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On the existence of weak solutions for the kinetic models of the motion of myxobacteria with alignment and reversals

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In this paper, we consider two non-linear kinetic partial differential equations that emerge in modeling rod-shaped bacteria's motion. Their motion is characterized by nematic alignment with neighboring bacteria, orientation reversals from cell polarity switching, and orientation diffusion. Our contribution lies in establishing the global existence of weak solutions for these equations. Our approach is based on applying the classical averaging lemma from the kinetic theory, augmented by a new version of that lemma, in which the transport operator is substituted with a uni-directional diffusion operator.

1. Introduction

Many rod-shaped bacteria are known to move on surfaces and self-organize into various spatial patterns due to mechanical interactions and biochemical signaling between bacteria, [6,12,27,39]. For instance, myxobacteria, studied for their multicellular interactions, can form dynamic patterns of clusters, streams, swirls, and aggregates, [4,1,31,34,40]. The formation of nematic order in myxobacterial colonies is very important for myxobacterial collective behavior [38,11].

These observations led to an increased interest in kinetic models for the motion of myxobacteria and, more broadly, in models of self-propelled rods with alignment. There are two common approaches to the mathematical modeling of alignment. The first one is the mean-field approximation [32,33,35,2,3,13,14,20]. The second one utilizes the Boltzmann framework [5,23,24,29,28,37,36]. Both approaches assume some independence in the distribution of particle states. The Boltzmann framework, which requires binary interactions, is more applicable in low-density configurations. In contrast, the mean-field approach is more suitable for high-density regimes.

Motivated by the problem of modeling the motion of a single layer of myxobacteria on a flat surface, we consider the following mean-field model for the probability distribution function $f(x,\theta,t)$ of bacteria at position $x \in \mathbb{R}^2$, with orientation angle of the bacteria's longitudinal axis $\theta \in (-\pi,\pi]$:

$$\partial_t f + e(\theta)\cdot\nabla_x f = -\partial_\theta(\Psi(V_f^0)f) + \mu\partial^2_{\theta\theta} f - \lambda f + \lambda\mathcal{T}_\pi[f]. \tag{1}$$

The left-hand side represents the active part: transport in the direction of orientation of the cell's longitudinal axis vector $e(\theta) = (\cos\theta, \sin\theta)$. The right-hand side of equation (1) accounts for changes in the orientation angle θ (passive part), including changes due to (from left to right) nematic alignment, random noise in orientation, and cell reversals generated by spontaneous switches in bacterial polarity. The alignment rate, $\Psi(V_f^0)$, is Lipschitz continuous and a bounded function of $V_f^0(x,\theta,t)$,

$$V_f^0(x,\theta,t) = \int_{-\pi}^{\pi} \sin(2(\theta'-\theta)) f(x,\theta',t)\, d\theta'. \tag{2}$$

Random changes in cell orientation are accounted for using orientational diffusion with diffusion coefficient μ. Cell reversals are accounted for by $-\lambda f + \lambda\mathcal{T}_\pi[f]$, $\lambda > 0$, where $\mathcal{T}_\pi$ is the translation operator in θ variable $\mathcal{T}_\pi[f(x,\theta,t)] = f(x,\theta+\pi,t)$. We will refer to this model as Model I. The model is based on the mean-field kinetic model from [32] for the motion of self-propelled rods with nematic alignment described by the Maier-Saupe interaction potential from the theory of liquid crystals. With $\Psi(x) = \gamma x$, the first two terms on the right-hand side of (1) represent the interaction operator from the one-dimensional Smoluchowski equation, [18]. However, this form of Ψ is unbounded and can lead to unrealistically fast alignment rates. Therefore, we consider Ψ to be a bounded function to limit the alignment rate as observed physically.

Alongside equation (1), we consider a kinetic model obtained in the asymptotic regime where the rate of reversals is much larger than both the rate of alignment and the rate of angular diffusion:

$$\partial_t f - \mu_1(e(\theta)\cdot\nabla_x)^2 f = -\partial_\theta(\Psi(V_f^0)f) + \mu\partial^2_{\theta\theta} f, \tag{3}$$

where the "active" part is the spatial diffusion in the direction $e(\theta)$ with the diffusion rate μ_1. We will refer to this model as Model II.

For space homogeneous models of alignment, including the Smoluchowski equation, the theory of the existence of solutions, their long-time behavior, and other properties, such as the phase transition, have been worked out in [9,10 ,15,13,14,16,20,26,19].

In the non-homogeneous setting, the mean-field alignment model was considered in [8], where the Smoluchowski equation is coupled with the Navier-Stokes equations for incompressible fluid flows. In that paper, the authors prove the global existence of classical solutions in 2 dimensions. A related result that establishes the global-in-time existence and uniqueness of solutions to a space-dependent alignment problem was obtained in [24]. In that work, the alignment is described in the Boltzmann framework, assuming the angular diffusion is large enough compared to the total bacteria mass.

Here, we establish the global existence of weak solutions to the Cauchy problem for equations (1) and (3). These main results are presented in Theorems 3.3 and 3.7. To prove theorems 3.3 and 3.7, we approximate both equations by introducing spatial viscosity and small-scale spatial averaging in the alignment rate. Due to the boundedness of the cut-off function Ψ, solutions to these approximate equations satisfy an L^2 "energy" estimate, independent of the viscosity and averaging parameters. This enables us to obtain a weakly compact sequence of solutions as the viscosity and averaging parameters vanish. To handle the non-linear alignment term in (1) and (3), we employ the theory of kinetic averaging [17,21,22,30].

The kinetic averaging applies directly to the approximate solutions of (1), while the situation is different with solutions of (3) because in (3), the kinetic density propagates in space by a diffusion process. However, since the direction of the diffusion $e(\theta)$ varies, we still expect improved regularity for θ-moments of the solutions. We prove this in Lemma 3.6 by showing that θ–moments of f belong to a fractional Sobolev space $H^{2\alpha,\alpha}_{x,t}$, $\alpha = \frac{1}{7}$, and bounded in this norm, independently of the approximating parameter. Such a bound implies the strong compactness of moments and, with that, the existence of weak solutions.

The outline of the paper is as follows. In Section 2.1, we derive equation (1) starting from an agent-based model of the motion of self-propelled rods. Then, in Section 2.2, assuming that we are interested in the evolution of cell density on the timescales much longer than a single reversal, we derive (3) from the asymptotic expansion of a solution of (1). In Section 3, we formulate and prove several theorems regarding the existence of approximate solutions and their convergence. Theorems 1 and 3 establish the existence and uniqueness of solutions of the equations that serve as an approximation of equations (1) and (3), respectively. The approximation is expressed by averaging the alignment rate V_f^0 over a ball of radius ϵ around point x. In Theorems 2 and 4, we take the limit of $\epsilon \to 0$ to obtain weak solutions of (1) and (3).

Keywords: Models for bacterial motion, multi-agent interacting systems, mean-field equations, kinetic theory, averaging lemmas.

Mathematics Subject Classification: Primary: 35F55, 35Q92; Secondary: 35Q84.

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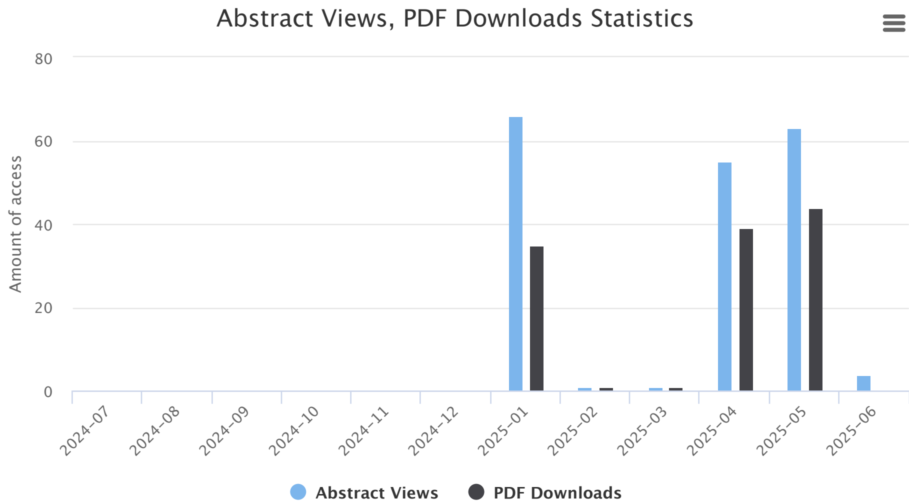

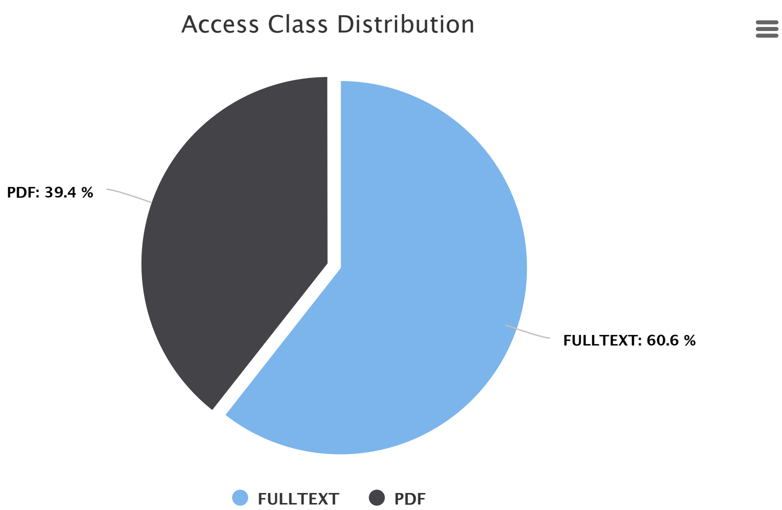

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