Living crystals of micro-swimmers.

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Recently, we have shown that micro-swimmers in 3D can generate coordinate behaviours like swimming in the same direction or create giant density fluctuations induced by the emergency of a dynamic cluster that percolates in the suspension. We found that the key factor to produce these collective motions (CM) is the hydrodynamic signature of the micro-swimmers [1]. On the other hand, since the set-up of many experiments is a suspension where particles can move in a quasi-2D geometry, we developed a systematic numerical study such that experimental parameters are simulated. We present here some results of numerical simulations of interacting micro-swimmers constrained to move in a slab. The results prove that our simulations can reproduce perfectly the living clusters obtained by experimentalists for either active colloids or bacteria. We also show some results of spherical swimmers trapped in a plane but embedded in an unconstrained fluid, swimmers can move along the interface and rotate freely in all directions, we found that interactions with the solvent become even more relevant than the 3D or the slab case since more interesting and striking collective motions emerge. To demonstrate that such coordinate behaviours are intrinsic to the hydrodynamic signature of the particles, we developed several systematic studies in terms of the system size. To do such studies it is important to have high performance computing, in our case we had access to the MareNostrum Supercomputer.

I. INTRODUCTION

Microorganisms in general are distributed in various aquatic environments in nature and industry. Despite their tiny size, micro-organisms play a vital role in a wide variety of phenomena. For example plankton, which plays a fundamental role in the ocean ecosystem, develops massive blooms which form the basis of the marine food web, regulate carbon in the atmosphere, and are responsible for half of the photosynthesis that takes place on our planet. Phytoplankton makes life on Earth possible. Algae bioreactors using to produce biomass constitute another relevant example. In the above examples, the behavior of such suspensions is tightly coupled the transport of chemical substances, momentum, and energy. In particular, to understand the micro-organism motility and transport, we should take into account that their collective behaviour emerges from their dynamic self-organization. Such collective behaviour has inspired researchers to deepen the understanding of the physics of motility to engineer complex emergent behaviours in model systems that promise advances in technological applications. With numerical simulations we are able to find the fundamental role that the hydrodynamic coupling through the embedding solvent has in the collective behaviour in model systems of self-propelled microswimmers. Such a fundamental understanding will help to identify new routes to design micro-robots that can imitate micro-organisms.

Many recent experiments with either artificial or living organisms have been done on quasi-two dimensional systems because of the relevant role of gravity. Accordingly, we have developed a systematic numerical study of interactive micro-swimmer suspensions where swimmers are confined in a slab, each micro-swimmer modelled individually using a very simple model called squirmer model which was introduced by Lighthill [2]. Such a model identifies systematically the basic features of the induced hydrodynamic flow around a spherical swimmer, hence the number of parameter that we have used are minima. We find that, tuning these parameters of activity and interaction we are able to find and characterize different kinds of collective behaviours. In particular, we find the key values where living crystals emerge like in the experiments. Here in this abstract we present the living crystals generated by numerical simulations with the squirmers confined in a slab and we compare with living crystals of bacteria or photoactive colloids. Additionally, we show what happens if the system is partially confined, as is the case in a membrane or when microorganisms are trapped at a liquid interface. In this confined geometry, squirmers swim in a plane but fluid in three dimensions. We find that the different types of confinement lead to qualitatively different collective patterns.

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II. INTERACTING MICROSWIMMERS IN A SLAB

We develop Lattice Boltzmann (LB) simulations [3] where a liquid is modelled by a discrete lattice in which each lattice node has distribution functions that represent the fluid. Embedded in this lattice, we put particles which interact with fluid nodes as boundary conditions that represent moving solid objects (often based on spheres) [4, 5]. Following this idea, we simulate our swimmers as spherical solid particles with an extra boundary condition in the surface of the particles to impose the active propulsion and stress. Both propulsion and stress are the activity of the swimmer, and they are modelled by the simplest version of the squirmer model [6], where only two parameters B_1 and B_2 are needed. B_1 is related to the polarity associated with squirmer propulsion and B_2 induces the active stresses in the fluid. To study the influence of activity we have taken the active stress relative to the polarity, quantified by $\beta = B_2/B_1$. In this way, swimmers can classified as pullers if B_2 is positive or as pushers if is negative. Most of bacteria swim as pushers while microorganisms like the motile algae Chlamydomonas behave like pullers.

Under this numerical scheme, we adapt the lattice such that we can have a slab of fluid with squirmers swimming in it. Additionally to the squirmer model, we introduce an isotropic Lennard-Jones interaction among the particles. Tuning systematically the activity parameter β and the interaction strength between particles, we are able to reproduce the living clusters observed in experiments with bacteria, or with active colloids. But squirmers not only reproduce the morphology of the living crystals, they also reproduce the dynamic of them once the crystals are formed. We quantify the rotational and translational velocity of the crystals to characterize them.

III. SWIMMING IN AN INTERFACE

We have developed numerical simulations of squirmer suspensions, where particles are confined to move only in a plane which is confined in a bulk solvent, and squirmers can re-orient freely in the three dimensional space. We have found that depending on the hydrodynamic stresses and self propelling velocity, particles can align either parallel or perpendicular to the swim plane. We analyse systematically the degree of ordering of active suspensions, by calculating the long-time polar and nematic order for all values of β. Squirmers confined to a plane, display global nematicity for apolar squirmers, a property absent otherwise. In order to develop a deeper understanding in how squirmers generate this collective motion, we have carried out a series of simulations where particles can re-orient given the hydrodynamic field around the particles, but they can not self-propel. We have found that particles are not able to generate polar order, but if particles are pullers, then a non-zero nematic order emerges.

IV. CONCLUSIONS AND REMARKS

We have been able to reproduce numerically, the living crystals observed in experiments with *Thiovulum majus*, one of the fastest swimming bacteria known, and with photoactive colloids. These results have been obtained from a systematic study tuning the parameters of interaction strength and hydrodynamic signatures of the squirmers confined in a slab.

When the squirmers are swimming at an interface, the nematic order generated by squirmers has a stronger dependence on β than their non-confined counterparts, and new classes of collective patterns are observed. The effect of confinement on the active particles opens the door to new states of CM such as non-zero nematicity for pullers with fixed positions, or the emergence of rotating clusters with a typical cluster size distribution without a system size dependence.

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