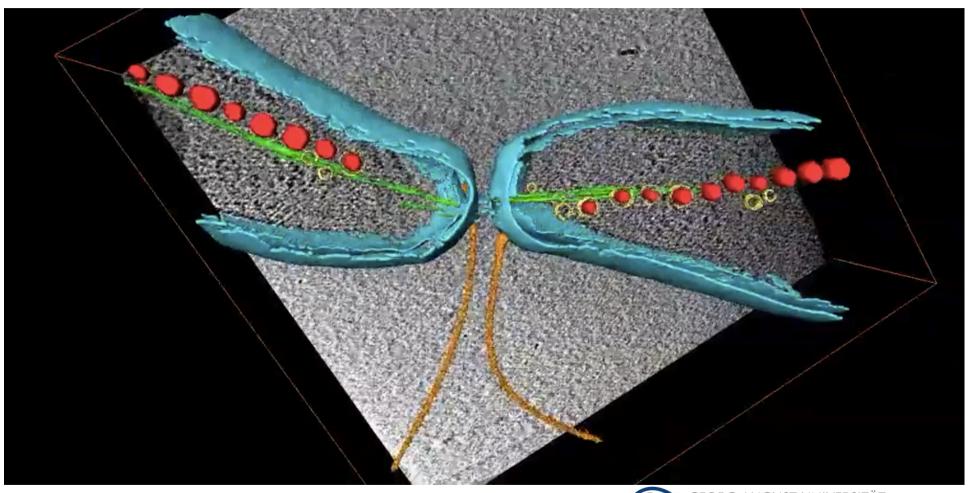
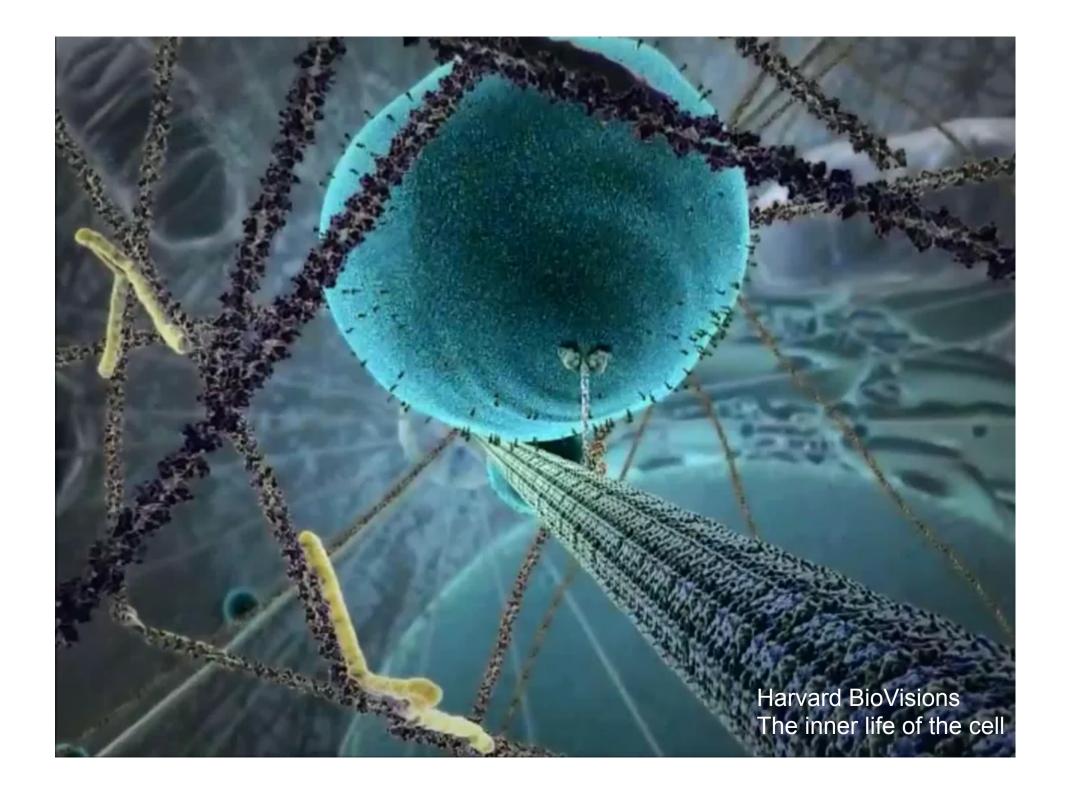
Traffic on filaments: molecular motors in difficult conditions



Stefan Klumpp







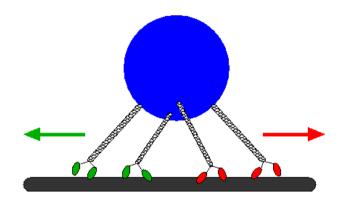


Hoogenraad lab A day in the life of a motor protein

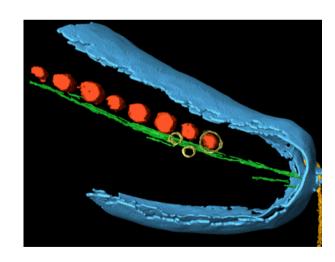
www.youtube.com/watch? v=tMKIPDBRJ1E

- stochasticity
- opposing force
 - other motors
 - external forces
- crowded conditions on filament/ in cytoplasm
- dynamic tracks

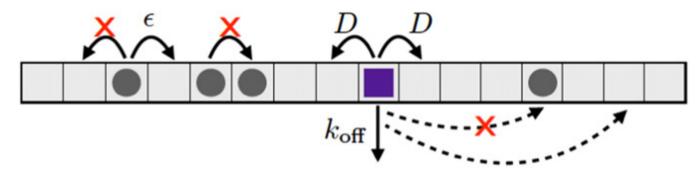
tug of war between teams of cytoskeletal motors



magnetosome filament in magnetotactic bacteria

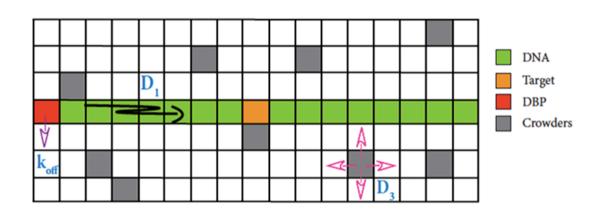


Roadblocks in exclusion processes (static or dynamic)





DNA binding in crowded conditions (obstacles on DNA, in cytoplasm)



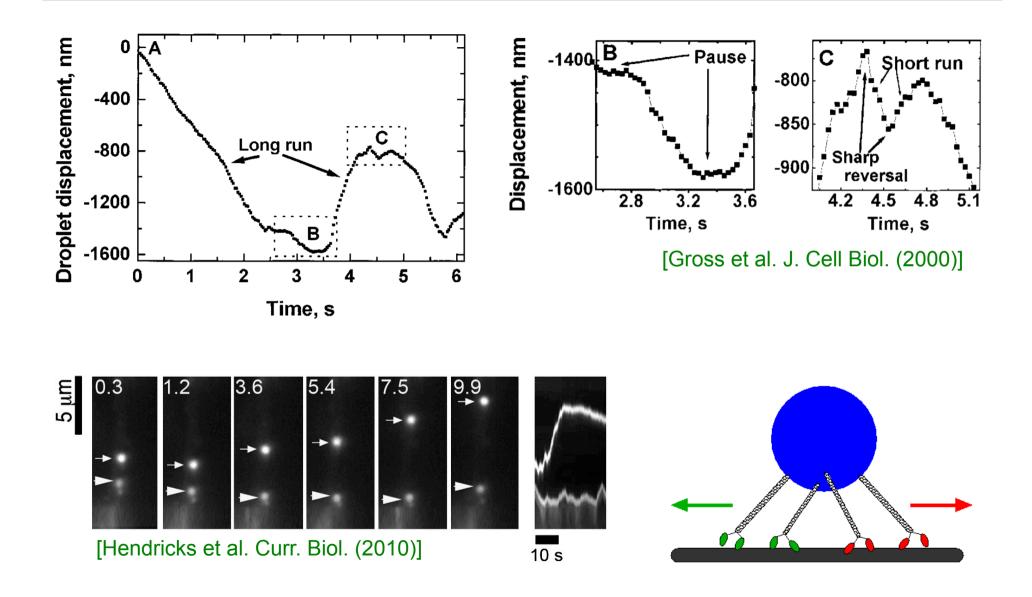




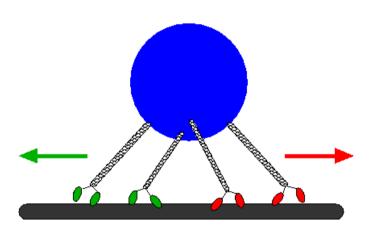
Traffic on the cytoskeleton

TUG OF WAR AND ALL THAT

Bidirectional transport: Tug of war and all that...



Bidirectional transport: Tug of war and all that...



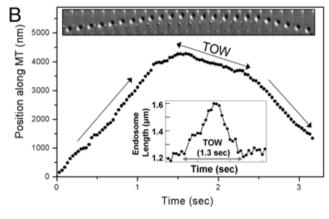
Tug-of-war model: mechanical forces coordinate opposite-direction motors

instability due to force-induced unbinding



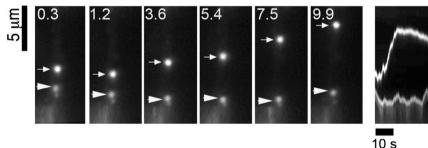


Experimental evidence for a tug-of-war



endosomes in Dictyostelium cells: endosome elongates during slow phase

Soppina et al., PNAS (2009)



neuronal vesicles:

observed motion quantitatively in agreement with tug-of-war model

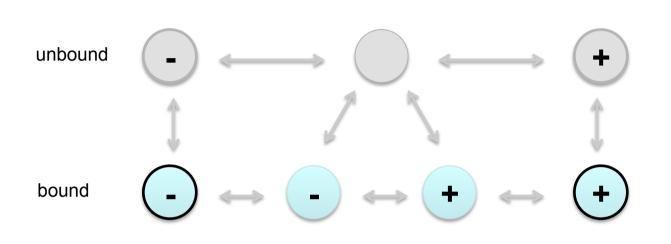
Hendricks et al., Curr Biol (2010)

but also: some observations point to additional biochem. regulation

- lipid droplets: long pauses Kunwar et al. PNAS 2012
- lipid droplets: same direction after unbinding Leidel et al. Biophys J 2012
- known regulator JIP1 Fu & Holzbaur 2013

→ control by generic mechanics + specific biochemistry

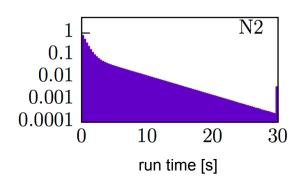
Toy model: bidirectional transport with regulation



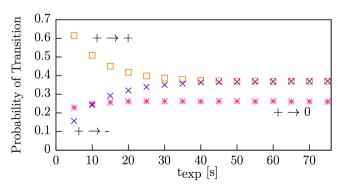
bidirectional transport

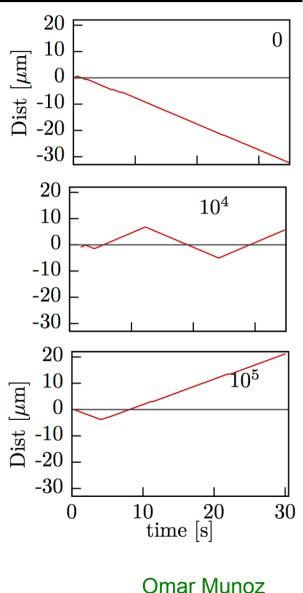
+ "locked-in" states due to regulation

rare very long runs

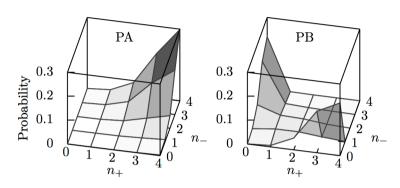


Memory upon unbinding

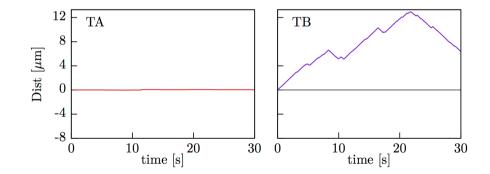




Tug-of-war with activation/inactivation

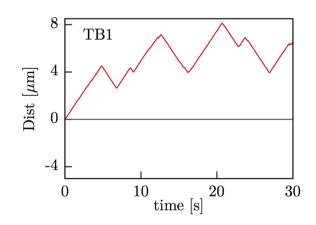


tug-of-war model



 $\begin{array}{c} 0.2 \\ \begin{array}{c} 0.2 \\ \begin{array}{c} 0.15 \\ \begin{array}{c} 0.15 \\ 0.05 \\ 0 \end{array} \\ 0 \end{array} \\ \begin{array}{c} 0.005 \\ 0 \end{array} \\ \begin{array}{c} 0.005 \\ 0 \end{array} \\ \begin{array}{c} 0 \\ 0 \end{array} \\ \begin{array}{c} 0$

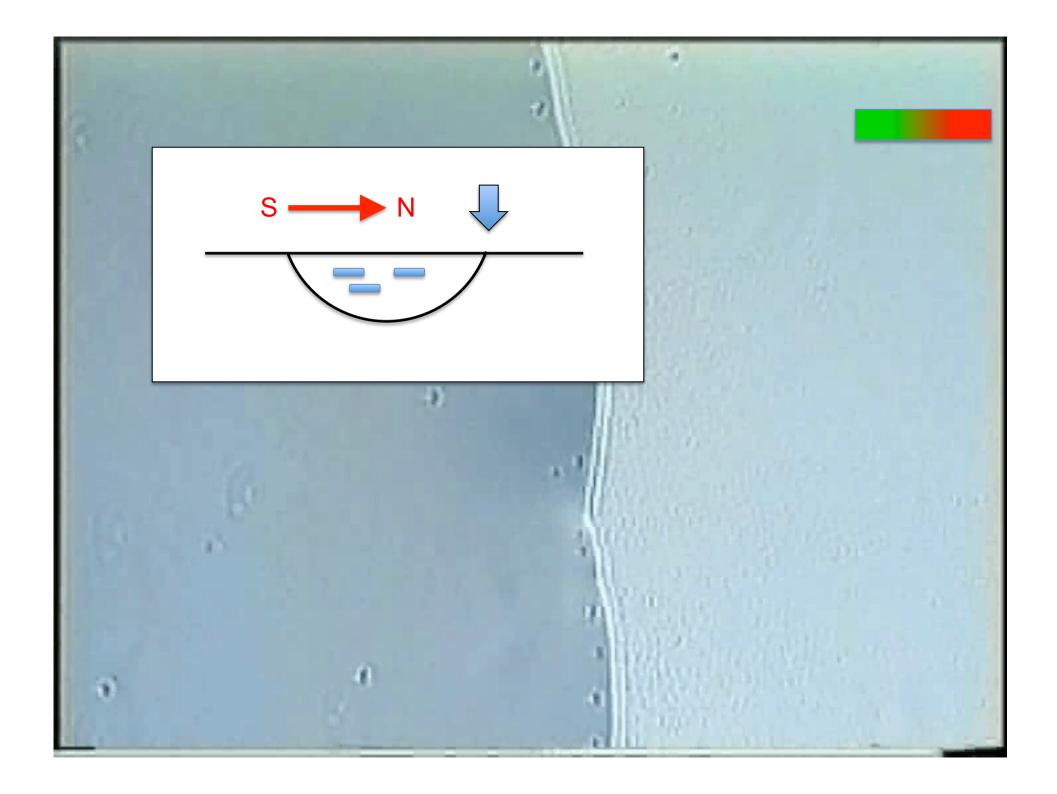
with motor activation

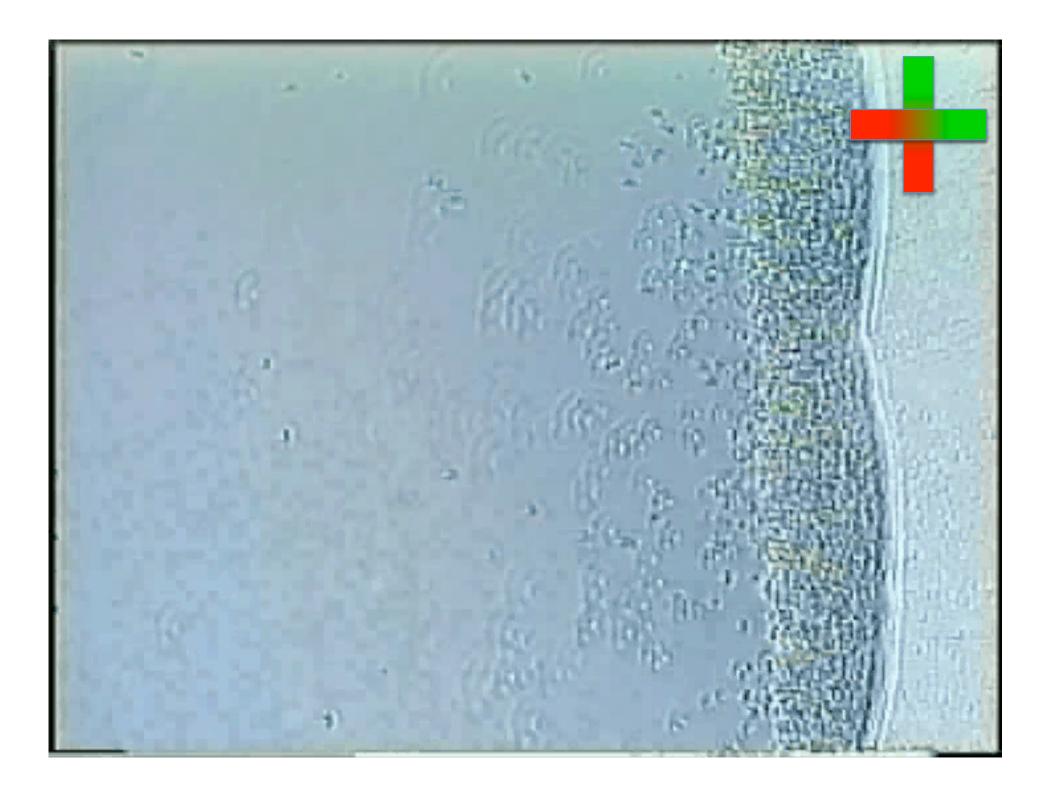


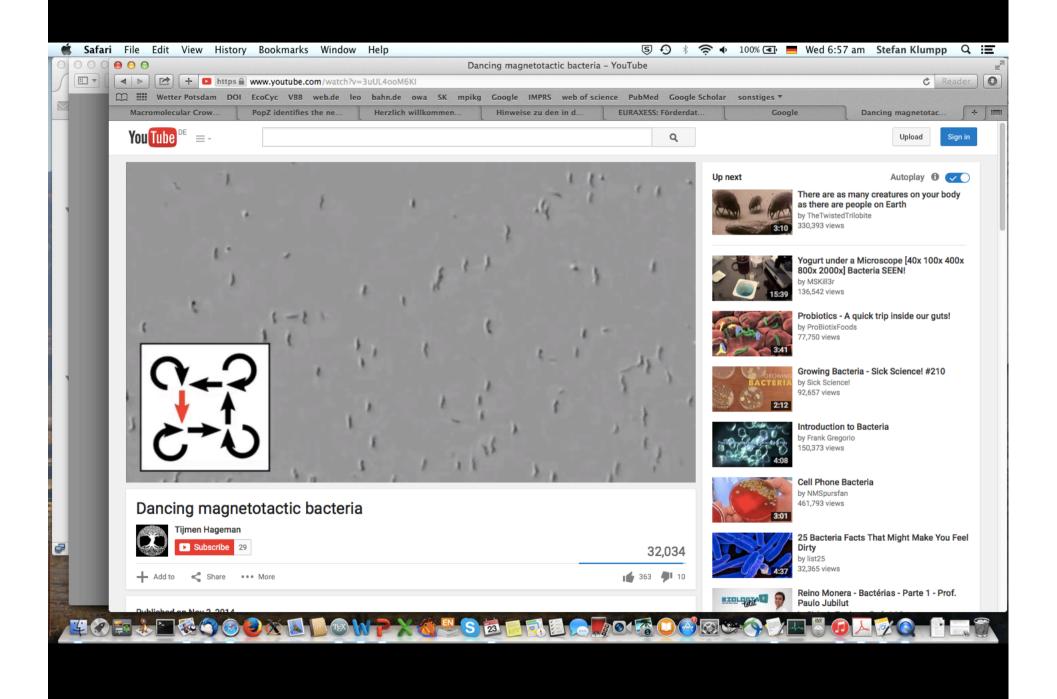
activation provides a mechanism for lock-in of direction abolishes parameter dependence

Traffic on a bacterial cytoskeleton

FILAMENTS IN MAGNETOTACTIC BACTERIA

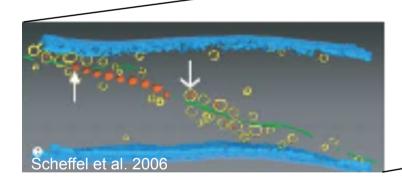




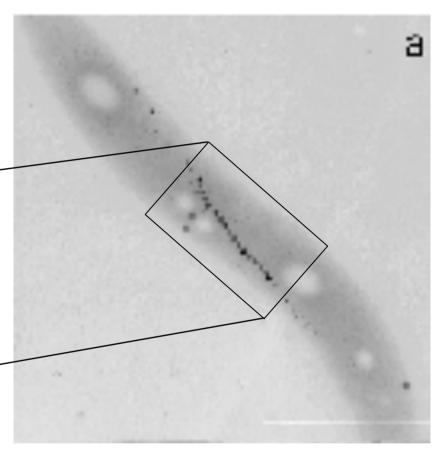


Magnetotactic bacteria

- form a chain of magnetic organelles (magnetosomes)
- → compass needle
- orient and navigate in magn. field of the earth

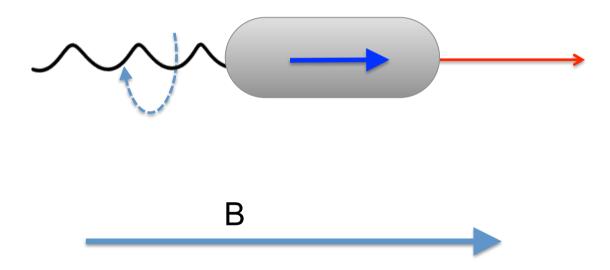


- ~40nm Fe₃O₄ crystals in vesicles, aligned on filament (MamK)
- permanent magnets, single-domain particles



Magnetospirillum gryphiswaldense MSR-1

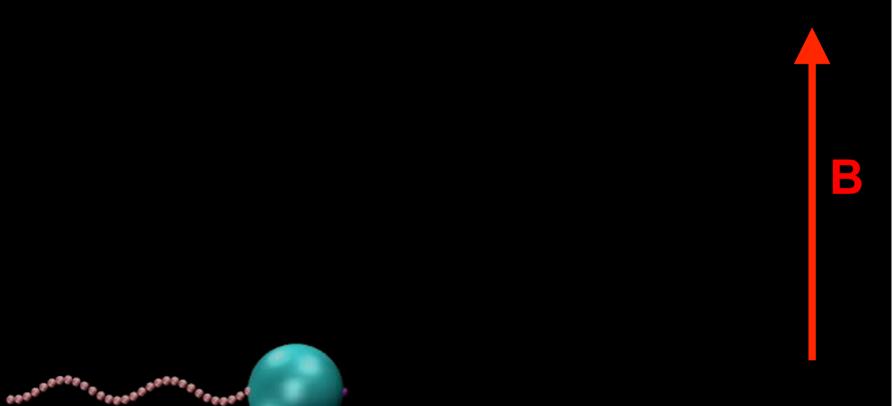
Passive alignment + active propulsion



"Self-propelled compass needle"

Homogeneous field: alignment but no attraction

Passive alignment + active propulsion



Sarah Mohammadinejad

Compass needle: structural requirement

Straight chain for high magnetic moment

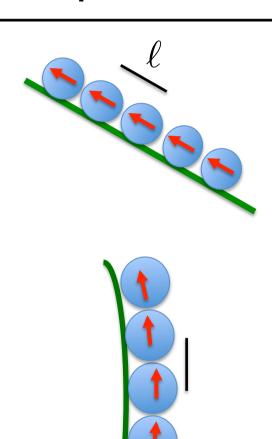
Bending rigidity
$$\kappa = \kappa_{\rm fil} + \kappa_{\rm magn}$$

$$E_{\mathrm{magn}} \approx E_{\mathrm{lin}} + \frac{1}{2} N \frac{\kappa_{\mathrm{magn}}}{\ell} \left(\frac{\ell}{R}\right)^2$$

$$\kappa_{\rm magn} \approx \epsilon \ell \frac{\zeta(3)}{4}$$

persistence length:
$$L_p=\frac{\kappa}{k_BT}$$

$$L_{p,\mathrm{magn}}=\frac{\kappa_{\mathrm{magn}}}{k_BT} ~ \text{~~3-4 } \mu \text{m~~cell length}$$

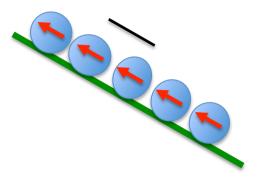


Compass needle: structural requirement

persistence length:

$$L_{p,\text{magn}} = \frac{\kappa_{\text{magn}}}{k_B T}$$

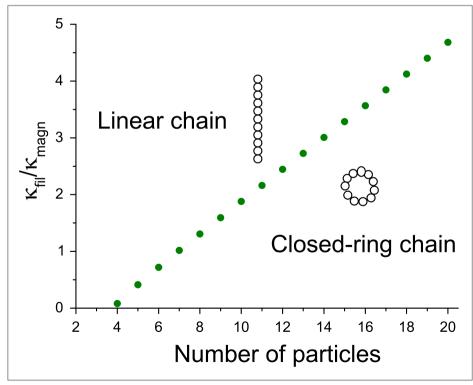
 \sim 3-4 μm \sim cell length





straight magnetic chain is metastable

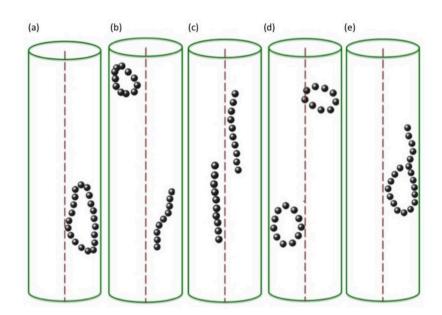
stabilized by filament



Kiani, Faivre, Klumpp, New J Phys 2015

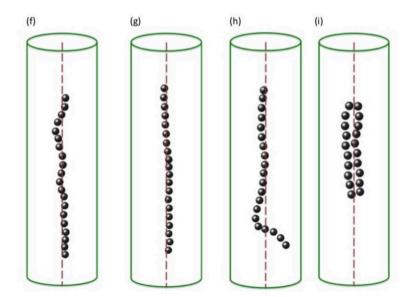
Compass needle: structural requirement

without binding to filament



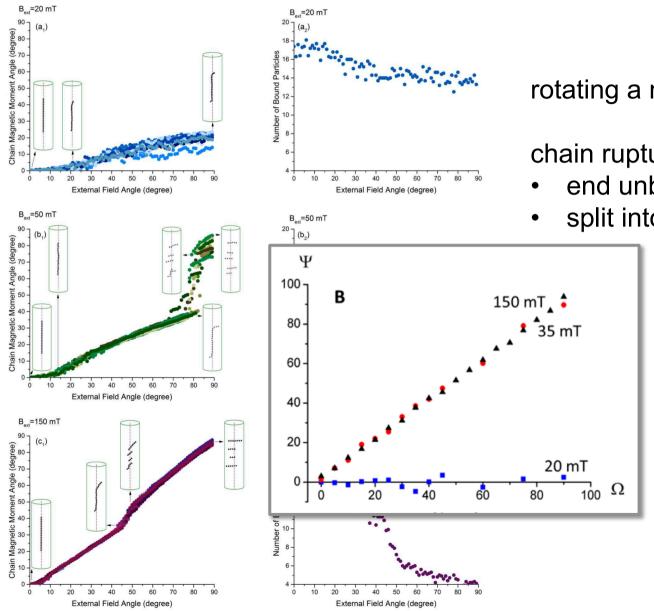
filament stabilizes chain: MC simulations

with binding to filament



Bahareh Kiani

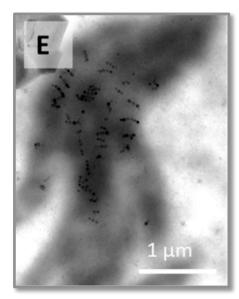
Probing mechanical stability



rotating a magnetic field

chain ruptures in 2 steps

- end unbinding
- split into short chains



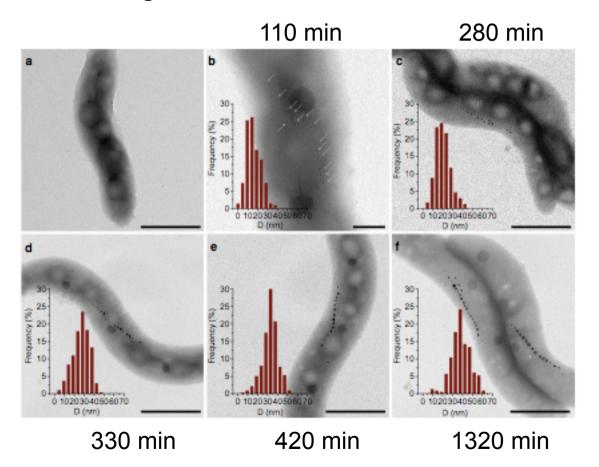
A. Körning et al. Nano Lett. 2014

Positioning of magnetosomes, chain formation, cell division

AN ACTIVE FILAMENT

Formation of magnetosome chains

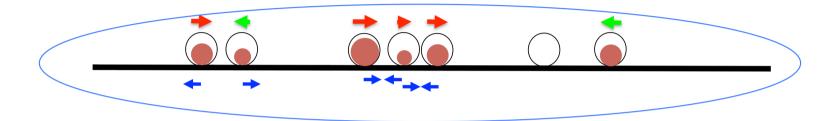
- experiment: iron-starved cells shifted to medium with iron, but no nutrients
- form magnetosome chains over 5-10 hours



- → role of magnetic interactions?
 (interplay of physics and biology)
- → diffusion + magn.
 interactions sufficient for chain formation?
 → role of MamK,J proteins?
- → idea: in-silico mutants defective in processes

[Faivre et al. Biophys. J. 2010]

Model for chain formation

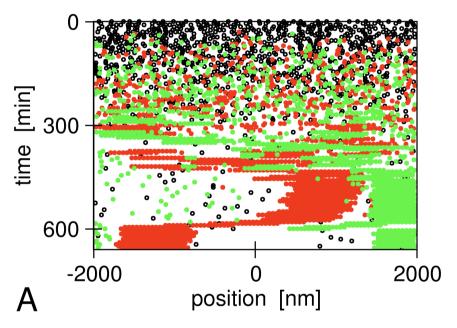


- hybrid Langevin dynamics—Monte Carlo simulation
- simulate ~10 hours of dynamics
- most parameters known, diffusion coeff. varied over wide range

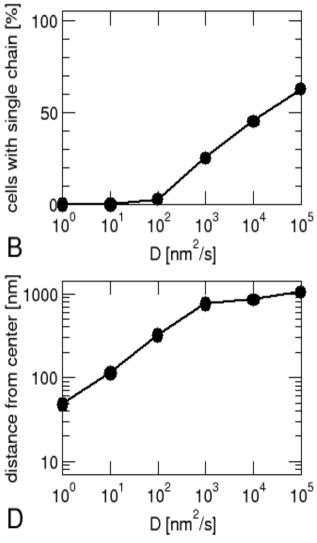
Diffusion + magn. interactions

diffusion + magn. interactions sufficient for chain formation?

analyze simulated cells 10 hours after induction

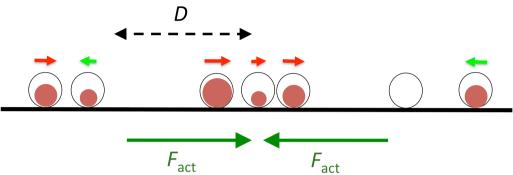


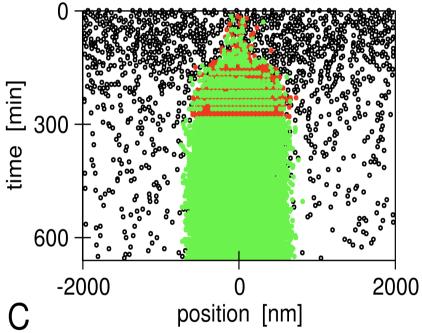
- substantial fraction of cells form ≥2 chains
- chains not centered
- onset of magnetization later than in expt.



Active transport to cell center

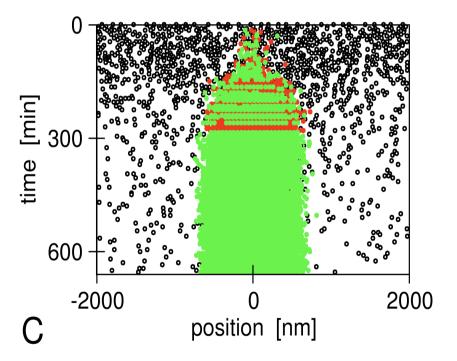
active transport, driven by (de)polymerization of cytoskeletal filaments? (MamK, FtsZ-like, others?)

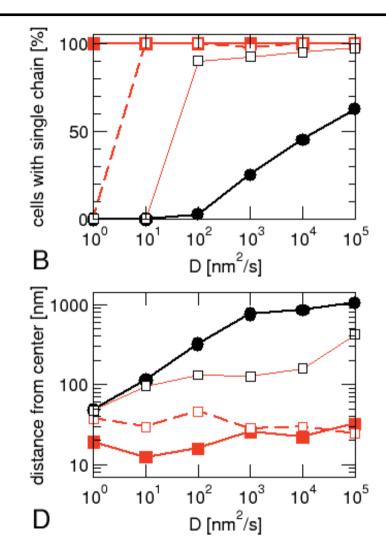




Active transport to cell center

active transport, driven by (de)polymerization of cytoskeletal filaments? (MamK, FtsZ-like, others?)





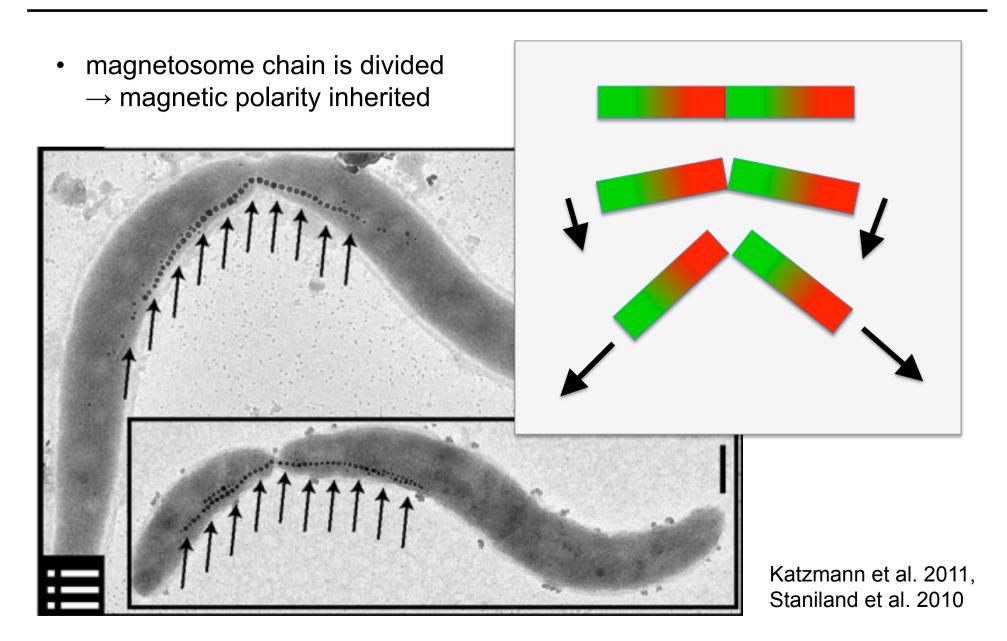
- \rightarrow robust chain formation above velocity threshold v= $DF_{act}/(kT) \approx 15$ nm/min
- → competition with local chain formation
- → forces/velocities in range for (de-)polymerization motors

mamK deletion mutant

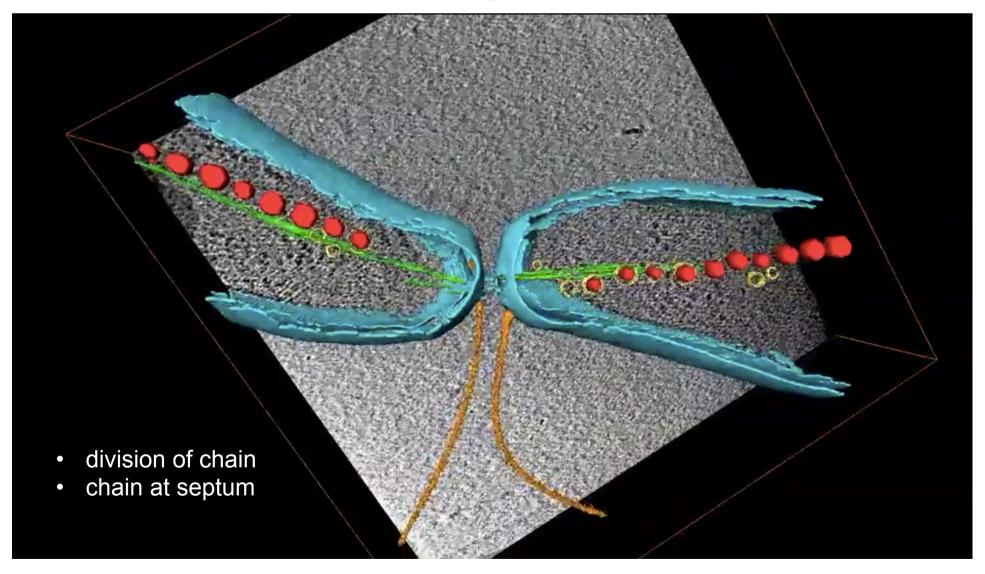
 MamK discovered as main protein of filaments time [min] 300 • mamK deletion in M. gryphiswaldense: shorter chains, cells with multiple chains [Katzmann et al. Mol. Micro 2010] 600 -2000 2000 position [nm] cells with single chain [%] simul. exp. with active movements (WT) 100 no active movements (∆mamK) ∆mamK with active movements active movements → role for *mamK* in active transport (motor?)

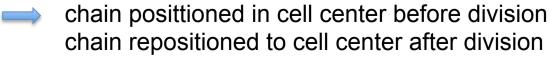
Klumpp & Faivre, PLoS One 7, e33562 (2012)

Cell division in magnetotactic bacteria



Repositioning of the chain

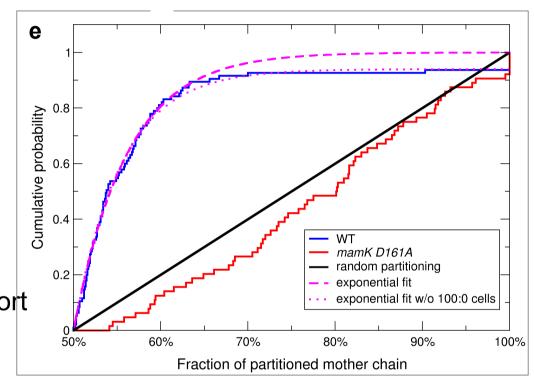




Before division: positioning in the cell center

quantitative analysis of chain partitioning:

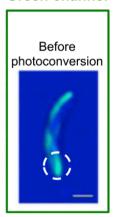
- WT: precise partitioning (~6 % or ~1 magnetosome)
- mamK D161A: approx. random
- → active positioning due to active filament
- → exp. fit: balance of active transport and diffusion

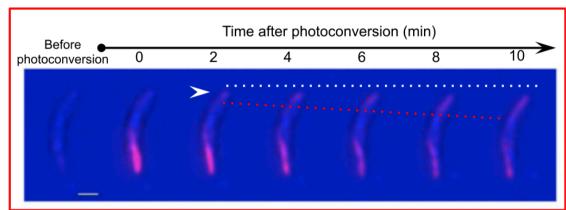


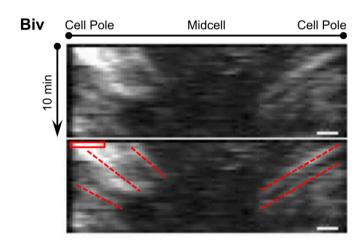
Active filament

Green channel

Red channel

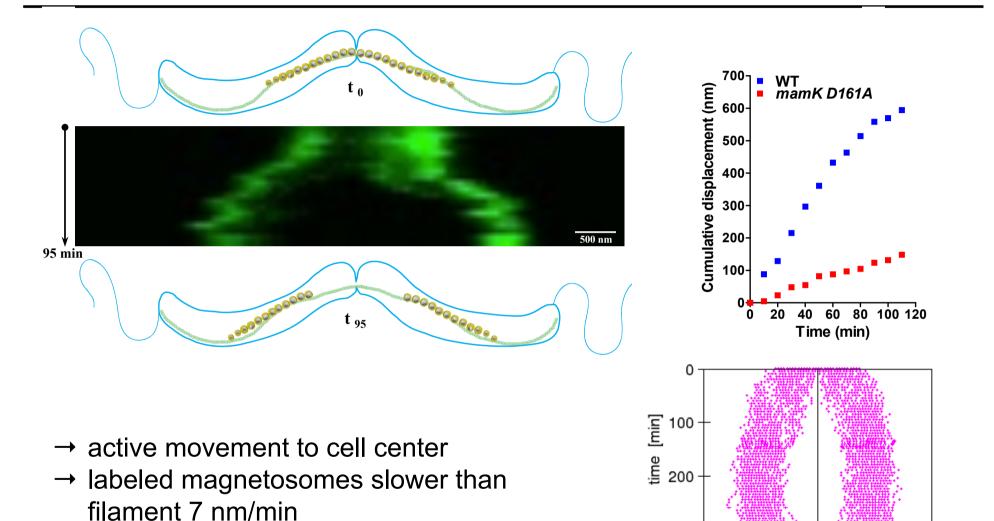






- labeled MamK travels to center from both poles
- speed 0.3 μm/min

Repositioning after cell division



→ dependent on hydrolysis by filament

Toro-Nahuelpan et al. BMC Biol. 2016

position [nm]

2000

300 -

-2000

Summary

magnetotactic bacteria: model system to study role of physics in biology

- magnetism: new functions + constraints
- many interesting problems to be studied
- key role of active processes
- challenge: generic physical forces and specific signals (chemotactic signaling etc.)

