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A corrected decoupled scheme for chemotaxis models

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Abstract

The main purpose of this paper is to present a new corrected decoupled scheme combined with a spatial finite volume method for chemotaxis models. First, we derive the scheme for a parabolic-elliptic chemotaxis model arising in embryology. We then establish the existence and uniqueness of the numerical solution, and we prove that it converges to a corresponding weak solution for the studied model. In the last section, several numerical tests are presented by applying our approach to a number of chemotaxis systems. The obtained numerical results demonstrate the efficiency of the proposed scheme and its effectiveness to capture different forms of spatial patterns.

Keywords: Chemotaxis, Decoupled scheme, Correction term, Time discretization
2010 MSC: 65M08, 65M12, 92C17 .

1. Introduction

Chemotaxis refers to a phenomenon that enables cells (or organisms) to migrate in response to a chemical signal. This process has sparked the interest of many scientists since it is encountered in several medical and biological applications, such as bacteria aggregation, tumour growth, integumental patterns in animals etc.

In [1], Oster and Murray discussed a cell-chemotaxis model involving motile cells that respond to a chemoattractant secreted by the cells themselves. In its dimensionless form, the model reads

$$\begin{cases} \partial_t u = \mu \Delta u - a \nabla \cdot (u \nabla c), \\ \partial_t c = \Delta c + \dfrac{u}{u+1} - c, \end{cases} \tag{1.1}$$

where μ and a are positive constants, u is the cell density and c is the concentration of chemoattractant.

The above system is based on the Keller-Segel model [2], which is the most popular model for chemotaxis. The migration of cells is assumed to be governed by Fickian

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