Abstract

Collective behavior is abundant in nature, from flocks of birds down to the coherent motion of microbes. At the small scale, microbes such as algae swim at low-Reynolds number $Re \sim \mathcal{O}(10^{-3})$, that is in an environment dominated by viscosity. Due the highly viscous environment the hydrodynamic forces imposed by the organism span over relative long range, therefore the collective behavior of microbes is with increasing interest to the fluid mechanics community. Understanding how microbes interact with different environments and each other has much relevance new lab-on chip applications, bio-film formation, and promising value to emergent microfluidic technologies. This thesis is an experimental study that focuses on the motile algae C. reinhardtii that is of length scale of $l_b = 10[\mu m]$ and propels its body by beating two flagella ($l_f = 10[\mu m]$). Based on the imposed flow signature by the algae there is interest two strains, the wild-type (cc125) that pulls it surrounding fluid in, and a mutant (mbo-1) with reverse swimming gait that pushes fluid out. The main goal of this thesis study the detailed motion and interactions of cells with planar physical boundaries as well as with each other. We study the motility of individual cells at varying density in relative dilute regime, with as well interest to possible phase transition of the cell suspension as a collective system.

We track multiple algae in 3 dimensions for sufficient long times using a 4 camera system to study their motility in an unconfined geometry of size $l \sim 1[mm]$. We triangulate the time position of the algae by use of an integer optimization technique (ILP) which we match different paths of particle images among the camera planes by a recursive divide and conquer strategy in MATLAB, and justify the performance towards the Pareto frontier. After having reconstructed the time positional information in the object domain, we study the motily of the microorganisms by the dynamics along their trajectories using the Frenet-Serret framework. In our results we find unexpected behavior of the wild-type (cc125) algae mostly swimming up and down the fluid domain. In case of the mutant (mbo-1) cells we find they mostly crowd the surface, therefore less to our interest. For the motile wild-type algae we find a non-uniform concentration profile over the height of the domain, which a significant portion remains at the boundary. For the algae that freely explore the bulk we find that they move along helical trajectories with a tendency to left-handed chirality. For the algae that are motile at the surface the majority is found to circle clockwise over the surface. Based on the concentration profile over the height of the domain, we define a boundary region that extends up to $l_{bnd} = 100[\mu m]$. In this region we find that most algae touch the boundary and swim either co-planar to the boundary or reflect of the boundary. For the reflecting cells there is strong correspondence between in incident and outgoing orientation of the cell along its trajectory with respect to the boundary. The cell-cell interaction have a much wider range of complex behavior, due the high degrees of freedom as the cell are freely suspended in the bulk. Therefore we only touch upon the complexity of these events in light of the cell-wall interactions. We find that the algae do not significantly reorient when coming close together as they tend to conserve their relative angle along the trajectories. This is not necessarily a trivial consequence of cells ignoring each other as they can perform complex motion during these events.

Our method is unique in the sense that the 4 camera system allows higher cell densities in the fluid domain than many single camera methods. We find for the cell-wall interactions that our study to sheds new light on the boundary action in comparison to studies in the confined geometry. We propose that the boundary action can explain the up and down swimming in the domain by a fixed point operation due the geometric aspect ratio of the flow-chamber. For the cell-cell interactions we conclude that we have not yet studied the right metric to study their complexity in detail. We propose that future work should include different unconfined flow geometries as an engineering outlook. Further we recommend different optimization techniques that could further improve the the tracking and triangulation of the multiple algae in the fluid domain. At last it would be very interesting to study the algae suspended in visco-elastic fluids as is widely found in biology, whereas this remains largely unexplored in experiments.

Keywords: low-Reynolds number, lagrangian particle tracking, micro-algae, collective behavior