



Initial–boundary value problems for a system of hyperbolic balance laws arising from chemotaxis

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Abstract

This paper is devoted to the analytical study of initial–boundary value problems for a system of hyperbolic balance laws derived from a repulsive chemotaxis model with logarithmic sensitivity. In the first part of the paper we show that, subject to the Dirichlet boundary conditions, classical solutions exist globally in time for large initial data. Asymptotically in time, the solutions are shown to converge to their boundary data at an exponential rate as time goes to infinity. Numerical simulations are supplied to corroborate the analytical results. The analytic approach developed herein can be utilized to handle a family of initial and initial–boundary value problems of the model and related models with similar mathematical structure. As a demonstration of the effectiveness of our approach, in the second part of the paper we show that, subject to the Neumann–Dirichlet boundary conditions, classical solutions exist and converge to constant equilibrium states for large initial data and for arbitrary values of the chemical diffusion coefficient. This improves a previous result obtained in [30] where the smallness of the chemical diffusion coefficient was required.

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1. Introduction

In contrast to random diffusion, chemotaxis is the biased movement of an organism in response to a chemical stimulus. Somatic cells, bacteria, and other single-cell or multicellular organisms direct their movements according to certain chemicals in their environment. This is important for bacteria to find food (for example, glucose) by swimming toward the highest concentration of food molecules, or to flee from poisons (for example, phenol). In multicellular organisms, chemotaxis is critical to early development (e.g., movement of sperm towards the egg during fertilization) and subsequent phases of development (e.g., migration of neurons or lymphocytes) as well as in normal function. In addition, it has been recognized that mechanisms that allow chemotaxis in animals can be subverted during cancer metastasis. There are two major types of chemotactic movement. Attractive chemotaxis occurs if the movement is toward a higher concentration of the chemical in question. However, repulsive chemotaxis occurs if the movement is in the opposite direction. It is a general belief that aggregation occurs in attractive chemotaxis, while cell populations usually collapse to uniform distributions in repulsive chemotaxis.

Mathematical modeling and analysis of chemotaxis have been carried on for many decades. In the last 30–35 years, among several works investigating taxes, chemotaxis research shows a significantly high ratio (> 95%). Between the year 1975 and 2006, more than 22,000 papers in the scientific and medical literature were devoted to this phenomenon (PubMed), with the frequency of publication continuing to increase, which points to the underlined importance of chemotaxis research both in biology and medicine. The Keller–Segel model [11–13] has provided a cornerstone for many works investigating the biological and mathematical properties of chemotaxis, due to its intuitive simplicity, analytical tractability and capability to model the basic dynamics of chemotactic populations. In its general form, the Keller–Segel model reads

$$\begin{cases} \partial_t u = D\Delta u - \nabla \cdot (\chi u \nabla \phi(v)), \\ \partial_t v = \varepsilon \Delta v + g(u, v), \end{cases} \quad (1.1)$$

where u and v denote the cell density and chemical concentration, respectively; $D > 0$ and $\varepsilon \geq 0$ are cell and chemical diffusion coefficients, respectively; and χ is the chemotactic sensitivity coefficient. The chemotaxis is called to be attractive if $\chi > 0$ and repulsive if $\chi < 0$, where $|\chi|$ measures the strength of the chemical signal. Here $\phi(v)$ is referred to as the chemotactic sensitivity (CS) function describing the signal detection mechanism and $g(u, v)$ is a function characterizing the chemical growth and degradation. In the original papers [11–13], along with the derivation of the model, the authors carried out rigorous mathematical analysis and successfully reproduced an important experimental result obtained by Adler [1] regarding the traveling bands of motile *Escherichia coli*. Since the initiation of (1.1), an extensive body of literature has been devoted to the mathematical analysis of such model, see e.g. the survey papers [14,15] and the references therein.

Up to date, most of mathematical studies on chemotaxis deal with the classical attractive chemotaxis model where $\chi > 0$, $\phi(v) = v$, $g(u, v) = u - v$, see [15]. In contrast, the studies of repulsive chemotaxis were much less. A few results on repulsive chemotaxis have been developed recently, see [6,28] and the references therein. This paper is concerned with the analytical study of the following Keller–Segel type repulsive ($\chi < 0$) chemotaxis model with logarithmic sensitivity in one space dimension:

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