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Comment on “Particle Diffusion in a Quasi-Two-Dimensional Bacterial Bath”

Recently, Wu and Libchaber (WL) reported on a fascinating experiment in which bacteria move freely within a fluid film seeded with polystyrene beads [1]. They studied the dynamics of these beads as they are moved around by the bacteria, and found superdiffusive motion ($\langle r^2 \rangle \sim t^\alpha$ with $\alpha \approx 1.5$) below some crossover scales t_c , ℓ_c , beyond which normal diffusion ($\alpha = 1$) is recovered. WL interpret these scales as characteristic of the structures (swirls, jets) that emerge from the collective motion of the bacteria. A simple Langevin equation with a force term correlated in time over the crossover scale t_c was used to fit the experimental data. Two problems arise from this description: First, the Langevin framework predicts ballistic behavior ($\alpha = 2$) at short scales, at odds with the nontrivial exponents recorded in the experiment. Second, no attempt is made to explain the origin of the collective motion and how or why the crossover scales change with the bacteria density ρ .

Here we show that a coherent and robust theoretical framework for this experiment is that provided by the “self-propelled XY spin” models studied recently [2] complemented by a collection of passive beads. Let us describe briefly the model used here (details will appear elsewhere, together with evidence that our results are largely insensitive to the particular modeling choices made [3]). Bacteria move at discrete time steps with fixed-amplitude velocity v_0 along a direction reflecting the action of two forces: a noisy tendency to align with neighboring objects within radius r_0 [2], and a two-body repulsive force conferring them a finite size r_b . A small number of passive beads of radius r_B is added. They interact with bacteria via hard-core repulsion plus some level of entrainment within range r_0 (i.e., they take part of the neighboring bacteria velocity).

Increasing ρ , ordered collective motion appears at a value ρ^* [2]. For $\rho < \rho^*$, bacteria motion is characterized by scales which diverge as $\rho \rightarrow \rho^*$ (Fig. 1). Bead motion is directly related to bacteria behavior, as evidenced by their respective diffusive properties which both reveal superdiffusion crossing over at the same time scale t_c to normal diffusion (Figs. 1b and 1c). The characteristic scales of bead motion are thus given by the collective scales of bacteria motion, as foreseen by WL, but the short-time behavior of the beads in our model is superdiffusive, which is more consistent with the experimental data than the simple Langevin ansatz.

The density dependence of the crossover scales is also naturally explained by our model: as ρ increases, the system is closer to the critical point ρ^* , and the superdiffusive behavior persists longer. The range of variation of crossover scales recorded by WL is small (e.g., the maximum value of ℓ_c is of the order of r_B). This explains why a linear variation was found to be a good approxi-

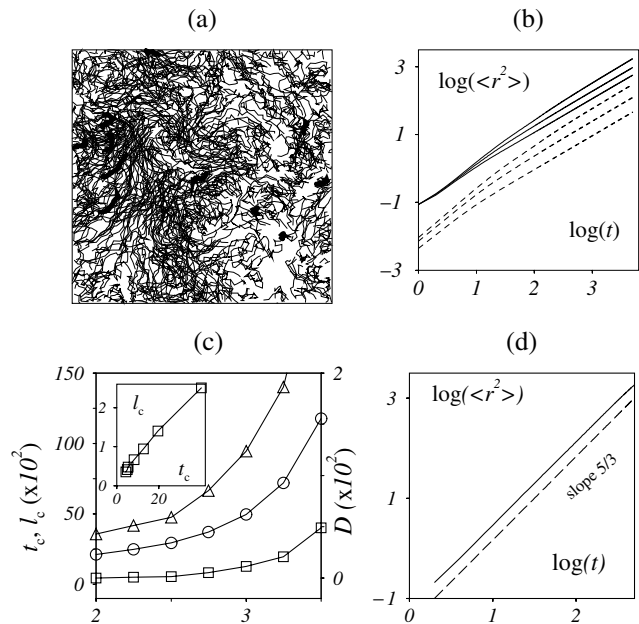


FIG. 1. Minimal model for bacterial bath with passive beads with $v_0 = 0.3$, $r_0 = 1.0$, $r_b = 0.13$, $r_B = 0.38$ (for other details, see [3]). (a) Short-time (30 time steps) trajectories of bacteria (thin lines) and beads (thick lines) for $\rho < \rho^*$ in a system of size 32×32 ; (b) mean square displacement $\langle r^2 \rangle$ vs time for bacteria (solid lines) and beads (dashed lines) for $\rho = 2, 3, 3.5 < \rho^* \approx 4.2$; (c) ρ variation of t_c (\square) and ℓ_c (\triangle) and diffusion constant $D = \lim_{t \rightarrow \infty} d\langle r^2 \rangle / dt$ (\circ); (d) superdiffusion at $\rho = \rho^*$ with exponent $\alpha \approx 1.65(15)$.

mation in [1], even though the scales are expected to diverge at threshold (Fig. 1c). We believe the framework proposed here is more consistent than the Langevin approach of WL. A firmer statement will be available only when experiments taking place closer to ρ^* (i.e., at higher densities) are conducted. They would allow for the superdiffusive behavior to be observed over a wide range of scales, and the expected universality of the associated exponent α (Fig. 1d) could be assessed.

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- [1] X.-L. Wu and A. Libchaber, Phys. Rev. Lett. **84**, 3017 (2000).
- [2] A. Czirok, H. E. Stanley, and T. Vicsek, J. Phys. A **30**, 1375 (1997); J. Toner and Y. Tu, Phys. Rev. E **58**, 4828 (1998).
- [3] G. Grégoire, H. Chaté, and Y. Tu (to be published).