

# Modeling of collective swimming in random bacterial suspensions.

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## *Abstract*

Bacteria are the most abundant organisms on Earth and they significantly influence carbon cycling and sequestration, decomposition of biomass, and transformation of contaminants in the environment. This motivates our study of the basic principles of bacterial behavior and its control. The principal mechanism behind the unique macroscopic properties of bacterial suspensions (e.g., 7-fold reduction of the effective viscosity and a 10-fold increase of the effective diffusivity) is self-organization of the bacteria at the microscopic level – a multiscale phenomenon. Our goal is the understanding the mechanism of self-organization, which is a fundamental issue in the study of biological and inanimate systems. Our work in this area includes

- *Analytical and numerical study of dilute and semi-dilute bacterial suspensions.* We introduced a so-called semi-dilute model for swimming bacteria that includes pairwise interactions and obtained an explicit asymptotic formula for the effective viscosity in terms of known physical parameters. This formula is compared with that derived in our PDE model for a dilute suspension of bacteria driven by a stochastic torque, which models random reorientation of bacteria (“tumbling”). This comparison leads to a phenomenon of stochasticity arising from a deterministic system is referred to as *self-induced noise*.

We also conducted numerical modeling of a large number of interacting bacteria using Graphical Processing Units (GPU).

- *Kinetic collisional model—work in progress.* We seek to capture a phase transition in the bacterial suspension – an appearance of correlations and local preferential alignment with an increase of concentration. Collisions of the bacteria, ignored in most of the previous works, play an important role in this study.

Collaborators: PSU students S. Ryan and B. Haines, and DOE scientists I. Aronson and D. Karpeev (both Argonne Nat. Lab)