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A Positivity-Preserving Fourier Spectral Moving Mesh Method for the Keller-Segel Chemotaxis Model

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Abstract. We develop a numerical method for the Keller-Segel chemotaxis system that is designed to

(i) preserve the model's fundamental structural properties (positivity/bound preservation, mass conservation, and energy dissipation),

(ii) efficiently and accurately resolve the near-singular dynamics associated with spike formation and finite-time blow-up.

Our approach combines a linear, positivity-preserving scalar auxiliary variable (SAV) scheme (following the framework in [15]) with a Fourier spectral spatial discretization and an moving-mesh PDE-based method. The SAV reformulation provides a convenient platform for stable, linear time stepping while maintaining energy dissipation; the Fourier spectral discretization delivers high accuracy in smooth regions; and the moving-mesh PDE mesh redistribution concentrates collocation points in regions of large gradients so that sharp, localized structures can be resolved without prohibitive cost. We show that the proposed moving mesh SAV scheme inherits positivity preservation, mass conservation, and discrete energy dissipation provided the mesh motion avoids element overlap. Two-dimensional tests demonstrate the method's ability to capture fine spike profiles and estimate blow-up times with substantially reduced computational effort; the formulation extends straightforwardly to

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three spatial dimensions. Numerical results show that the proposed method is a practical and effective method for accurate simulation of chemotactic aggregation.

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Key words: Keller-Segel chemotaxis model, moving mesh PDE, scalar auxiliary variable, positivity preserving, finite-time blowup.

1 Introduction

Chemotaxis describes the directed movement and aggregation of organisms (such as microorganisms or cells) in response to chemical signals (commonly called chemoattractants). The classical Keller-Segel model (see Eqs. (2.1) and (2.2) in Section 2), proposed by Keller and Segel [19–21], uses the cell density $u(x,t)$ and the chemical concentration $\phi(x,t)$ as primary variables and models the competition between diffusion (Brownian motion) and aggregation driven by chemical gradients via advection-diffusion equations. As a result, the Keller-Segel system has become a fundamental mathematical model for studying biological aggregation, pattern formation, and processes such as tumor growth. The most common Keller-Segel system is written as a parabolic-parabolic system, i.e., for each organism and the chemical concentration, the evolution is described by a parabolic equation. In many cases, the chemical signals respond to the concentration of the organism much faster than the organism responds to the chemical signal. Therefore, it is common to simplify the parabolic equation for the chemical signal as an elliptic equation, which leads to a parabolic-elliptic system.

From a theoretical viewpoint, the Keller-Segel system has been intensively studied and has generated a rich body of results. In two spatial dimensions, it is well known that, for sufficiently large initial total mass, the parabolic-elliptic case [28] and certain fully parabolic cases [14] can develop finite-time aggregation (blow-up), where the solution concentrates toward Dirac-delta–type measures. Besides the classical δ-type singularity, self-similar profiles of the form $C(T-t+|x|^2)^{-1}$ have been identified and provide alternative descriptions of blow-up behavior in the 3D parabolic-elliptic case [13,30]. In three dimensions, global well-posedness results for the fully parabolic Keller-Segel system have been established under smallness assumptions on the initial data [3,22,27,32]. At the same time, a complete characterization (criteria and profile) of finite-time singularity formation in 3D for the fully parabolic case remains largely open.

Numerical simulations of the Keller-Segel model confront two distinct challenges. The first is to design discretizations that respect the model's fundamental