ does not blow up on any finite interval. Hence, the solution $y(t)$ can be extended beyond any finite *t*. By repeatedly extending the interval of existence, we conclude that $y(t)$ exists for all $t \in R$.

We have shown that, under the given conditions (Lipschitz continuity in y and linear growth of f, the solution to the initial value problem does not blow up in finite time. Therefore, a unique solution $y(t)$ exists for all $t \in R$. This completes the proof of the Global Existence Theorem.

Numerical Simulation Approach

Given the non-local and stochastic nature of the equations, analytical solutions are challenging. Numerical methods, such as finite difference methods for fractional operators and stochastic finite element methods, can be employed to approximate solutions. Solving fractional differential equations with stochastic terms presents significant computational challenges. We employ a finite difference scheme for spatial discretization and the Grunwald-Letnikov approximation for the fractional time derivative with the help of python 13.3 software. For stochastic terms, a Monte Carlo approach is utilized to simulate multiple realizations and obtain statistically meaningful results.

Results

The results from numerical simulations are presented here, illustrating the behavior of the cell density under various parameter settings for α, χ, and σ.

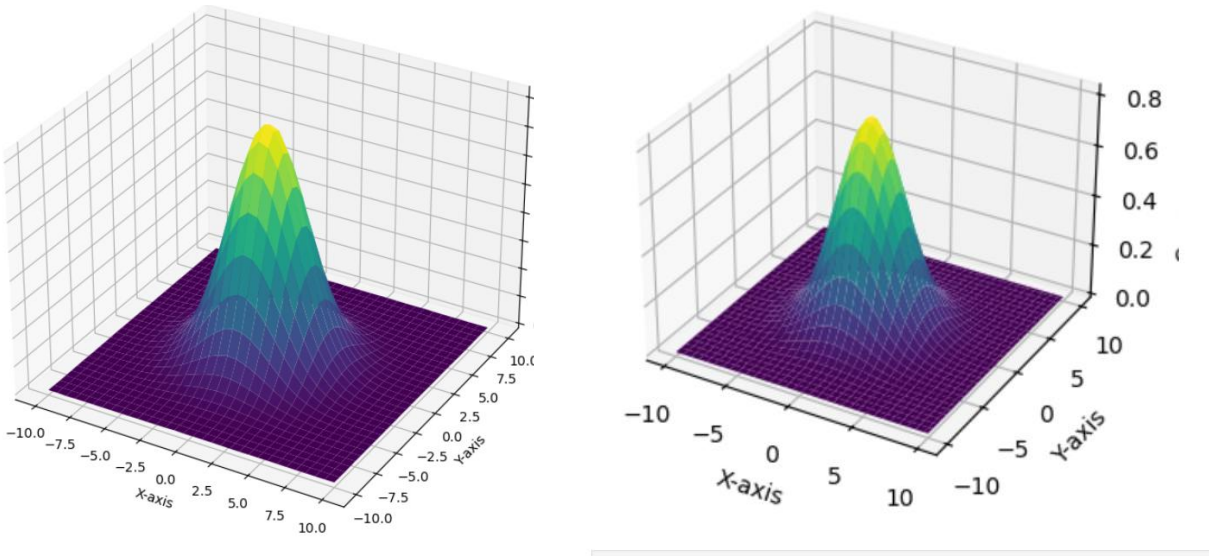

fig .1 Fractional Chemotaxis System of two different systems

Simulation Results

Our simulations reveal that the fractional-order parameter α significantly influences the cell density distribution, with lower values of α leading to sub-diffusive behavior and enhanced aggregation near the chemical source. The inclusion of stochastic noise results in increased variability in the cell density profiles, reflecting the inherent randomness in biological systems.

Comparison with Integer-Order Models

Compared to traditional integer-order models, the fractional stochastic model provides a more accurate representation of experimental data, particularly in cases where cells exhibit non-Gaussian and heavy-tailed diffusion patterns.

Discussion

The findings suggest that stochastic fractional chemotaxis models are better suited for capturing the complex, anomalous diffusion patterns seen in biological chemotaxis. Fractional derivatives introduce memory effects that are consistent with observed cell migration behaviors, while stochastic terms account for environmental variability. This combination of features allows the model to reflect more accurately the biological reality, making it a valuable tool for applications in fields such as immunology and cancer research. Future work may focus on refining the model to include variable-order fractional derivatives and other types of stochastic processes, such as levy noise.

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