The Positivity-Preserving Finite Volume Coupled with Finite Element Method for the Keller–Segel–Navier–Stokes Model

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Received 21 November 2023; Accepted (in revised version) 5 March 2024

Abstract. We propose a linear decoupled positivity-preserving scheme for the chemotaxis-fluid system, which models the interaction between aerobic bacteria and the fluid flow surrounding them. This scheme comprises the finite element method (FEM) for the fluid equations on a regular triangulation and an upwind finite volume method (FVM) for the chemotaxis system on two types of dual mesh. The discrete cellular density and chemical concentration are represented as the piecewise constant functions on the dual mesh. They can also be equivalently expressed as the piecewise linear functions on the triangulation in the sense of mass-lumping. These discrete solutions are obtained by the upwind finite volume approximation satisfying the laws of positivity preservation and mass conservation. The finite element method is used to compute the numerical velocity in the triangulation, which is then used to determine the upwind-style numerical flux in the dual mesh. We analyze the Mproperty of the matrices from the discrete system and prove the well-posedness and the positivity-preserving property. By using the L^p -estimate of the discrete Laplace operators, semigroup analysis, and induction method, we are able to establish the optimal error estimates for chemical concentration, cellular density, and velocity field in $(l^{\infty}(W^{1,p}), l^{\infty}(L^p), l^{\infty}(W^{1,p}))$ -norm. Several numerical examples are presented to verify the theoretical results.

AMS subject classifications: 65M08, 76M10, 76D05, 35Q92, 92C17

Key words: Finite volume method, finite element method, chemotaxis-fluid system, conservation law, positivity preserving, error estimates.

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Introduction 1

We develop and analyze a numerical scheme that preserves positivity and mass conservation for the 2D chemotaxis-fluid system, also known as the Keller-Segel-Navier-Stokes equations, in a polygonal domain Ω . This approach combines the finite volume method and the finite element method. The PDE model represents the complex interplay between chemotaxis, diffusion of signaling chemicals, and the buoyancy-driven effect of bacterial mass on the fluid motion:

$$\int c_t + \mathbf{u} \cdot \nabla c - \nu_c \Delta c = -nf(c) \qquad \text{in } \Omega \times (0,T), \qquad (1.1a)$$

$$n_t + \mathbf{u} \cdot \nabla n - \nu_n \Delta n + \nabla \cdot (n\chi(c)\nabla c) = 0 \quad \text{in } \Omega \times (0,T),$$
(1.1b)

$$+ \mathbf{u} \cdot \nabla \mathbf{u} - \nu \Delta \mathbf{u} + \nabla p = n \nabla \Phi \qquad \text{in } \Omega \times (0, T), \qquad (1.1c)$$

$$\begin{cases} n_t + u \cdot \nabla n - \nu_n \Delta n + \nabla \cdot (n\chi(c)\nabla c) = 0 & \text{in } \Omega \times (0,T), \\ u_t + u \cdot \nabla u - \nu \Delta u + \nabla p = n\nabla \Phi & \text{in } \Omega \times (0,T), \\ \nabla \cdot u = 0 & \text{in } \Omega \times (0,T), \\ u = 0, \quad \nabla_n n = \nabla_n c = 0 & \text{on } \Gamma \times (0,T), \end{cases}$$
(1.1e)

$$\begin{aligned} u(\cdot,0) &= u_0, \quad n(\cdot,0) = n_0, \quad c(\cdot,0) = c_0 \quad \text{in } \Omega, \end{aligned}$$
(1.1c)

where the unknown (n(x,t),c(x,t),u(x,t),p(x,t)) represents the density of cells, the concentration of chemical material, the velocity and pressure of the fluid flow, ∇_n denotes the differentiation along the outer unit normal vector *n* on the boundary $\Gamma = \partial \Omega$, $\nu_c > 0$ and $\nu_n > 0$ the diffusion parameters, and $\nu > 0$ the viscosity. The functions for chemotactic sensitivity, signal consumption rate, gravitational potential, and initial values are given as $\chi(\cdot)$, $f(\cdot)$, $\Phi(x,t)$ and (u_0, n_0, c_0) . Experiments have shown that this chemotaxis-fluid interaction produces structures with high concentrations of cells in local areas. The case of upward oxygen taxis and downward gravitational forcing are studied by [56], which demonstrates that the dynamics of oxygen diffusion and consumption, chemotaxis, and viscous flow cause the formation of fluid vortices and high concentrations of cells in local areas. Several analytical findings on the well-posedness of the chemotaxis-fluid equations are summarized by [3].

Extensive research has been conducted on the PDE theories of the Keller-Segel system [16,25,30,31,43,44,57], as well as various numerical methods. These include the (masslumping) finite element method [41, 47, 48, 52], the discontinuous Galerkin method [18, 19], the finite volume method (FVM) [2,4,10,22,63], the finite difference method [17,49], and the hybrid finite-volume-finite-difference (HFVFD) scheme [8] which is suitable for singular solutions. Moreover, the stochastic particle method [28] has also been explored.

For the chemotaxis-fluid system, the weak and global existence theory has been established by [58,59], and various simulation methods have been proposed, including the finite-difference method and finite element method (FEM) [23, 24, 36, 39, 53], the conservative finite difference scheme [26], the FEM with biquadratic quadrilateral element [15], the finite-volume-nonconforming-finite-element method [7], the particle method mixed with FVM [29]. The vorticity-based HFVFD scheme proposed by [9] constructs numerical approximations based on the finite element method, however, there is a limitation for the estimation of pressure. In the case of the chemotaxis-Stokes system, [21, 35] proposes a