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# Semi-implicit finite volume schemes for a chemotaxis-growth model

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**Abstract**

This paper is concerned with finite volume approximations for a nonlinear parabolic–elliptic system for chemotaxis-growth in $\mathbb{R}^d$, $d = 2, 3$. This model describes a process of pattern formation by some chemotactic biological individuals. We present two schemes which make use of a semi-implicit time discretization and an upwind finite volume approximation. For both schemes, we prove existence, uniqueness and nonnegativity of the approximate solutions under some conditions on the time step, and we show (for one of the schemes) that the numerical solution converges to a corresponding weak solution for the studied model. Numerical simulations are performed in two dimensional spaces to demonstrate the efficiency of the schemes to capture the pattern formations and to verify our theoretical results.


*Keywords:* Finite volume scheme; Semi-implicit scheme; Convergence analysis; Chemotaxis; Pattern formation; Growth

## 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 pattern formation, immunology,

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and tumor growth. For a better understanding of the behavior of population of chemotactic bacteria, various mathematical models have been proposed over the last decades. The most known one has been introduced by Patlak [23], and Keller and Segel [15]. The classical form of this model reads:

$$\frac{\partial u}{\partial t} = \Delta u - \nabla \cdot (\chi\, u \nabla c) \quad \text{in } \Omega \times (0, T), \tag{1.1}$$

$$\frac{\partial c}{\partial t} = \Delta c - c + u \quad \text{in } \Omega \times (0, T), \tag{1.2}$$

with homogeneous Neumann boundary conditions and initial conditions. Herein, $\Omega$ is an open bounded domain in $\mathbb{R}^d$ ($d \in \mathbb{N}^*$) and $T > 0$. In this model, $u(x, t)$ and $c(x, t)$ denote respectively the cell density and the chemoattractant concentration in $(x, t) \in \Omega \times (0, T)$, and $\chi$ is a positive constant describing the chemotactic sensitivity. In an other version of the Patlak–Keller–Segel model, Eq. (1.2) has been replaced by the elliptic equation

$$\Delta c - c + u = 0 \quad \text{in } \Omega \times (0, T). \tag{1.3}$$

In this case, the diffusion of the chemoattractant is neglected. This substitution can be justified by the assumption that the diffusion of the chemoattractant is much faster than that of the cell.

This model describes the aggregation of some kind of bacteria in response to chemical signal. The Patlak–Keller–Segel system (1.1)–(1.2) and its simplified form (1.1), (1.3) may blow up in finite time. This blow up occurs for specific initial conditions for $u$. The occurrence of the blow-up depends also on $\chi$. Several works are devoted to mathematical analysis of these systems (see, e.g., [19,12,13]).

From numerical point of view, several authors discussed numerical methods for Patlak–Keller–Segel systems (1.1)–(1.2),(see, e.g., [29,9,8,25]) and (1.1), (1.3) (see, e.g.,[17,26,24,11]). In [11], Filbet proposes a fully implicit finite volume scheme and provides a convergence proof. The main challenge encountered in his work was getting a priori estimates which are necessary to prove the convergence of his scheme. After proving the existence and uniqueness of the numerical solution, he shows that the numerical approximation converges to the weak solution of the problem under a smallness condition on the initial cell density for $d = 2$.

Numerical methods were discussed also for a class of volume-filling chemotaxis models [2,14,7]. In these models, the chemotactic sensitivity $\chi(u)$ is assumed to vanish when the cell density reaches a certain threshold value $u_m$. As a consequence, the boundedness of the solution is assured for all values of the initial cell density.

In the above model, the total mass is conserved in time, which means that growth of bacteria (or cell) is ignored. However, growth can have an important effect on the dynamics of bacteria [16]. In [4,5], Budrene and Berg found that motile cells of Escherichia coli aggregate to form stable patterns of remarkable regularity when grown from a single point on certain substrates. One of the models which describes this process of pattern formation reads

$$\frac{\partial u}{\partial t} = D_u\, \Delta u - \nabla \cdot (\chi\, u \nabla c) + f(u) \quad \text{in } \Omega \times (0, T), \tag{1.4}$$

$$\frac{\partial c}{\partial t} = D_v\, \Delta c - \beta c + \mu u \quad \text{in } \Omega \times (0, T), \tag{1.5}$$

where $f(u)$ is a logistic source representing the growth rate of $u$, and $\chi$, $D_u$, $D_v$, $\beta$, $\mu$ are positive constants. In this paper we are concerned with the parabolic–elliptic version of the above model with the generalized logistic source (see, e.g., [20]), $f(u) = au(b - u^{\alpha-1})$ defined for $u > 0$,