Mechanics of cell-motility and selfpropulsion in viscous fluids

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Motility



Motility is the capability of exhibiting directed, purposeful movement.

Motile cells provides fascinating examples of motility at microscopic scales (1-50 μ m)

Tumor cells (crawling on a solid surface)

Sperm cells (swimming in a fluid)

Bacteria (**swimming** in a fluid)





Need better understanding of underlying mechanisms



Control mechanisms and interactions with surroundings to enhance (infertility) or reduce (metastasis) motility

Engineer self-propelled artificial micro-motile systems (nano-robots inside the human body for diagnostics and therapy)

We are currently unable to obtain self-propulsion at microscopic scales artificially

Maybe we can learn from Nature ? (bio-mimetic or bio-inspired design)

Using Nature as a template is sometimes naive (airplanes don't flap their wings)

PeregrinFalconTrim.flv



4

Aniso2.mov



red blood cell + flexible magnetic filament

H. Stone et al., Nature (2005)

polymer film + muscle cells

G. Whitesides et al., Science (2007)



Molecular motors



3. Types of molecular motors

Cells generally store chemical energy in two forms: highenergy chemical bonds, such as the phosphoanhydride bonds in ATP (adenosine triphosphate); and asymmetric ion gradients across membranes, such as the electrical potential seen in nerve cells. These sources of chemical energy drive all cell processes, from metabolism through DNA replication. The subset of cell proteins and macromolecular complexes that convert chemical energy into mechanical force are generally called *molecular motors*. Their astonishing variety reflects the diversity of cell movements necessary to life.

Known biological molecular motors may be divided into five general groups: (1) rotary motors, (2) linear stepper motors, (3) assembly and disassembly motors, (4) extrusion nozzles, and (5) prestressed springs. All of the various cell movements already described are performed by ensembles of molecular motors that fall into these categories (see table 1). Coordinated actions of many small individual components can give rise to large-scale (cellular or organismal) movements. Because the molecular motor appears to be the fundamental unit of biological motility, much experimental and theoretical effort has focused on understanding these motor elements.



Linear stepper motors. They drive sliding among adjacent fibers causing muscle contraction, bending of flagella,)



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Cell Motility



Cell movement	Cell structure needed	Molecular motor	Motor category
Movements through liquid	and and an and		
Bacterial swimming	Flagella (bacterial)	Flagellar rotor (MotA/MotB)	Rotary
Eukaryotic swimming	Cilia, flagella (eukaryotic)	Dynein	Linear stepper
Metaboly	Unknown	Unknown	Unknown
Movements on solid surfaces			
Amoeboid motility (crawling)	Lamellipodia, filopodia, pseudopodia	Actin	Assembly/disassembly
		Myosin (several)	Linear stepper
Bacterial gliding	Junctional pore complex	Slime extrusion nozzle	Extrusion
Parasite gliding	Pellicle	Myosin (class XIV)	Linear stepper (probably)
Bacterial twitching	Type IV pili	Pilus base motor (PilT)	Assembly/disassembly?
			Linear Stepper?
Intracellular movements			
Chromosome segregation	Mitotic spindle	Kinesin (several), dynein	Linear stepper
		Tubulin	Assembly/disassembly
Organelle transport	Microtubule arrays	Kinesin (several), dynein	Linear stepper
	Actin gels	Myosin (class V, class VI, others?)	Linear stepper
	Actin comets	Actin	Assembly/disassembly
Rapid cell shape changes			
Muscle contraction	Sarcomere	Myosin (class II)	Linear stepper
Cytokinesis	Division furrow	Myosin (class II)	Linear stepper
Stalked ciliate recoil	Spasmoneme	Spasmin	Prestressed spring
Acrosome extension (Thyone)	Acrosomal vesicle	Actin	Assembly
Acrosome extension (Limulus)	Acrosomal bundle	Actin	Prestressed spring

Table 1. Cell movements and their molecular mechanisms.



Actin-based motility





fibroblasts



neuronal growth cones Neuron1.flv



macrophages





cellix.imba.oeaw.ac.at fileadmin conferences Videotour_.mov

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listeria Listeria monocytogenes.mp4

keratocytes



Actin polymerization at the leading edge drives sissa motility of crawling cells*





(* metastatic tumor cells, immune system response ...)

FishKeratocytes2.mov	

K. Keren et al. (2008)





Protrusion

Governed by a large number of well identified bio-chemical reactions mediated by actin-binding proteins

T. D. Pollard and J. Berro (2009)



Long range order: where from?





Long range order at the μm scale of the cell (the front is flat)

emerging from uncoordinated growth at the nm scale of the individual filaments.

Hypothesis:

self-organized growth is orchestrated by long range **mechanical interactions** mediated by the membrane.

After all, it's filaments pushing against the membrane (Mogilner, Theriot, Keren, Marenduzzo, Prost, Sykes, Plastino...)



Trout keratocytes, M. Prass et al., J. Cell Biol. (2006)

Growth velocity rather insensitive to opposing force, up to a stall force.



Actin filaments symmetrically oriented with respect to the protrusion direction.



A mechanical model for the active layer at the leading edge (2d horizontal slice)





An "active" layer of growing actin network between

the plasma membrane (above)

and the previously grown, immobilized network (entanglements, crosslinks, and adhesion to substrate mediated by moleular clutches, below)



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Starting from a set of fixed "seeds", at each time step *i* a random filament grows at its barbed end, and a branch originates at a random location with probability *Pb.* (growth and branching)

At exposed pointed ends, filaments get depolymerized at speed D. (depolymerization)

Growth events that would lead to overlap with existing filaments are not allowed. (steric hindrance)

Contact among filaments and between filaments and membrane explicitly accounted for .

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Stresses are computed by minimizing total elastic energy at each growth step

$$\mathscr{E}_{i}^{\text{actin}} = \sum_{a} \frac{1}{2} E_{a} \varepsilon_{a}^{2} l_{a}, \quad \mathscr{E}_{i}^{\text{membrane}} = \sum_{m} \frac{1}{2} E_{m} \varepsilon_{m}^{2} l_{m}, \quad \mathscr{E}_{i}^{\text{bending}} = \sum_{m} \kappa \rho_{m}^{2} d, \quad \mathscr{E}_{i}^{\text{contact}} = \sum_{h} \sum_{k \neq h} \psi(d_{hk}).$$
$$\mathscr{E}_{i} = \mathscr{E}_{i}^{\text{actin}} + \mathscr{E}_{i}^{\text{membrane}} + \mathscr{E}_{i}^{\text{bending}} + \mathscr{E}_{i}^{\text{contact}} - \mathscr{L}_{i}^{\text{ext}}, \quad \{u^{eq}\}_{i} = \underset{\{u\}_{i}}{\operatorname{argmin}} \mathscr{E}_{i}(\{u\}_{i}).$$

Monomers with stress exceeding threshold (filam. rupture bend. mom.) are cleaved away; equilibrium states are computed iteratively until no monomer exceed the critical stress.



Growth periods alternate with retractions (avalanches of local rupture events).

Sustained growth when structures fit for pushing (uniform stress distribution thanks to mutual support between neighbors) emerge spontaneously (evolution: mutation through random growth and branching; selection: through failure of overstressed filaments).

Active sites for growth and branching are localized near the membrane



Self-organization of the orientation (optimal shape design ?)





Flexible filaments: large deformations (elastic deflections compensate misalignment)

Stiff filaments: selection (cleavage of misoriented filaments)



Force vs growth Velocity





1/2

force [F,]

1/3

1/6



Growth velocity depends only weakly on the opposing force, up to stall force when growth becomes impossible

Growth against higher values of opposing force requires higher density of actin monomers

5/6

2/3



L. Cardamone et al.: Proceedings of the National Academy of Sciences, 108: 13978–13983 (2011)

- Mechanical stresses may govern the emergence of long range order through the following evolutionary scheme:
 - Filaments that try to grow alone break and depolymerize away.
 - Only when filaments happen to grow cooperatively they can support each other and manage to push the membrane without being crushed.
- Accumulation of mechanical stresses in randomly growing, breakable filaments that push against the membrane. This simple model exhibits ("explains") :
 - Characteristic F vs V and the ability of the network to self-organize its orientation,

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Appendix: values of material parameters



Table S1. Model parameters. Parameters for the benchmark simulations in units of filament thickness d and filament rupture force F_r .

parameter	description	value	References
d	actin filament thickness	7 nm	[8,9]
β	characteristic angle of the truss structure	60°	1000000
a	monomer edge length	$d\cos(\beta/2)$	
θ	initial orientation of seeds	±30°	
φ	branching angle	60°	[5, 10, 11]
P_b	branching probability	0.3	
D	depolymerization speed	10	
E	filament persistence length	$10^{3}d$	[4, 12]
Ê _r	filament rupture force	100 pN	[1]
f_c	edge rupture force	$F_r/2$	
$\stackrel{f_c}{E_m}$	membrane stretching stiffness	$2\dot{F}_r$	[13, 14]
κ	membrane bending stiffness	0.1 $F_{\tau} \cdot d^2$	[11]
с	contact stiffness	30 pN·nm	100 Be
δ	contact length	0.5a	

d = 7 nm

 F_r in the range between 100 and 600 pN







Reynolds Number (Re)





Velocity (typical order of magnitude) V Diameter (typical length scale) L Mass density of the fluid ρ Viscosity of the fluid η

For water at room temperature $\rho/\eta = 10^6 (m^2 s^{-1})^{-1}$.

Re is a dimensionless measure of relative importance of inertia vs. viscosity

Orders of magnitude for swimmers:

Men, tuna, sharks:L=1m, V=1-10 ms^{-1}Re= $10^{6}-10^{7}$ Bacteria:L=1x10^{-6}m, V=1-10x10^{-6} ms^{-1}Re= $10^{-6}-10^{-5}$



G.I Taylor and low Re flows



National Committee for Fluid Mechanics Films: http://web.mit.edu/hml/ncfmf.html

G.I. Taylor's movie on low Re flows:

http://modular.mit.edu:8080/ramgen/ifluids/ Low_Reynolds_Number_Flow.rm



Modern classical physics through the work of G.I. Taylor:

One scientist's work provides material for an entire course, covering topics ranging from hydrodynamic stability and turbulence to electrohydrodynamics and the locomotion of small organisms.

-- Michael P. Brenner and Howard A. Stone

http://www.deas.harvard.edu/brenner/taylor/physic_today/taylor.htm

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Flow past a sphere (Stokes formula)



25

Re = 0



Re > 250



Drag = $6 \pi \mu R V$ (Stokes, 1851)

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Resistance matrix for ellipsoidal shapes SISSA The reversauce matrix & succes the symmetries of D: if Dissymmetric them the e-vecto ore along the arocs of supmenting 0 ð K= GTLu I = GTLu Sphere 0 001 4-1 Q → 10 polate ellipsort of revolution ₹h € (1 + 00 ē 0 EL 0 56 0 K= Grou <u>5α</u> ε(1, 112) 5. 00 linteb

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Lecture 4: from mobility to motility



Swimming: a definition

the ability to advance in water by performing a cyclic shape change (a *stroke*) in the absence of external propulsive forces



It's a control problem: Can we reach B from A (with B≠A) by executing (periodic) shape changes (or by prescribing suitable internal forces) ?

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Two conceptual ingredients



1.

How does the surrounding medium react (namely, which forces does it exert ?) to shape changes of the swimmer?

(equations of motion of the surrounding medium)

2.

How does the swimmer move in repsonse to the forces that the surrounding medium applies to it ?

(equations of motion of the swimmer)



Outer Stokes problem



Find u induced in the fluid surrounding swimmer Ω by its shape changes:



$$\begin{aligned} -\eta \Delta u + \nabla p &= 0 \quad \text{on } \mathbb{R}^3 \setminus \Omega, \\ \operatorname{div}(u) &= 0 \quad \text{on } \mathbb{R}^3 \setminus \Omega, \end{aligned}$$

 $u = V_{Dir}$ on $\partial \Omega$

 $u \to 0$ at infinity.

 $\sigma n = DN_{\Omega}[v_{Dir}]$ viscous "reactive" force p.u. area on $\partial \Omega$





The motion of the swimmer induced by its shape changes is a-priori unknown.

Equations of motion:

0

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m
$$(x_c)_{,tt} = F_{tot}$$

 $0 = F_{tot}$ neglecting swimmer's inertia

$$F = F_{ext} + F_{visc}$$

= F_{visc} self-propulsion

Similarly, total viscous torque = 0.







The <u>flexible</u> oar

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The corkscrew

in a flow regime obeying Stokes equations, a scallop cannot advance through the reciprocal motion of its valves

whatever forward motion will be produced by closing the valves, it will be exactly canceled by a backward motion upon reopening them (see Marta's talk)

G.I. Taylor, 1951 H. Berg, 1973 H. Derg, 1973 (bacterial flagella)

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A. Najafi and R. Golestanian: Simple swimmer at low Reynolds numbers: three linked spheres, PRE **69**, 062901 (2004)

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Mathematical swimming in a nutshell





shape

 $c = \frac{1}{3} \sum_{i=1}^{3} x^{(i)}$

 $\xi_1 = x^{(2)} - x^{(1)}$

 $\xi_2 = x^{(3)} - x^{(2)}$

position

Swimming is

 $\xi_1(t), \xi_2(t)$ periodic of period T

executing cyclic shape changes

producing

$$\Delta c = \int_{0}^{T} \dot{c} dt \neq 0$$

 $f^{(1)} + f^{(2)} + f^{(3)} = 0$

net positional change after one period

under

no external force (self-propulsion)

Positional change from shape change (axisym.)

$$\overrightarrow{t} = \underbrace{f(0)}_{i} \underbrace{f(0)}_{i$$

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Swimming at max efficiency (geodesic strokes) (strokes of max Lighthill efficiency)

Rescale to unit time interval. Minimize expended power

$$\int_{0}^{1} \int_{\Omega} \sigma \mathbf{n} \cdot \mathbf{v} \, dt = \int_{0}^{1} \int_{\partial\Omega} DN_{\xi} [\mathbf{v}_{\text{Dir}}] \cdot \mathbf{v}_{\text{Dir}} \, dA \, dt = \int_{0}^{1} G(\xi) \dot{\xi} \cdot \dot{\xi} \, dt \qquad \text{stroke "length"}$$

at given
$$\Delta c = \int_{0}^{1} V(\xi) \cdot \dot{\xi} = \int_{\omega} \operatorname{curl} V(\xi) \, d\xi \qquad \text{enclosed area}$$

Euler-Lagrange eqn.

$$-\frac{d}{dt}(G\dot{\xi}) + \frac{1}{2} \begin{pmatrix} \partial_1 G\dot{\xi} \cdot \dot{\xi} \\ \partial_2 G\dot{\xi} \cdot \dot{\xi} \end{pmatrix} + \lambda \operatorname{curl} V(\xi) \, \dot{\xi}^{\perp} = 0$$

Optimal paths are sub-riemannian geodesics. Optimal strokes exist. They can be computed numerically.









Summary and perspectives



- Self-propulsion yields the key equation(s) giving positional change from shape change
- Swimming problem as a problem of controllability
- Optimal strokes of low Re swimmers computable; sub-riemannian geodesics
- The picture is qualitatively similar for general swimmers with finitely many shape dofs. (6 ODEs rather than 1 equation of motion. But: rotations !)
- What about the genuinely infinite-dimensional case ?





Metaboly of Eutreptiella sp.

- What is the biological function of metaboly motion (swimming ???)
- Is there something being optimized by the stroke of this micro-organism ?





G.I. Taylor: Analysis of the swimming of microscopic organisms, Proc. Roy. Soc. A **209**, 447- 461 (1951).

> G. Gray and G.J. Hancock: The propulsion of sea-urchin spermatozoa, J. Exp. Biol. **32**, 802- 814 (1955).

G. Dal Maso, ADS, M. Morandotti: An existence and uniqueness result for the self-propelled motion of micro-swimmers, SIAM J. Math Analysis **43**, 1345-1368 (2011).



Solve for the fluid velocity ${\bf u}$ in the surrounding fluid. No-slip plus fluid at rest at infinity.

BCs in a frame moving with the sheet:

 $\mathbf{u}(x, h(x, t)) = -b\omega\cos(kx - \omega t)\mathbf{e}_y,$

 $\lim_{y \to \infty} \mathbf{u}(x, y) = -\mathbf{U}.$

where $\ensuremath{\mathbf{U}}$ is the swimming speed of the sheet.

Wave travels to the right

Transversal (bending/shape) wave: sheet moves to the left

Solving the outer Stokes problem:

$$\mathbf{U} = -\frac{1}{2}\omega\mathbf{k}b^2.$$

Longitudinal (stretching) wave: sheet moves to the right (see Ezio's talk on Monday)



Wave travels to the right

Transversal (bending/shape) wave: sheet moves to the left

If the sheet is blocked: the sheet pumps fluid towards right

Gray-Hancock beating flagellum



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Local drag approximation (??) or "resistive force theory"

$$\mathbf{f} = -\xi_{\parallel} \mathbf{u}_{\parallel} - \xi_{\perp} \mathbf{u}_{\perp},$$

Eq. of motion:

$$\mathbf{F}_{head} + \int \mathbf{f} = \mathbf{0}$$

Solve for the unknown swimming velocity:

 $U = \frac{(\xi_{\perp} - \xi_{||}) \int_0^L \dot{h} h' \,\mathrm{d}x}{\xi_{||}L + \xi_0 a}.$

Average over one period of oscillation:
$$\langle U \rangle = -\frac{\xi_{\perp} - \xi_{||}}{2\xi_{||}} \frac{\omega k d}{1 + (\xi_0 a)}$$

Remark: get back Taylor's formula with L > > α (head radius) and $\xi_{\perp} = 2 \xi_{\parallel}$ (??)



B.M. Friedrich et al., High precision tracking of sperm swimming fine structure provides strong test of resistive force theory. J. Exp. Biol. 213, 1226-1234 (2010).





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