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Local Discontinuous Galerkin Methods with Decoupled Implicit-Explicit Time Marching for the Growth-Mediated Autochemotactic Pattern Formation Model

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Abstract. In this paper, two fully-discrete local discontinuous Galerkin (LDG) methods are applied to the growth-mediated autochemotactic pattern formation model in self-propelling bacteria. The numerical methods are linear and decoupled, which greatly improve the computational efficiency. In order to resolve the time level mismatch of the discretization process, a special time marching method with high-order accuracy is constructed. Under the condition of slight time step constraints, the optimal error estimates of this method are given. Moreover, the theoretical results are verified by numerical experiments. Real simulations show the patterns of spots, rings, stripes as well as inverted spots because of the interplay of chemotactic drift and growth rate of the cells.

AMS subject classifications: 65M15, 65M60

Key words: Local discontinuous Galerkin methods, implicit-explicit time-marching scheme, error estimate, growth-mediated autochemotactic pattern formation model.

1 Introduction

Complex pattern appears in active systems, such as bacterial colonies, birds flocking, fish schools, insect swarms and other self-propelled particles [2, 9, 14, 15]. Several different mechanisms underlying pattern formation in bacteria have been explored, for example, temporal control of gene expression, density-dependent motility, quorum sensing, and the phenomenon of chemotaxis. The model we focus on in this paper was proposed by Mukherjee [13], which has shown interactions of bacterial growth kinetics, autochemotactic movement and cell movement. In addition, growth is a key adjustment parameter that can determine the spatiotemporal dynamics of a colony.

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Suppose $\Omega \subset \mathbb{R}^2$ be a rectangular domain. The growth-mediated autochemotactic pattern formation model [13] for self-propelling bacteria is demonstrated as follows in dimensionless form:

$$\frac{\partial \rho}{\partial t} = -\nabla \cdot (\rho \mathbf{p}) + \nabla^2 \rho + g\rho(1-\rho), \tag{1.1a}$$

$$\frac{\partial c}{\partial t} = \mathcal{D}_c \nabla^2 c + \rho - c + \kappa \nabla \cdot (\rho \mathbf{p}), \tag{1.1b}$$

$$\frac{\partial \mathbf{p}}{\partial t} = -\Gamma \mathbf{p} + \mathcal{D}_p \nabla^2 \mathbf{p} + S\nabla c - \Gamma_2 |\mathbf{p}|^2 \mathbf{p}, \tag{1.1c}$$

where ρ is the bacterial density, c is the self-secreted chemical density, and $\mathbf{p} = (p_1, p_2)$ is the polarization. The variables and parameters in the model are defined as

$$|\mathbf{p}|^2 = p_1^2 + p_2^2, \quad g = \frac{\alpha}{k_d}, \quad \Gamma = \frac{\gamma}{k_d}, \quad \mathcal{D}_p = \frac{D_p}{D_\rho}, \quad \mathcal{D}_c = \frac{D_c}{D_\rho}, \quad \kappa = \frac{k_a k_d}{k_0 \nu_0} \quad \text{and} \quad \Gamma_2 = \frac{\gamma_2 D_\rho}{\nu_0^2},$$

where α is the growth rate, γ is the decay rate of $\mathbf{p}$, k_d denotes a rate of natural degradation, D_p and D_ρ are the translational diffusion constant and the diffusion constant, respectively, D_c is the diffusion constant, k_a is the anisotropic correction term, k_0 is the local rate, ν_0 is the self-propulsion speed of the bacteria, γ_2 describes saturation in $\mathbf{p}$ at strong alignment, g is the growth rate, and S is chemotactic strength. Here, the parameter S represents chemoattraction and chemorepulsion, for positive ($S > 0$) and negative ($S < 0$) values, respectively.

There are few of numerical simulations for the growth-mediated autochemotactic pattern formation model in self-propelling bacteria. In [13], the authors used the finite difference method to carry out numerical simulation, but there was no theoretical support for numerical analysis. When there is not any growth dynamics (i.e., $g = 0$), [10] explored a mass-preserving characteristic finite element approach, and the convergence analysis was well studied, yet only the first-order time scheme was developed. However, the circumtance that $g = 0$ is not particularly practical since bacteria density cannot expand locally in the absence of any bounds. Because the change in density is not minor, which is a characteristic of this problem in some circumstances, we must explore approaches with high resolution. As a result, for the model in this paper, we use local discontinuous Galerkin (LDG) methods. To the best of the authors' knowledge, this is the first paper that discusses error estimates for the model with this method.

Inspired by Bassi and Rebay [3], the LDG method was introduced by Cockburn and Shu [4] to solve the convection-diffusion equations. Thereafter, the LDG method has developed successfully and been employed in numerous models with higher-order and dispersive terms [21,22]. The principle of the LDG approach is to introduce certain auxiliary variables to reduce the higher-order derivatives in the equations to the first-order, so that the discontinuous Galerkin (DG) approach can then be used. Hence, the LDG approach inherits advantages of the DG method, including good stability, high-order precision, as well as flexibility on hp-adaptivity and complex geometry.