Advances in Mathematics 330 (2018) 834–875

Contents lists available at ScienceDirect

Advances in Mathematics

www.elsevier.com/locate/aim

Large global-in-time solutions to a nonlocal model of chemotaxis ☆

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ARTICLE INFO

Article history:
Received 12 June 2017
Received in revised form 1 March 2018
Accepted 28 March 2018
Available online xxxx
Communicated by Camillo De Lellis

Czesław Ryll-Nardzewski (1926–2015), in memoriam

MSC:
35Q92
35B44
35K55
35A01

Keywords:
Model of chemotaxis
Fractional Laplacian
Global existence of solutions
Blowup of solutions

ABSTRACT

We consider the parabolic–elliptic model for the chemotaxis with fractional (anomalous) diffusion. Global-in-time solutions are constructed under (nearly) optimal assumptions on the size of radial initial data. Moreover, criteria for blowup of radial solutions in terms of suitable Morrey spaces norms are derived.

☆ The authors were supported by the NCN grant 2013/09/B/ST1/04412 and 2016/23/B/ST1/00434 (the first named author, for the revision of the paper) and UMO-2014/15/B/ST1/00060 (the third author).

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https://doi.org/10.1016/j.aim.2018.03.036
0001-8708/

1. Introduction

1.1. Formulation of the problem

We consider the following version of the parabolic–elliptic Keller–Segel model of chemotaxis in $d \geq 2$ space dimensions

$$u_t + (-\Delta)^{\alpha/2} u + \nabla \cdot (u \nabla v) = 0, \quad x \in \mathbb{R}^d, \ t > 0, \tag{1.1}$$

$$\Delta v + u = 0, \quad x \in \mathbb{R}^d, \ t > 0, \tag{1.2}$$

supplemented with the nonnegative initial condition

$$u(x, 0) = u_0(x). \tag{1.3}$$

Here the unknown variables $u = u(x,t)$ and $v = v(x,t)$ correspond to the density of the population of microorganisms (*e.g.* swimming bacteria or slime mold) and the density of the chemical substance secreted by themselves that attracts them and makes them to aggregate. In this work, a diffusion process described by model (1.1)–(1.3) is given by the fractional power of the Laplacian $(-\Delta)^{\alpha/2}$ with $\alpha \in (0, 2)$ which is a pseudodifferential operator with a symbol $|\xi|^\alpha$, see *e.g.* [25] for a comprehensive treatment of nonlocal diffusion operators. In case of sufficiently regular functions, we also have the following well-known representation of the fractional Laplacian with $\alpha \in (0, 2)$

$$-(-\Delta)^{\alpha/2} \omega(x) = \mathcal{A} \lim_{\delta \searrow 0} \int\limits_{\{|y| > \delta\}} \frac{\omega(x-y) - \omega(x)}{|y|^{d+\alpha}} \, \mathrm{d}y, \tag{1.4}$$

where, by *e.g.* [21, Th. 1], [31],

$$\mathcal{A} = \mathcal{A}(d, \alpha) = \frac{2^\alpha \Gamma\left(\frac{d+\alpha}{2}\right)}{\pi^{\frac{d}{2}} \left|\Gamma\left(-\frac{\alpha}{2}\right)\right|}. \tag{1.5}$$

The initial datum in (1.3) is a nonnegative function $u_0 \in L^1(\mathbb{R}^d)$ of the total mass $M = \int_{\mathbb{R}^d} u_0(x) \, \mathrm{d}x$ which is conserved during the evolution of (suitably regular) solutions

$$M = \int\limits_{\mathbb{R}^d} u(x,t) \, \mathrm{d}x \qquad \text{for all} \quad t \in [0, T). \tag{1.6}$$

Note, however, that a natural scaling for system (1.1)–(1.2)

$$u_\lambda(x,t) = \lambda^\alpha u(\lambda x, \lambda^\alpha t) \ \text{ for each } \ \lambda > 0, \tag{1.7}$$

leads to the equality $\int_{\mathbb{R}^d} u_\lambda(x,t) \, \mathrm{d}x = \lambda^{\alpha - d} \int_{\mathbb{R}^d} u(x,t) \, \mathrm{d}x$, *i.e.* for $\alpha \neq d$, the total mass of a rescaled solution u_λ can be chosen arbitrarily with suitable $\lambda > 0$.