The role of fluid dynamics in micro-swimmer suspensions

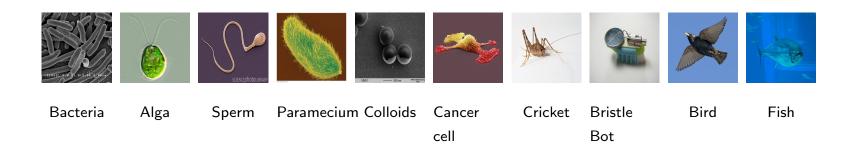
Enkeleida Lushi

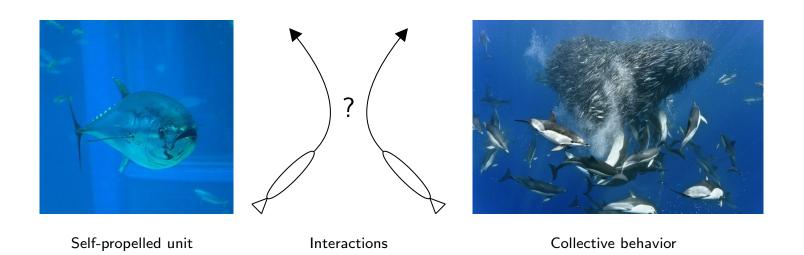
Brown University, Engineering

Collaborators:

Hugo Wioland & Raymond Goldstein,DAMTP, University of Cambridge& Vasily KantslerUniversity of Warwick & SkolTech

Active matter -> collective motion of self-propelled agents

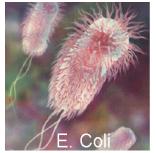




Background: swimming at low Reynolds number

In nature, several swimming mechanisms are observed: e.g. flagellar propulsion (E Coli, B Subtilis, C. Rheinhardii...)

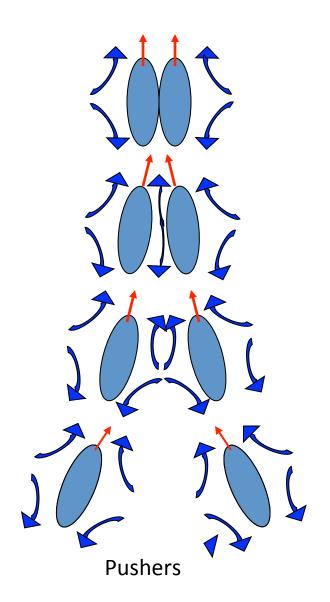
Reynolds number is very small $\sim 10^{-4}$

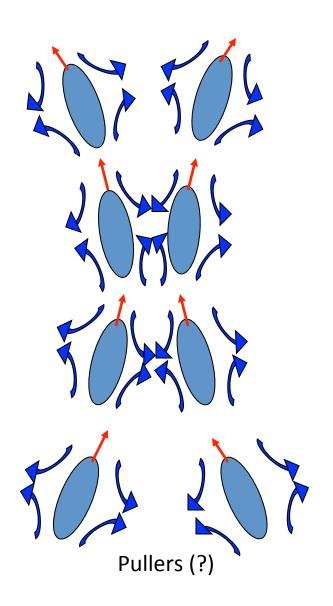




We look at micro-swimmers classified into **pusher** or **puller** types due to **the leading order** force dipole / stresslet they create due to locomotion. Drag Thrust Motion Thrust Drag pusher particle Extensile force dipole E.g: B. subtilis Drag Motion Drag Thrust Contractile force puller particle dipole E.g: Chlamydomonas

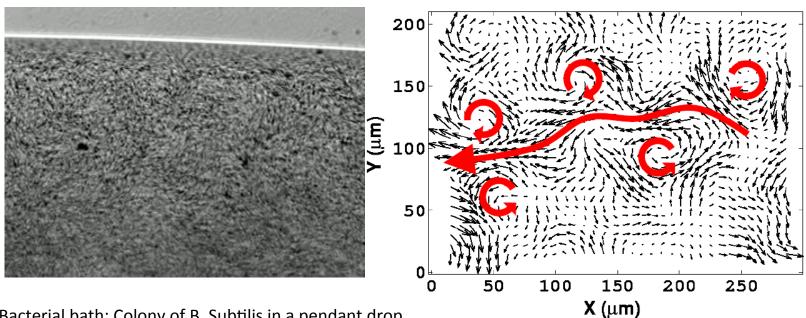
Schematic interaction of two swimmers





Interactions in suspensions of micro-swimmers

Bacterial "turbulence".



Bacterial bath: Colony of B. Subtilis in a pendant drop,

Dombrowski, Kessler and Goldstein, 2004

Observations:

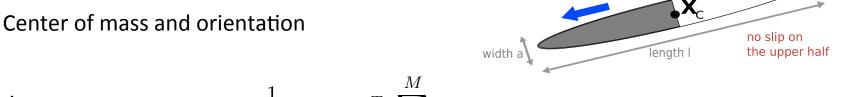
collective behavior drives the fluid

swimming speed 20-30 μm/sec not much tumbling

Bacterium Subtilis rod-shaped ~4 µm long

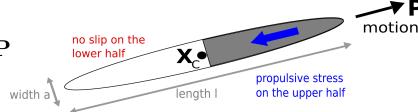
- correlated motions over large length scales, collective speed ~10 times individual speed
- density fluctuations, self-organization -> jets, vortices
- enhanced transport and diffusion, etc.

Minimal swimmer model: leading order dynamics in swimmer slenderness



$$\dot{\mathbf{X}}_i = \mathbf{u}\delta(\mathbf{x} - \mathbf{X}_i) + V\mathbf{P} + \frac{1}{2}(\mathbf{I} + \mathbf{P}_i\mathbf{P}_i^T)\sum_{j \neq i}^{M} \mathbf{F}_{ij}^e$$

$$\dot{\mathbf{P}}_i = (\mathbf{I} - \mathbf{P}\mathbf{P}^T)[\nabla \mathbf{u}\delta(\mathbf{x} - \mathbf{X}_i)]\mathbf{P} + 6\sum_{j \neq i}^{M} \mathbf{T}_{ij}^e \times \mathbf{P}$$



motion

propulsive stress on

the lower half

Low Re flow with extra stress (active + due pairwise steric interactions)

$$-\nabla^2 \mathbf{u} + \nabla q = \nabla \cdot \mathbf{\Sigma}$$
$$\nabla \cdot \mathbf{u} = 0$$

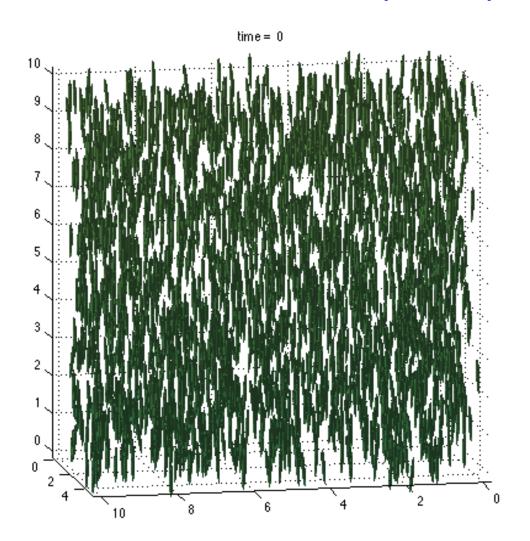
$$egin{aligned} oldsymbol{\Sigma} &= \sum_{i=1}^{M} \left[\mathbf{S}_{i}^{a} + \mathbf{S}_{i}^{e}
ight] \delta(\mathbf{x} - \mathbf{X}_{i}) \ \mathbf{S}_{i}^{a} &= lpha \mathbf{P}_{i} \mathbf{P}_{i}^{T} \ \mathbf{S}_{i}^{e} &= \sum_{i>i}^{M} \mathbf{F}_{ij}^{e} \mathbf{r}_{ij}^{T} \end{aligned}$$

Numerical Methodology

- Coupled dynamics of the micro-swimmers (Lagrangian) and the fluid equations (solved in an Eulerian grid)
- We use an Immersed Boundary Framework.
- Triply periodic fluid domain we solve the fluid equations spectrally.
- Steric interactions done via a soft anisotropic potential.
- Computational cost O(N log N + M) with N the total number of mesh points, M total swimming particles.

- Methodology extendable to include domain boundaries (e.g. thin films), curved surfaces, obstacles, etc.
- The particles need not be uniform in speed, shape or type.

3D simulation: initially nearly-aligned pusher swimmers



10³ box, triply-periodic (slice of the domain shown)

4000 swimmers, length 1, diameter 1/10, initially nearly aligned in the vertical direction

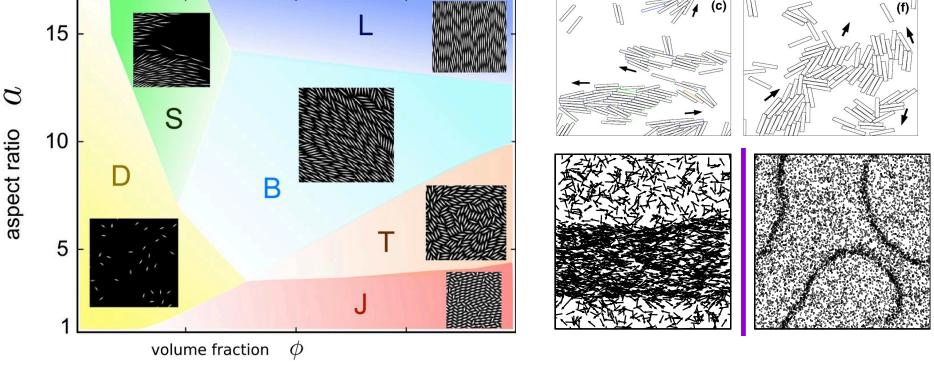
volume fraction <10%

We observe the emergence of large-scale fluid flows.

Suspension becomes isotropic on the whole, but swimmers locally align.

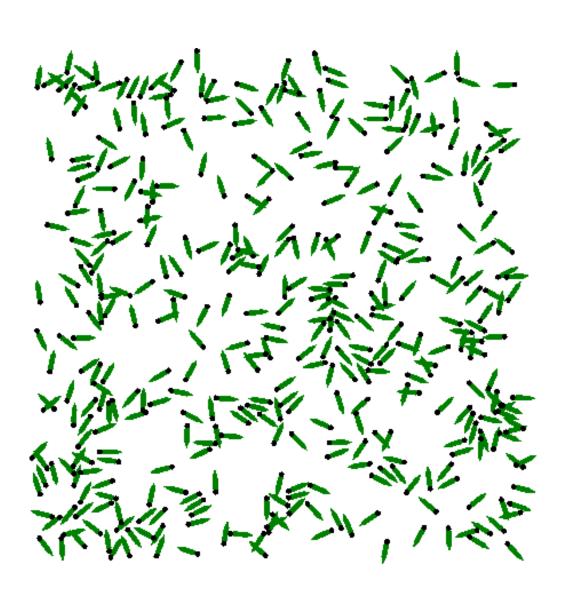
Collective dynamics of SPP-s

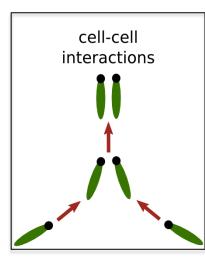
- Direct measurements of the flow field around <u>a single micro-swimmer</u> by Drescher et al PNAS 2011 indicate that direct collisions and noise are significant factors in the motion of such organisms, especially at short range.
- Recently there have been many studies of suspensions of SPP (self-propelled particles) with no hydrodynamics but sometime with aligning interactions.



Wensink et al, PNAS 2012, Peruani et al, PRE 2007, Ginelli et a, PRL 2010

2D, dilute, NO hydrodynamics

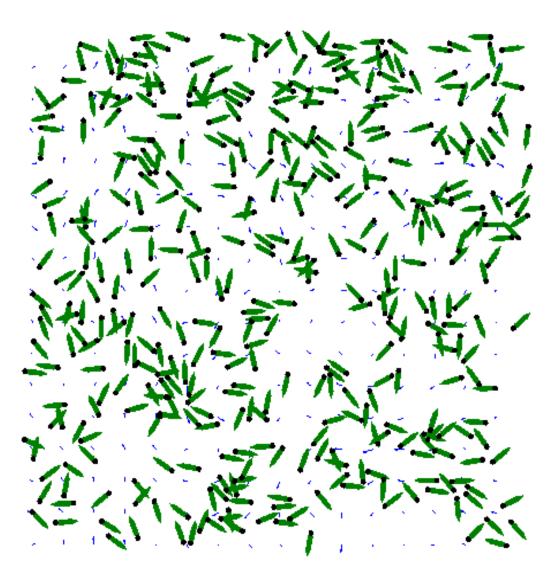


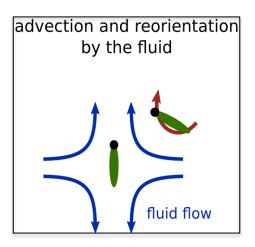


Bionematic or Swarming state

Observe large clusters co-moving.

2D, dilute, with hydrodynamics



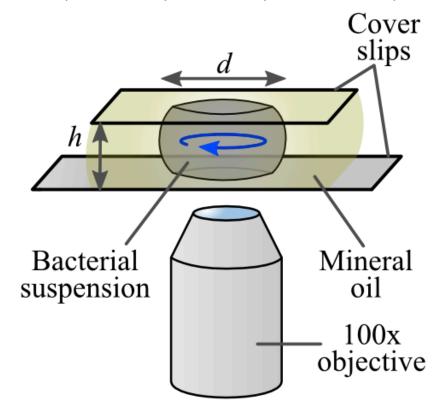


Observe smaller and more dynamic clusters of swimmers.

So hydrodynamics makes a difference.

Organization in a bacterial drop

H. Wioland, F. Woodhouse, J. Dunkel, J. Kessler, R. Goldstein, PRL 110(26) 268102 (2013)

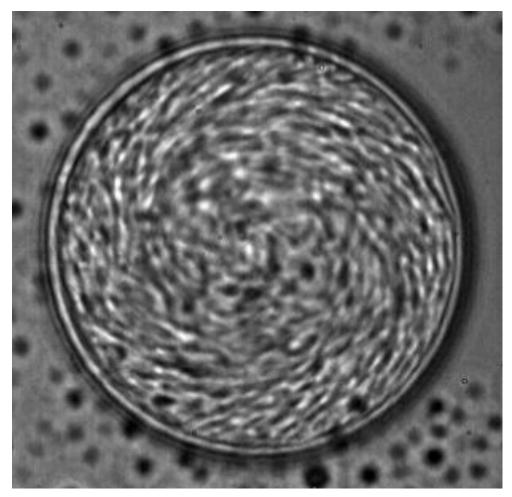


An emulsion of dense bacteria is confined between two coverslips to create flattened drops.

 $d = 10-100 \mu m$; $h \sim 25 \mu m$.

Organization in a bacterial drop

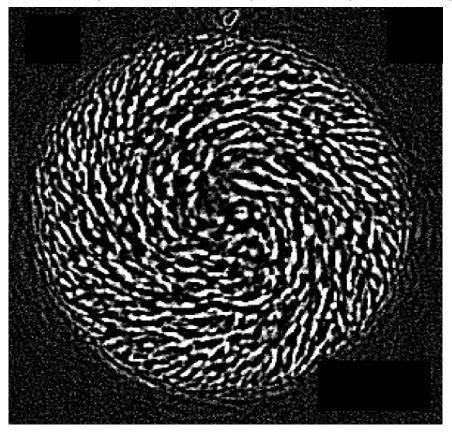
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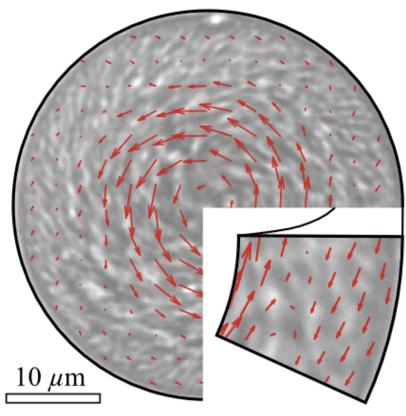


The suspension self-organizes into a spiral vortex, stable for tens of minutes.

Experiments: B. Subtilis in a drop

H. Wioland, F. Woodhouse, J. Dunkel, J. Kessler, R. Goldstein, PRL 110(26) 268102 (2013)

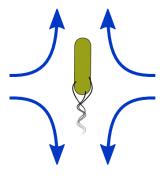




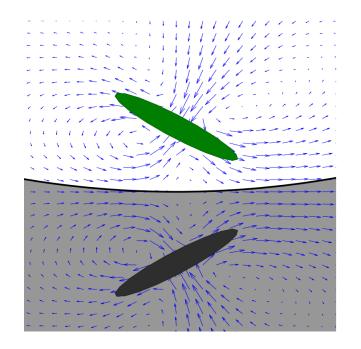
Spontaneous organization of the suspension into a spiral vortex.

bacteria flow (PIV)

Modeling & Simulation Method







Swimmers are ellipsoidally-shaped, propel along their main axis, etc. Need to trace only their centers of mass \mathbf{X} and orientations \mathbf{P} .

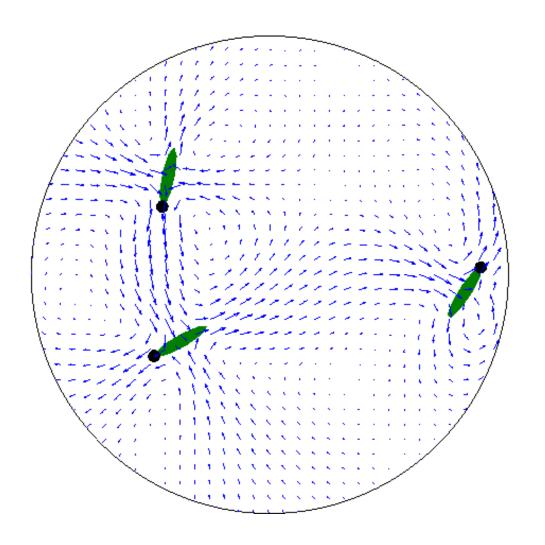
Each swimmer generates instantaneously a dipolar fluid disturbance.

Pair interactions between the swimmers are done via the repulsive part of a soft potential (so there can be some overlaps).

Near a boundary, use an image (this approximates a no-stress condition at the water-oil <u>drop interface</u>. Steric repulsions with the image swimmer effectively gives confinement.

In 2D, free space fluid flow u decays as 1/r. When there is a wall, u decays as 1/r^2.

A Swimmer in a Circle

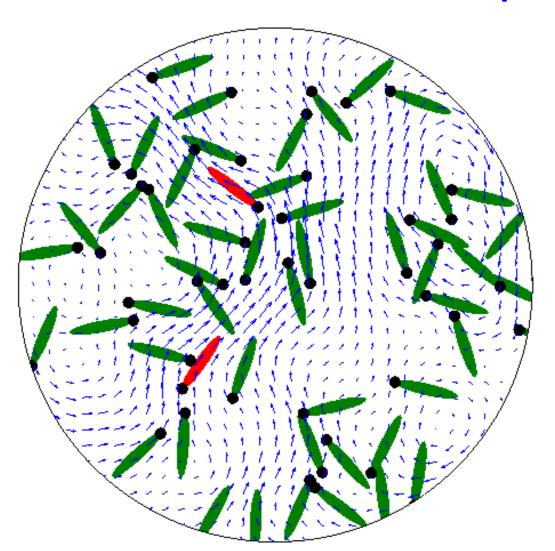


Swimmers end up at the boundary and swim at a very low angle.

Just as in the experiments.



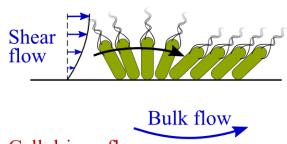
A Dilute Suspension



Swimmers head to the boundary and stay there.

The outer layer forms first and then it is stable.

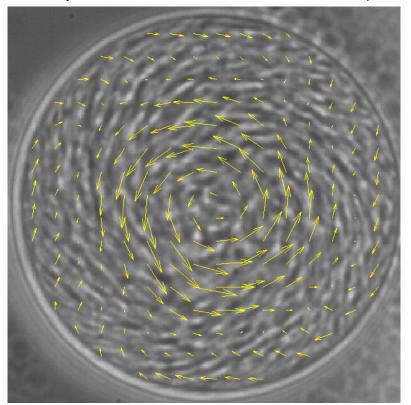
The pusher swimmers produce fluid flow in the opposite direction of their circulation.

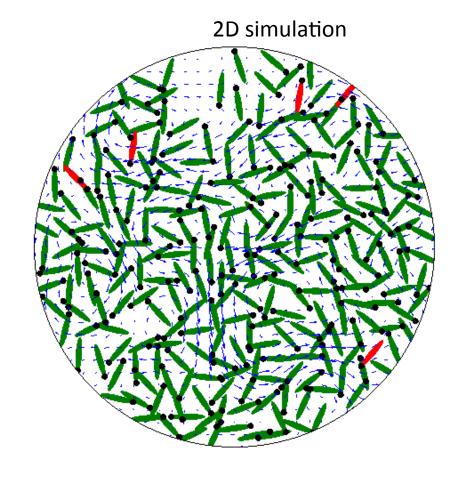




B. Subtilis in a drop, pushers in a disk

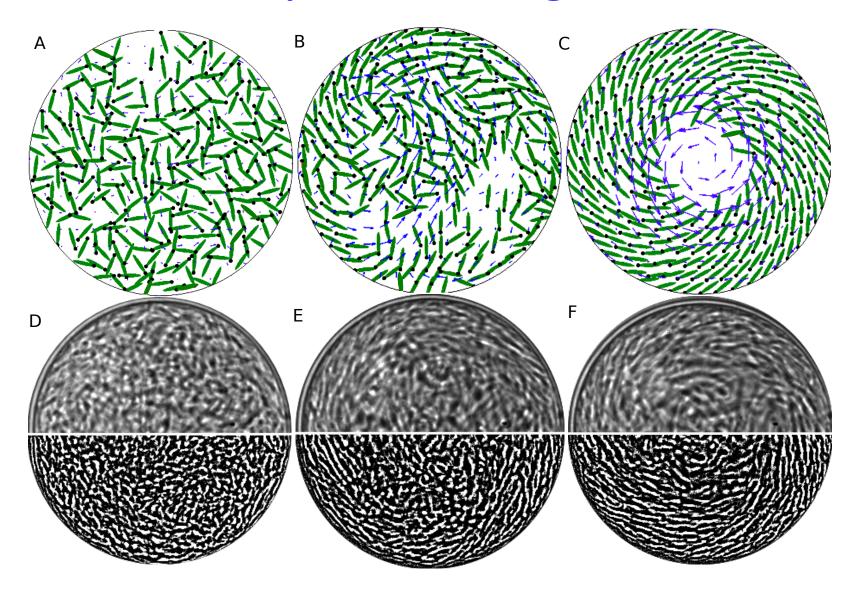
Experiments of H. Wioland et al. (2013)





2D simulation captures dynamics \rightarrow vortex flow, ordering of swimmers, etc.

Boundary-driven organization

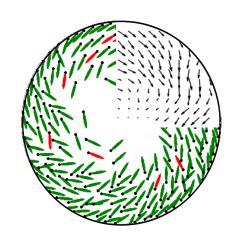


Causes for the self-organization

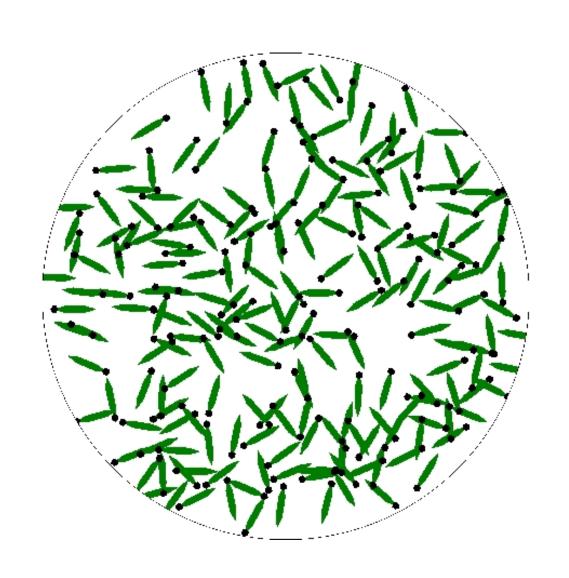
The usual ingredients include confinement and self-propulsion.

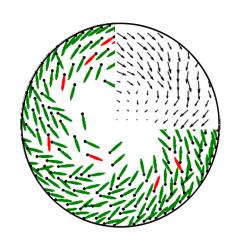
- Elongated swimmer shape (needed for steric interactions and boundary packing)
- Hydrodynamics (in some fashion)
- ? Noise ? Lubrication hydrodynamics? Some kind of other (prescribed) alignment ?

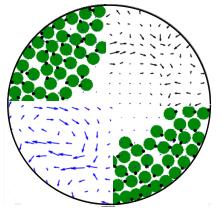
- Some previous studies have shown spontaneous vortex motion of self-propelled disk-like particles under some prescribed alignment, e.g. .Grossman et al, N. J. Phys. (2008).
- But the circulation in all of these is unidirectional.



- self-propulsion
- elongated particles
- no hydro
- -> (spiral) organization
- -> slow unidirectional circulation.

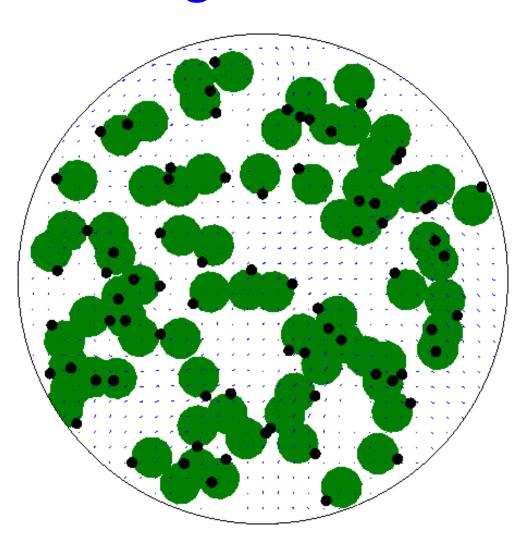


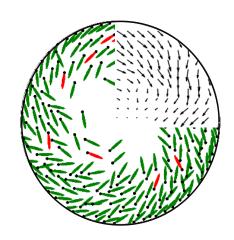




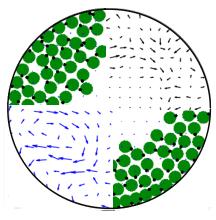
- self-propulsion
- elongated particles
- no hydro
- -> (spiral) organization -> layers form
- -> slow unidirectional circulation.

- self-propulsion
- disks
- with hydro
- -> no organization
- -> unstable circulation spurts

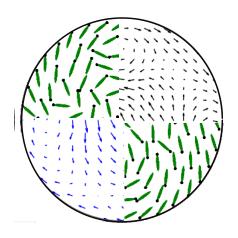




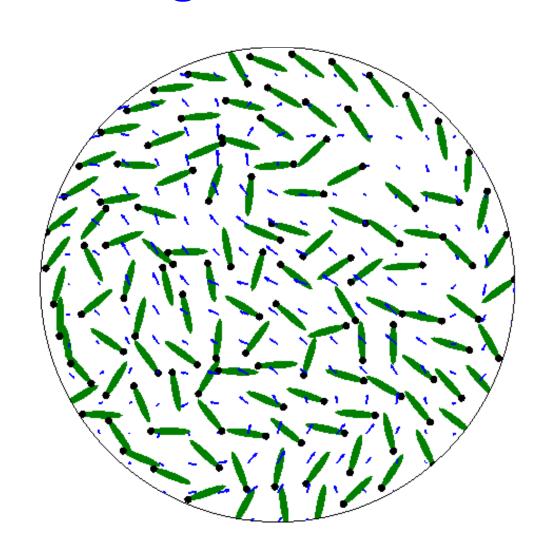
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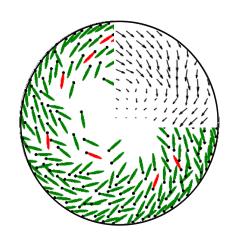


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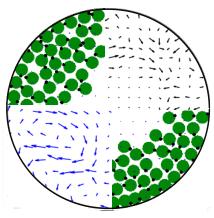


- self-propulsion
- elongated particles
- disk steric repulsions
- with hydro
- -> layers form
- -> spiral organization
- -> double circulation (so the ordering is due to hydrodynamics!)

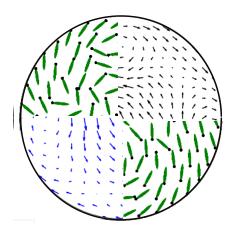




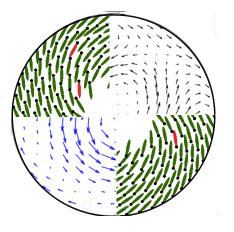
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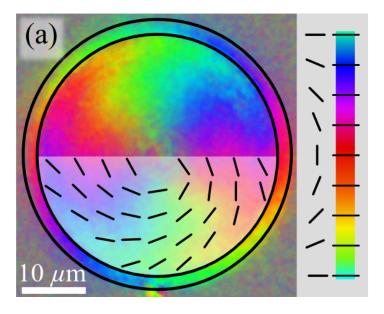
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Swimmer Orientation

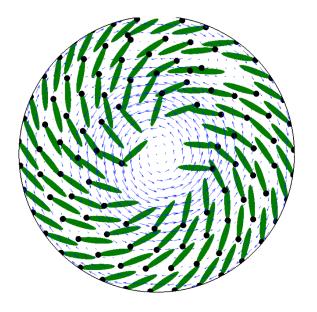
Experiments: observe a spiral ordering



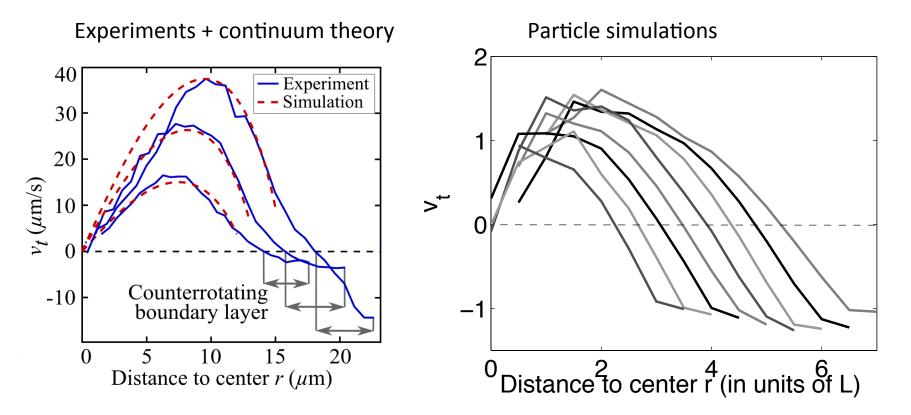
Cells move at an angle to tangential



Direct simulations: spiral ordering there too.

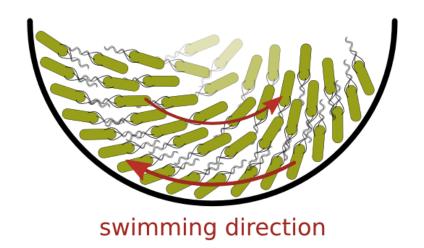


"Bacterial flow"



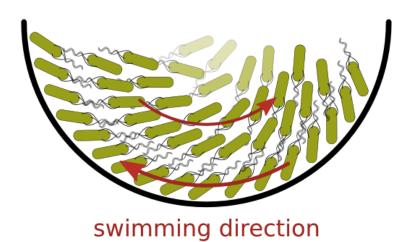
Counter-rotating boundary layer is about 1-2 swimmer lengths in both. Counter-rotating bacterial flow magnitude about 0.5-1V (V is individual swimmer speed) Max bulk bacterial flow magnitude about 1-2V.

Swimming Orientation

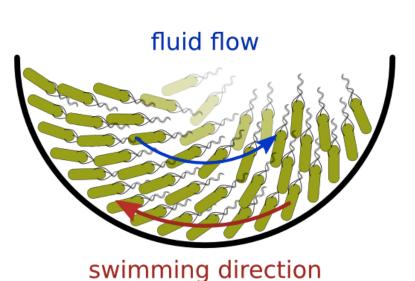


Initial interpretation of experiments (Wioland et al, PRL, 2013): cells in the bulk point inwards...

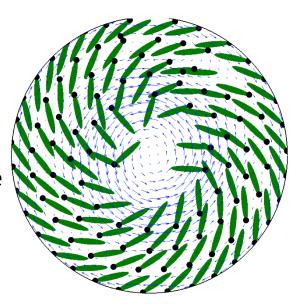
Swimming Orientation



Initial interpretation of experiments (Wioland et al, PRL, 2013): cells in the bulk point inwards...



Simulations however reveal that cells in the bulk point outwards...

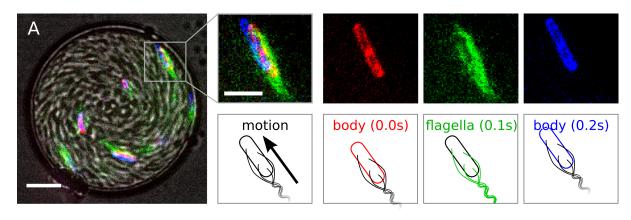


Motion of B. Subtilis at the Boundary and in the Bulk

New experiments to determine the configuration of the swimmers.

Mutant B. Subtilis (DS1919 3610) are labeled with Alexa Fluor 488 C5 maleimide on the flagella and FM4-64 on the cell membrane. These two-colored bacteria are mixed with a large amount of wild-type cells (strain 168) to form drops of dense suspensions.

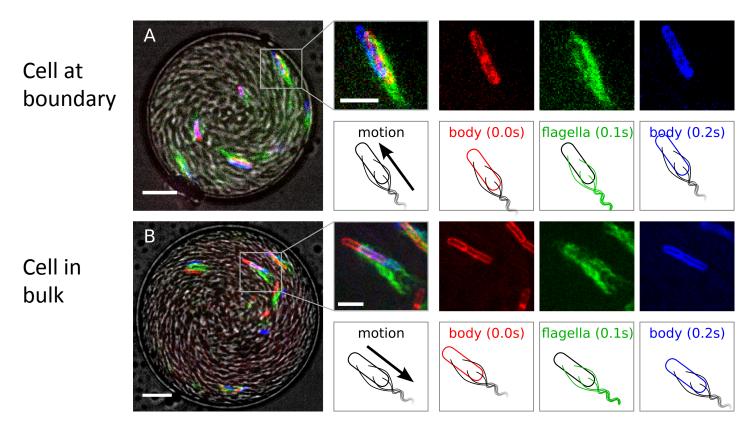
Cell at boundary



Motion of B. Subtilis at the Boundary and in the Bulk

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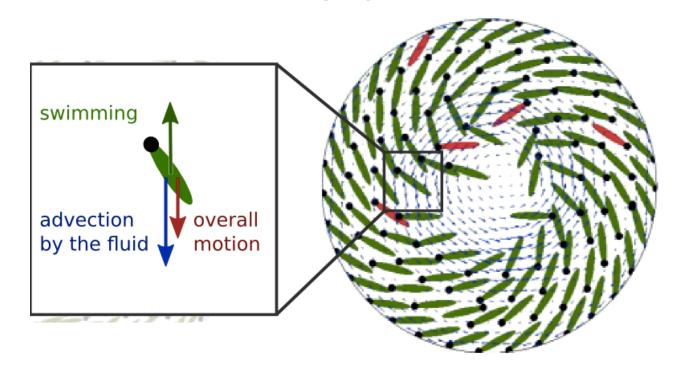
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E. Lushi, H. Wioland, R.E. Goldstein, Proc. Nat'l Acad Sci. 111(27) 9733-9738 (2014)

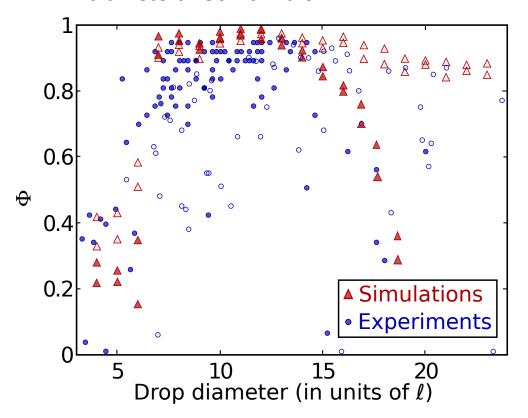
Motion of B. Subtilis at the Boundary and in the Bulk

Cell-fluid interactions are necessary and sufficient to reproduce the organization and dynamic of the drop. Cells in the center move backward as the fluid flow is stronger than their swimming speed.



Drop size range for self-organization

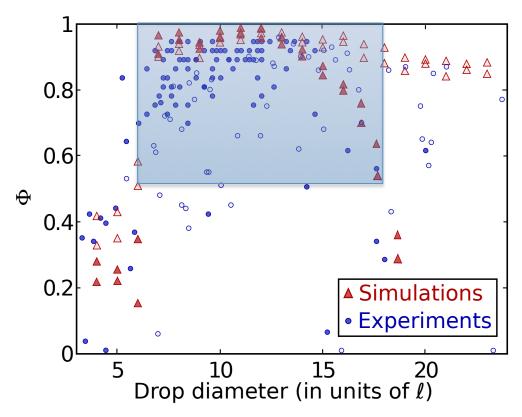
In experiments with drops 15 micron high the vortex emerges for drops with diameters ~30-70micron



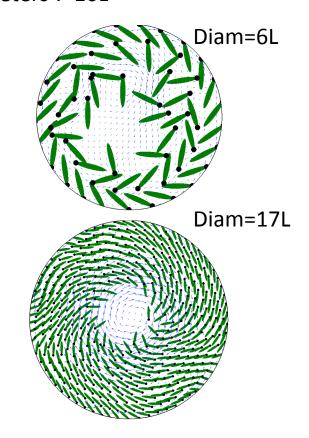
Vortex order parameter
$$\Phi = \frac{\sum_{i} |\mathbf{v}_{i} \cdot \mathbf{t}_{i}|/\sum_{j} ||\mathbf{v}_{j}|| - 2/\pi}{1 - 2/\pi}$$
 ~1 for a vortically-ordered suspension

Drop size range for self-organization

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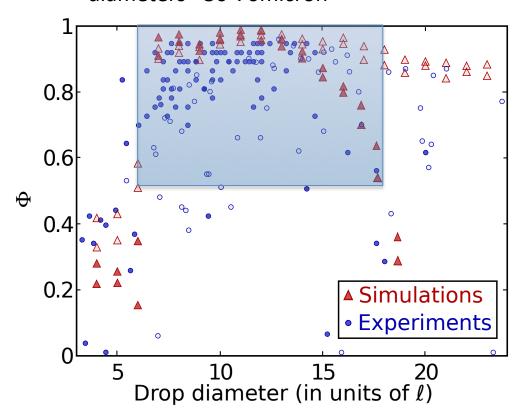
In particle simulations the spiral vortex spontaneously emerges for circle diameters 7-16L



Vortex order parameter $\Phi = \frac{\sum_{i} |\mathbf{v}_{i} \cdot \mathbf{t}_{i}|/\sum_{j} ||\mathbf{v}_{j}|| - 2/\pi}{1 - 2/\pi}$ ~1 for a vortically-ordered suspension

Drop size range for self-organization

In experiments with drops 15 micron high the vortex emerges for drops with diameters ~30-70micron



This suggests this length-scale range for confinement is important.

Indeed, it plays an important role in suspension self-organization in other domain geometries (current work with H. Wioland and R.E. Goldstein).

E. Lushi, H. Wioland, R.E.Goldstein, Proc. Nat'l Acad Sci.111(27) 9733-9738 (2014)

Vortex order parameter
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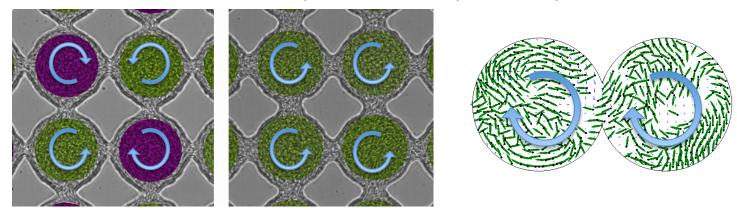
Summary and Discussion

- Minimalistic model that captures the physics of swimming and interactions.
 Fast numerical simulation allows us to trace a very large number of swimmers.
 Method is amendable for domains with static (or moving) boundaries, particles need not be uniform in shape, speed, etc.
- Method captures well the dynamics as observed in experiments.
- In the bacterial drop case, the simulations correctly predicted what drives the dynamics and give new insights into the microscopic arrangement of the bacteria.
- Most importantly, that study clearly shows that hydrodynamics is crucial in obtaining and reproducing the bacterial organization observed in the experiments.

E. Lushi, H. Wioland, R.E. Goldstein, Proc. Nat'l Acad Sci. 111(27) 9733-9738 (2014)

Some other adaptations & current directions

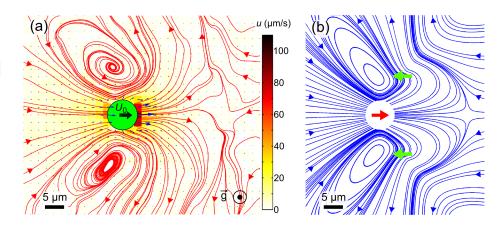
• Interactions of many bacterial vortices, ferromagnetic & antiferromagnetic order in a vortex lattice. With H. Wioland, F. Woodhouse, J. Dunkel, R. Goldstein.



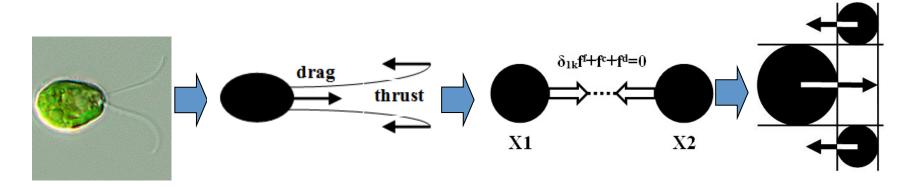
Other geometries; directing collective motion. With H. Wioland, R. Goldstein.

More ``realistic'' models for micro-swimmers

Inspired by the experimental observations of Drescher at al, PRL 2010



Develop <u>minimalistic mathemathical models</u> that correctly capture the essential dynamics of a microswimmer, in bulk or near boundaries.



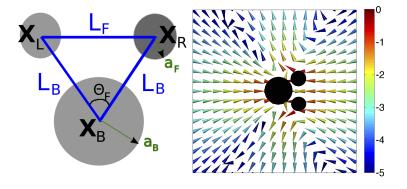
- a) C. Rheinhardii
- b) Forces on fluid
- c) 2 beads model
- d) 3 beads model

Behavior of a biflagellate near walls

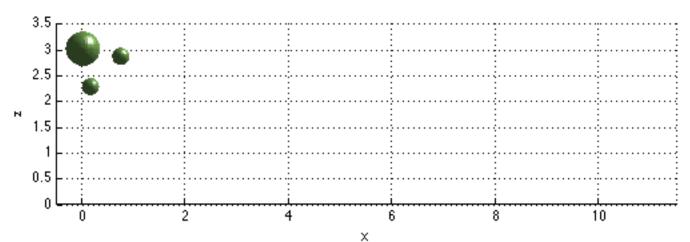
Most minimal models of C. Rheinhardii neglect the fore-aft asymmetry of the swimmer and particulars of the geometry. But that can quite affect the near-wall dynamics.

So we build a model that consists of **3** spherical beads connected by FENE springs

$$\frac{d\mathbf{x}_k}{dt} = \frac{1}{\xi_k} \left[\delta_{k,(L,R)} \mathbf{f}_k^f + \mathbf{f}_k^c + \mathbf{f}_k^x \right]
+ \sum_{j=(B,L,R)} G_{a_j}(\mathbf{x}_k, \mathbf{x}_j) \left[(1 - \delta_{k,j}) \mathbf{f}_j^c + \mathbf{f}_j^x \right]
+ \sum_{j=(B,L,R)} \tilde{G}_{a_j}(\mathbf{x}_k, \mathbf{x}_j) \left(\mathbf{f}_j^c + \mathbf{f}_j^x \right)$$

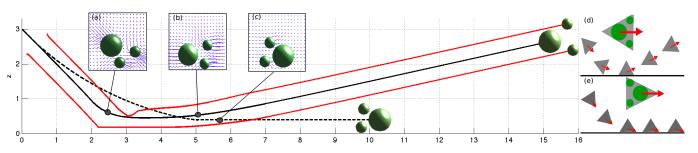


Direct interactions with walls done via the repulsive part of the LJ potential for spheres. Model captures what is seen in experiments of Kantsler et al, 110(4) 1187-1192 PNAS 2013.



Scattering from a wall

Turning chlamydomonas at a wall → ciliary contact with walls is important.

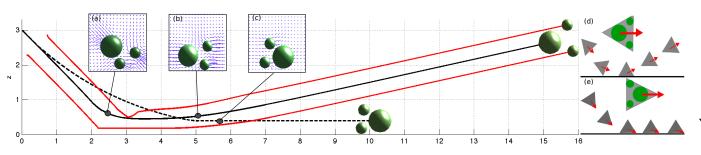


"Puller" chlamy scatters off but at angle different from incident angle

"Pusher" chlamy swims near wall

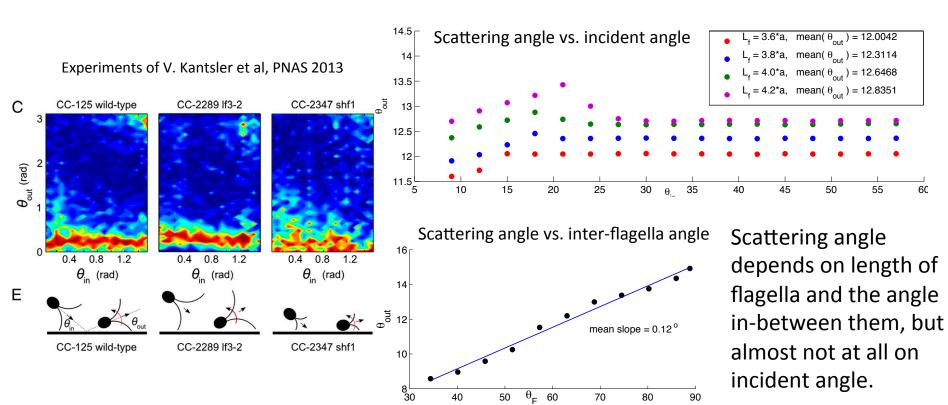
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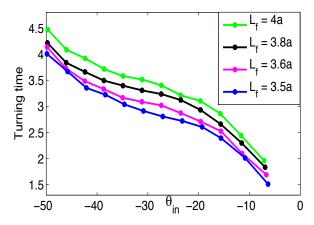
"Puller" chlamy scatters off but at angle different from incident angle

``Pusher'' chlamy swims near wall

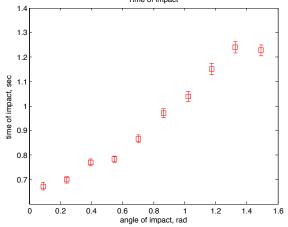


Turning Time & Trapping

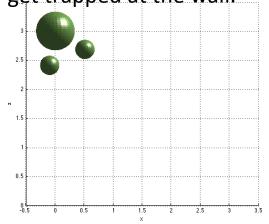
The time it takes a "puller" chlamy to turn at the wall vs. incident angle.



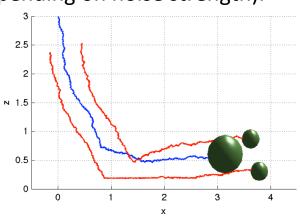
Depends on incident angle, approx. linearly. Flagella length makes very little difference.



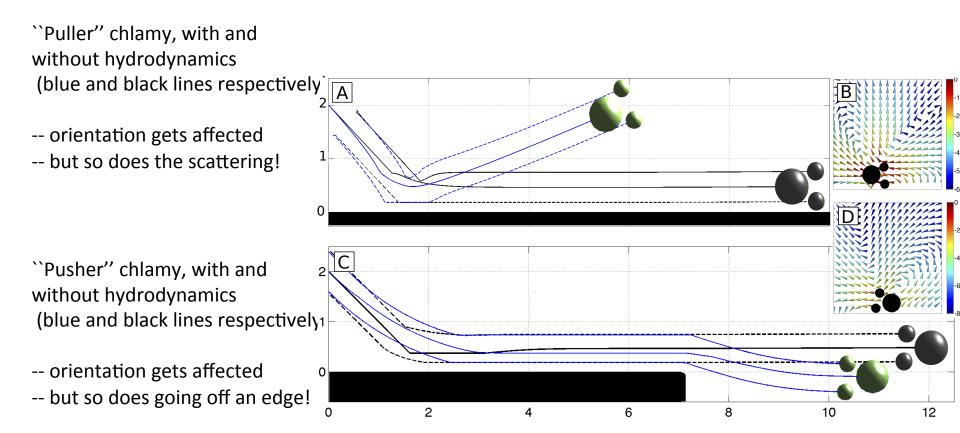
If incident angle is too steep, the chlamy may get trapped at the wall.



Adding noise can help it escape (depending on noise strength).



So does hydrodynamics matter?



Lushi, Kantsler, Goldstein, in preparation (2014).