Hydrodynamic Interactions

in Colloidal and Biological Physics

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The talk reports on recent work on hydrodynamic interactions (HI), a typical feature of colloidal systems. It presents examples from colloidal physics, which illustrate the special properties of HI, and then applies HI to problems connected with locomotion in biology. The latter is also the content of the introduction.

In biological systems, small organisms move in a Newtonian fluid or fluid itself is transported with the help of beating filaments (cilia) or rotating flagella. The motion is governed by small Reynolds numbers, i.e., by a regime where inertial effects can be neglected. Thus directed motion can only occur in systems where time-reversal symmetry is broken as indicated by Purcell and illustrated with his famous Purcell swimmer.

After these general remarks, hydrodynamic interactions and the methods to treat them are introduced. To illustrate their specific properties, a system of particles circling in a ring are considered. The particles are driven by a constant tangential force and they are restricted to the ring by radial harmonic forces. A linear stability analysis shows that the rotational motion of regular clusters are unstable. For a strong radial trap constant, the limit cycle consists of a pair of fastly moving particles (due to reduced friction) which catch up with a slower moving single particle whereby a new particle pair forms. Christoph Lutz in the group of Clemens Bechinger in Stuttgart realizes the limit cycle experimentally with the help of a laser tweezer scanning along a circle. If in addition, the laser intensity is modulated, the particles move in a tilted sawtooth potential. Via the stationnary Smoluchowski equation the average particle velocity for a single particle is calculated. It agrees well with experiments. For small amplitudes of the sawtooth potential, the motion is basically deterministic. Increasing, however, the amplitude further leads to potential wells in the tilted sawtooth which make the motion stochastic. A pair of particles seems to overcome the potential barriers with ease due to hydrodynamic interactions. The associated caterpillar-like motion is deterministic but starts and ends by thermal fluctuations. The experimental

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observations agree well with a Brownian-dynamics modelling.

In the third part of the talk, first a system that mimics flagella or cilia is introduced. It consists of superparamagnetic particles that form a line in an external field. Since the particles are charged, they do not touch. The particles can be linked together by so-called linker molecules, e.g, DNA. The result is a flagellum that can be driven by an external magnetic field whose direction is oscillating. Attached to a red-blood cell, it is able to transport the cell through water, as demonstrated by Remi Dreyfus in the group of Jérome Bibette in Paris. We modeled this system by implementing a discrete version of the worm-like chain bending energy and by letting the particles interact via HI. For constant magnetic field strength, both the swimming velocity and the efficiency of the swimmer exhibit maxima as a function of the field's oscillation frequency. The maxima are close to each other so the swimmer can be used in an optimal mode.

The last biological example deals with bacteria that move forward by cranking a bundle of helical filaments. If the sense of rotation of one filament is reversed, it leaves the bundle. The bacterium tumbles, changes its direction, and resumes its motion after the filament has joined the bundle again. All helical filaments in the bundle necessarily move in phase. We are interested if this synchronization can be achieved by hydrodynamic interactions. We introduce a simplistic model of two flagella by approximating them by rigidly connected spheres. Each of the two helices is fixed in space by a pair of terminal beads that move in harmonic traps and, therefore, allow for some sort of flexibility. The helices are each driven by the same constant torque and indeed show the synchronization towards a zero phase difference. Interestingly, the synchronization speed tends to zero when the trap stiffness of the terminal beads increases. Perfectly parallel helices do not synchronize. Calculations within the helical worm-like chain model show that intrinsic flexibility of the helical flagella considerably speeds up the synchronization.