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Numerical analysis of a chemotaxis–swimming bacteria model on a general triangular mesh

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ABSTRACT

This paper is devoted to the numerical study of a model arising from biology, consisting of chemotaxis equations coupled to Navier–Stokes flow through transport and external forcing. A detailed convergence analysis of this chemotaxis–fluid model by means of a suitable combination of the finite volume method and the nonconforming finite element method is investigated. In the case of nonpositive transmissibilities, a correction of the diffusive fluxes is necessary to maintain the monotonicity of the numerical scheme. Finally, many numerical tests are given to illustrate the behavior of the anisotropic Keller–Segel–Stokes system.

1. Introduction

Chemotaxis is a biological process, in which cells move towards a chemically more favorable environment. This behavior enables them to locate nutrients or to avoid predators and the chemical can be produced or consumed by the cells. For example, bacteria often swim towards higher concentration of oxygen to survive. The best studied model of chemotaxis phenomenon in mathematical biology is the Keller–Segel system introduced in [21] and the article [20] has provided a detailed introduction into the mathematics of this model. In nature, cells often live in a viscous fluid and meanwhile the motion of the fluid is under the influence of gravitational forcing generated by aggregation of cells. Unfortunately, chemotaxis systems do neglect the surrounding fluid and they are unable to predict the influence of the fluid on the anisotropic chemotaxis phenomenon. Thus, it is interesting and important to study some phenomenon of chemotaxis on the basis of the coupled cell–fluid model. For that, we investigate in this paper a system consisting of the parabolic Keller–Segel equations with general tensors coupled to Navier–Stokes equations,

$$\begin{cases} \partial_t N - \nabla\cdot(S(x)a(N)\nabla N) + \nabla\cdot(S(x)\chi(N)\nabla C) + u\cdot\nabla N = f(N), \\ \partial_t C - \nabla\cdot(M(x)\nabla C) + u\cdot\nabla C = h(N,C), \\ \partial_t u - \nu\Delta u + (u\cdot\nabla)u + \nabla P = -N\nabla\phi, \\ \nabla\cdot u = 0, \end{cases} \tag{1.1}$$

where the unknowns N and C are the concentrations of cells and chemical, respectively and u is the velocity field of a fluid flow governed by the incompressible Navier–Stokes equations with pressure P and viscosity ν. We denote by Ω a spatial

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domain where the cells and the fluid move and interact. We assume that Ω is an open bounded domain in $\mathbb{R}^d$, $d = 2$ or 3 with smooth boundary $\partial\Omega$. The experimental set-up corresponds to mixed type boundary conditions. For simplicity we use no-flux conditions for N and C and zero Dirichlet for u to reflect the no-slip boundary conditions of the flow. Therefore, the system (1.1) is supplemented by the following boundary conditions on $\Sigma_t = \partial\Omega \times (0, T)$,

$$S(x)a(N)\nabla N \cdot \eta = 0,\ M(x)\nabla C \cdot \eta = 0,\ u = 0, \tag{1.2}$$

where η is the exterior unit normal to $\partial\Omega$. The initial conditions on Ω are given by,

$$N(x,0) = N_0(x),\ C(x,0) = C_0(x),\ u(x,0) = u_0(x). \tag{1.3}$$

Anisotropic and heterogeneous tensors are denoted by $S(x)$ and $M(x)$. The function $\chi(N)$ is usually written in the form $\chi(N) = N\tilde{h}(N)$ where $\tilde{h}$ is commonly referred to as the chemotactic sensitivity function. Moreover, the density-dependent diffusion coefficient is denoted by $a(N)$. The function $h(N, C)$ describes the rates of production and degradation of the chemical signal (chemoattractant); here, we assume it is of birth–death structure, i.e., a linear function,

$$h(N, C) = \alpha N - \beta C;\ \alpha, \beta \geq 0\,. \tag{1.4}$$

It can be seen in the model (1.1) that the coupling of chemotaxis and fluid is realized through both the transport of cells and chemical substrates $u \cdot \nabla N$, $u \cdot \nabla C$ and the external gravitational force $g = -N\nabla\phi$ exerted on the fluid by cells. In fact, this external force can be produced by different physical mechanisms such as gravity, electric and magnetic forces but in our study, we are only interested in the case of gravitational force $\nabla\phi =$ "$V_b(\rho_b - \rho)\tilde{g}$"$z$ exerted by a bacterium onto the fluid along the upwards unit vector z proportional to the volume of the bacterium V_b, the gravitation acceleration $\tilde{g} = 9.8\ \mathrm{m/s^2}$ and the density of bacteria is ρ_b (bacteria are about 10% denser than water).

Furthermore, since the fluid is slow, we can also consider the simplified chemotaxis–Stokes system taking the following form

$$\begin{cases} \partial_t N - \nabla \cdot \big(S(x)a(N)\nabla N\big) + \nabla \cdot \big(S(x)\chi(N)\nabla C\big) + u \cdot \nabla N = f(N), \\ \partial_t C - \nabla \cdot (M(x)\nabla C) + u \cdot \nabla C = h(N, C), \\ \partial_t u - \nu\Delta u + \nabla P = -N\nabla\phi, \\ \nabla \cdot u = 0, \end{cases} \tag{1.5}$$

where compared with (1.1), the nonlinear convective term $(u \cdot \nabla)u$ is ignored in the fluid equation.

The questions of global existence of weak solutions of the model (1.1) and uniqueness of solutions of the model (1.5) have been answered in [7] and thus our model (1.1) is well-posed. Motivated by experiments described in [5,6] which explain the dynamics of anisotropic chemotaxis models in a fluid at rest ($u = 0$) and interested by numerical issues related to the dynamics of these models coupled to a viscous fluid through transport and gravitational force, we investigate in this paper the numerical analysis of models (1.1) and (1.5). One should also note the experiments given in [8,26,19] of bacteria only consuming the chemical with another function $h(N, C) = -k(C)N$ where a cut-off function k is introduced to describe the aggregation of a part of bacteria below an interface between two fluids, while other bacteria are rendered inactive wherever the oxygen concentration has fallen below the threshold of activity. To our knowledge, there are only a few numerical results given for related systems (see [8,22]). For example, the finite element method has been used to illustrate the behavior of the elliptic–parabolic Keller–Segel–Stokes system with different numerical examples in [22].

In the sequel and for the sake of clarity, we will divide our model (1.1) into two systems:

$$\begin{cases} \partial_t N - \nabla \cdot (S(x)a(N)\nabla N) + \nabla \cdot (S(x)\chi(N)\nabla C) + u \cdot \nabla N = f(N), \\ \partial_t C - \nabla \cdot (M(x)\nabla C) + u \cdot \nabla C = h(N, C), \\ S(x)a(N)\nabla N \cdot \eta = 0,\ M(x)\nabla C \cdot \eta = 0, \\ N(x,0) = N_0(x),\ C(x,0) = C_0(x)\,, \end{cases} \tag{1.6}$$

and

$$\begin{cases} \partial_t u - \nu\Delta u + (u \cdot \nabla)u + \nabla P = -N\nabla\phi, \\ \nabla \cdot u = 0, \\ u = 0 \qquad x \in \partial\Omega, \\ u(x,0) = u_0(x). \end{cases} \tag{1.7}$$

Assuming a vanishing fluid velocity field u and neglecting the hydrodynamic force f between cells, the system (1.6) is then reduced to an anisotropic Keller–Segel model. A scheme recently developed in the finite volume framework (see [1]) treats the discretization of the isotropic Keller–Segel model in a homogeneous domain where the diffusion tensors are considered to be the identity matrix. In this case, the mesh used for the space discretization is assumed to satisfy the