CLUSTERING OF GYROTACTIC MICROORGANISMS IN TURBULENT FLOWS

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Abstract   We study the spatial distribution of gyrotactic microorganisms swimming in a three-dimensional turbulent flow by means of direct numerical simulations. We find that gyrotaxis combines with turbulent fluctuations to produce small scales patchiness with fractal clustering. We explain our observations by showing that gyrotactic swimming cells behave like tracers transported by an effective compressible flow. We derive an explicit expression for the compressibility in the limit of fluid acceleration much smaller than gravity.

Microbial patchiness in oceans is important for ecological and evolutionary dynamics and for biogeochemical processes [6, 4]. In motile aquatic microorganisms, self-propulsion provides a mechanism to escape fluid pathlines, potentially leading to small-scale patchiness. Remarkably, motility combined with fluid flows can also generate large-scale inhomogeneities. For instance, spectacular aggregation of phytoplankton cells (in layers centimeters to meters thin, horizontally extending from hundreds of meters to kilometers) can result from vertical shears and *gyrotactic swimming* [2]. Gyrotaxis characterizes several species of motile microalgae whose swimming direction is determined by the balance of viscous and gravitational torques, due to the displacement between the cell center of mass and buoyancy. As an effect of such balance gyrotactic algae aggregate in the center of descending vertical pipe flows [5].
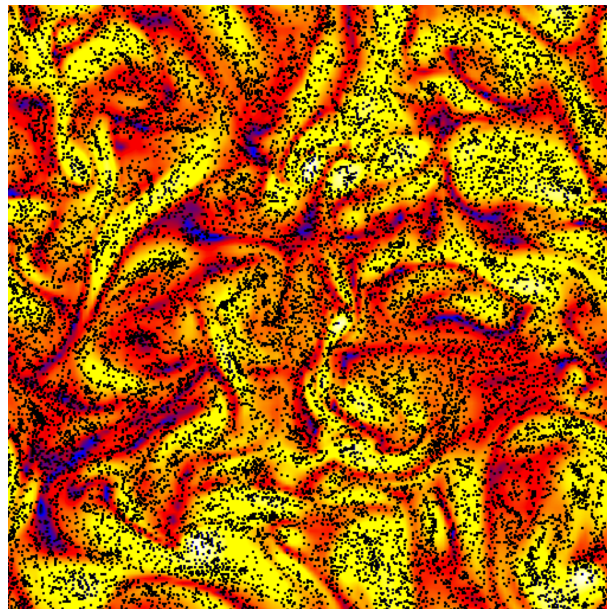

Figure 1. Spatial distribution of gyrotactic swimmers evolving according to (1-2) in a slab of a 3D turbulent flow. Colors represent vorticity magnitude, black points are the positions of the swimmers.

We investigate the interplay between gyrotactic motility and realistic turbulent flows, as occurring in the sea, by means of direct numerical simulations. We numerically integrate the forced Navier-Stokes equations on a tri-periodic grid at moderate Reynolds number up to $R_\lambda \simeq 100$. In stationary conditions of the flow, we introduce the swimmers at initial positions $\mathbf{X}(0)$ and follow their motion by integrating

$$\frac{d\mathbf{X}}{dt} = \mathbf{u}(\mathbf{X}, t) + V_s \mathbf{p} \tag{1}$$

$$\frac{d\mathbf{p}}{dt} = \frac{1}{2B}(\hat{\mathbf{z}} - p_z\mathbf{p}) + \frac{1}{2}\omega \times \mathbf{p} \qquad (2)$$

where V_s represents the swimming velocity, the unit vector $\mathbf{p}$ is the swimming direction, B is the characteristic cell orientation time driven by gravity and ω is the vorticity of the flow. The initial positions $\mathbf{X}(0)$ of the swimmers are uniformly distributed in the computational box, with random orientation of swimming direction $\mathbf{p}$.

The equations of motion (1-2) formally represent a dissipative dynamical system in the $2d$-dimensional phase space with contraction rate

$$\Gamma = -\frac{d+1}{2B}p_z \qquad (3)$$

therefore, as $\mathbf{p}$ orients in the vertical direction, Γ is expected to be negative and swimmers will move onto a dynamical attractor of dimension smaller that the phase space. In these conditions we expect to observe clustering of cells in the physical space, as it is shown in the examples of Fig. 1. We remark that clustering is a consequence of swimming: for $V_s = 0$ the motion of swimmers (1) recover that of fluid particles which cannot clusterize in an incompressible flow.

For $B \to 0$, the direction of swimming becomes aligned to the vertical direction and the effective velocity for the swimmers is $\mathbf{v} = \mathbf{u} + V_s\hat{\mathbf{z}}$, which is again incompressible and no clustering is possible. The absence of clustering is expected also for $B \to \infty$, because in this case $\Gamma \to 0$. Clustering is possible for intermediate values of the orientation time B, and we find numerically that maximum clustering is indeed observed for the dimensionless parameter $B\omega_{rms} = O(1)$. As shown in Fig. 2, for intermediate value of B, the fractal dimension of cell distribution attains a minimum at a value which decreases with the swimming velocity [1].
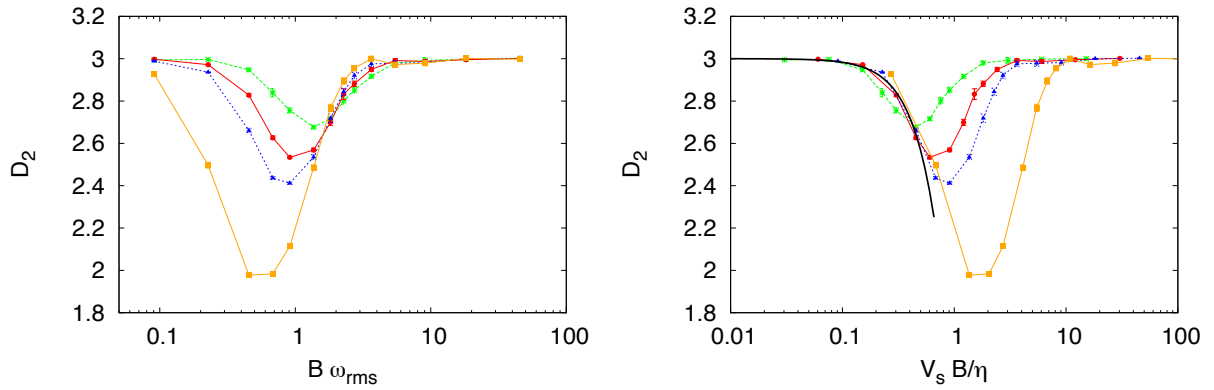

Figure 2. Clustering of swimmers as a function of parameters. Left: correlation dimension D_2 vs orientation time B for different values of swimming velocity $V_s = 0.1$ (green), $V_s = 0.2$ (red), $V_s = 0.3$ (blue) and $V_s = 0.9$ (orange). Right: the same data plotted as a function of the dimensionless parameter V_sB/η. The black line represents the prediction $D_2 = 3 - a(V_sB/\eta)^2$.

The mechanism which lead to clustering of cells can be fully understood in the limit of fast orientation time. Indeed, for $B\omega_{rms} \ll 1$ the cell swimming direction is well approximated by $\mathbf{p} = (B\omega_y, -B\omega_x, 1)$. This gives an effective velocity $\mathbf{v} = \mathbf{u} + V_s\mathbf{p}$ for the swimmers with a non-vanishing divergence $\nabla \cdot \mathbf{v} = -(V_sB/\eta)\nabla^2 w$ (η is the Kolmogorov scale and w the vertical velocity). In these conditions, particles transported by the velocity $\mathbf{v}$ clusterize on a fractal set of codimension $3 - D$ proportional to the square of $\nabla \cdot \mathbf{v}$ [3]. We can therefore predict that for $B\omega_{rms} < 1$ the fractal dimension of cell clusters behaves like $D_2 \simeq 3 - a(V_sB/\eta)^2$ as indeed shown in Fig. 2.

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