

09:01 kokejcha:~/demo> |

issaso@kokeicha: ~/demo 94x44

sohpc-ffea / FFEA -- Bitbucket - Mozilla Firefox

sohpc-ffea / FFEA -- ... x

Multi-scale Modelling of Molecular Motors with Fluctuating Finite Element Analysis

Sarah Anne Harris

School of Physics and Astronomy

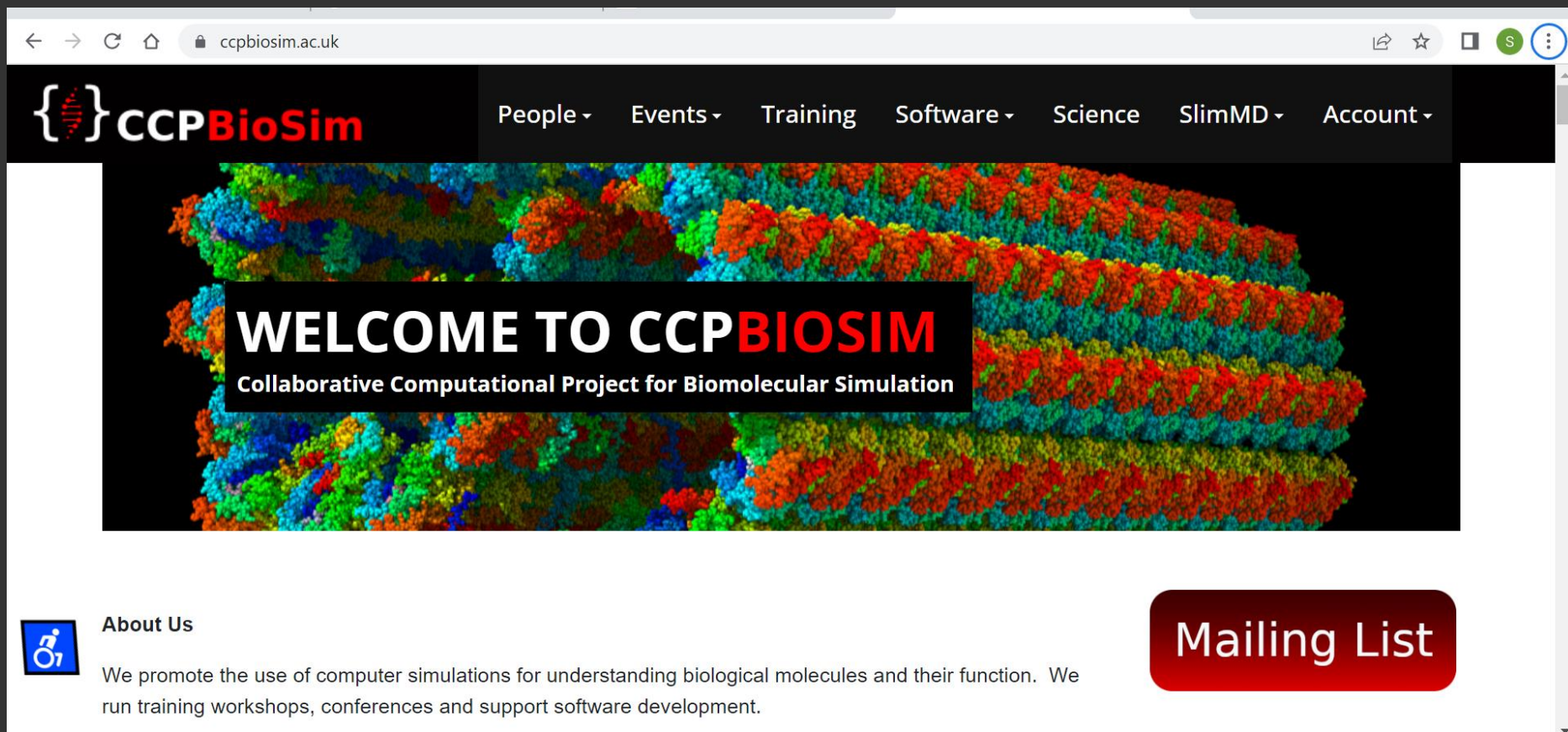
Astbury Centre for Structural and Molecular Biology

University of Leeds, UK

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CCPBioSim Network – Please join us!!

<https://www.ccpbiosim.ac.uk/>



The screenshot shows the CCPBioSim website homepage. At the top, there is a navigation bar with the CCPBioSim logo on the left and a menu with items: People, Events, Training, Software, Science, SlimMD, and Account. Below the navigation bar is a large banner image featuring a colorful, multi-layered molecular simulation structure. Overlaid on this image is a black box containing the text: "WELCOME TO CCPBIOSIM" in large white and red letters, and "Collaborative Computational Project for Biomolecular Simulation" in smaller white text below it. At the bottom left, there is an "About Us" section with a small icon of a person and a computer, followed by the text: "We promote the use of computer simulations for understanding biological molecules and their function. We run training workshops, conferences and support software development." At the bottom right, there is a prominent red button with the text "Mailing List".

CCPBioSim

People ▾ Events ▾ Training Software ▾ Science SlimMD ▾ Account ▾

WELCOME TO CCPBIOSIM
Collaborative Computational Project for Biomolecular Simulation

About Us

We promote the use of computer simulations for understanding biological molecules and their function. We run training workshops, conferences and support software development.

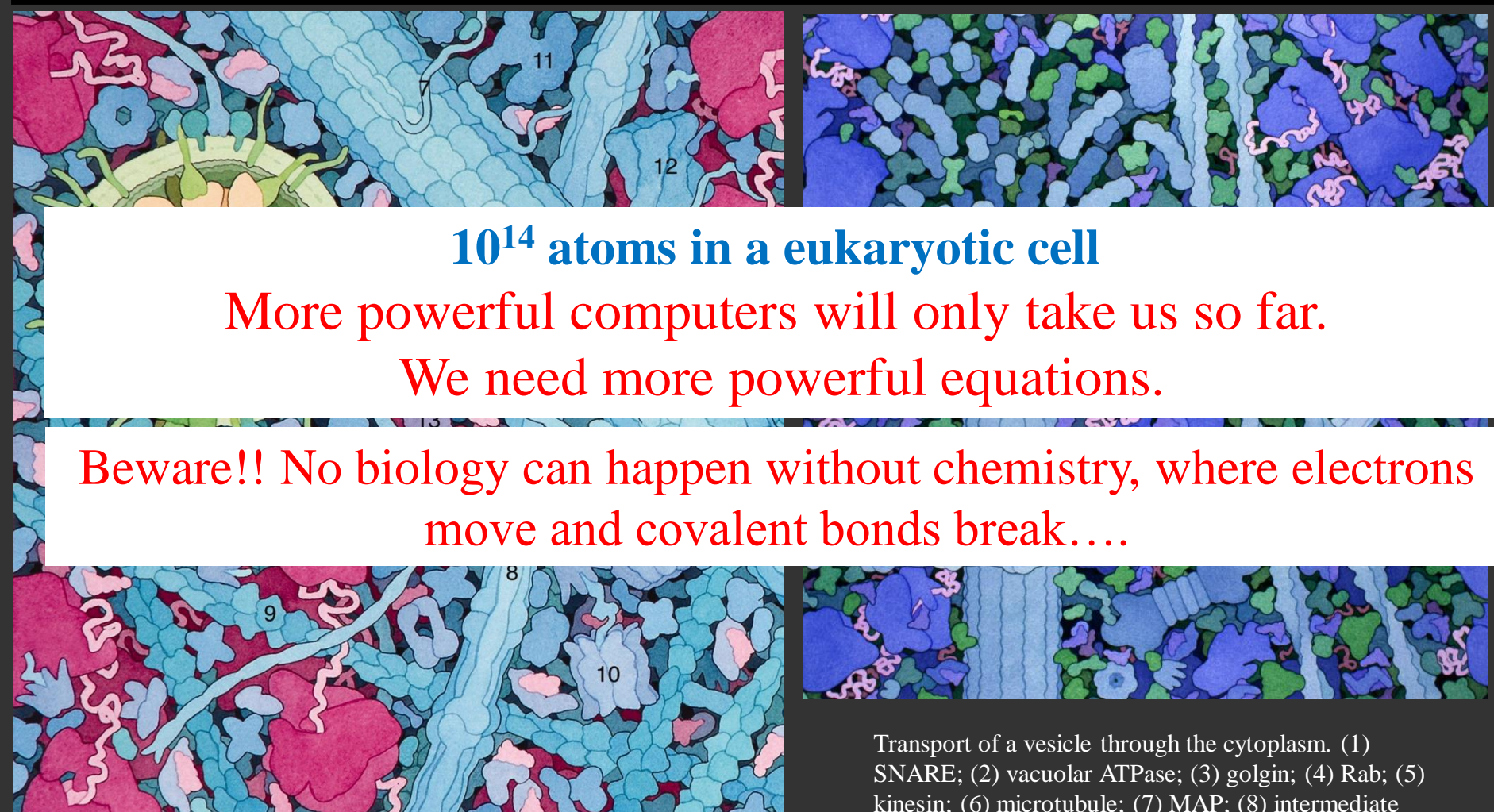
Mailing List

The Cytoplasm is Packed with Motors

10^{14} atoms in a eukaryotic cell

**More powerful computers will only take us so far.
We need more powerful equations.**

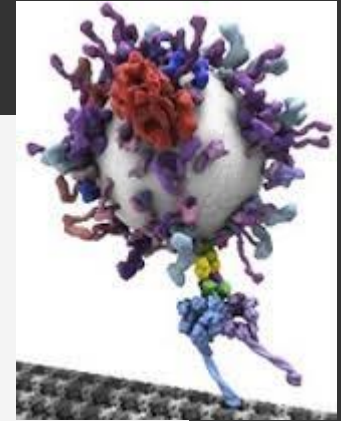
Beware!! No biology can happen without chemistry, where electrons move and covalent bonds break....



Transport of a vesicle through the cytoplasm. (1) SNARE; (2) vacuolar ATPase; (3) golgin; (4) Rab; (5) kinesin; (6) microtubule; (7) MAP; (8) intermediate filament; (9) actin; (10) TRiC/CCT chaperonin; (11) fatty acid synthase; (12) calcium/calmodul independent protein kinase II; (13) caspase 7 and XIAP

Cytoplasmic Dynein Walking

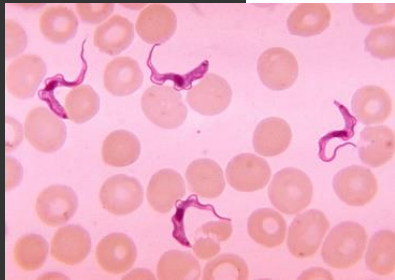
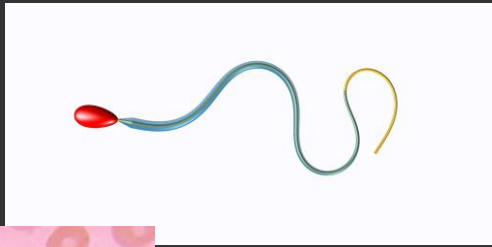
Cytoplasmic dynein transports cargo along microtubules
(towards the cell center!)



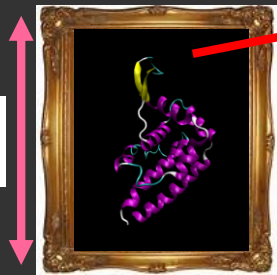
The Axoneme ~ A Macromolecular Machine

Hermes Gadelha, York

Sperm

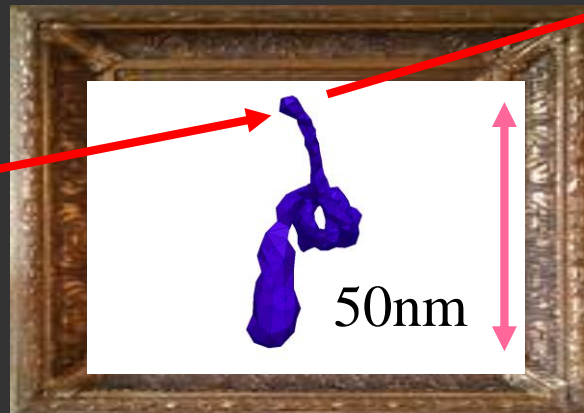


Trypanosomes



10nm

Dynein MTBD



50nm

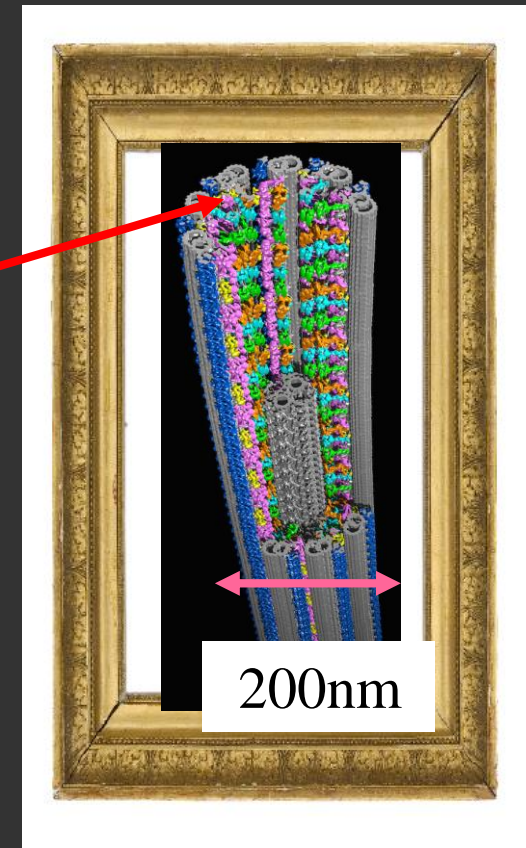
Dynein Motor

~1 million atoms in water (no tail)

16 dyneins in 96nm repeat; 9 MT doublets

50-100×96nm = 5-10μm length

6×10⁸ atoms (non solvent)

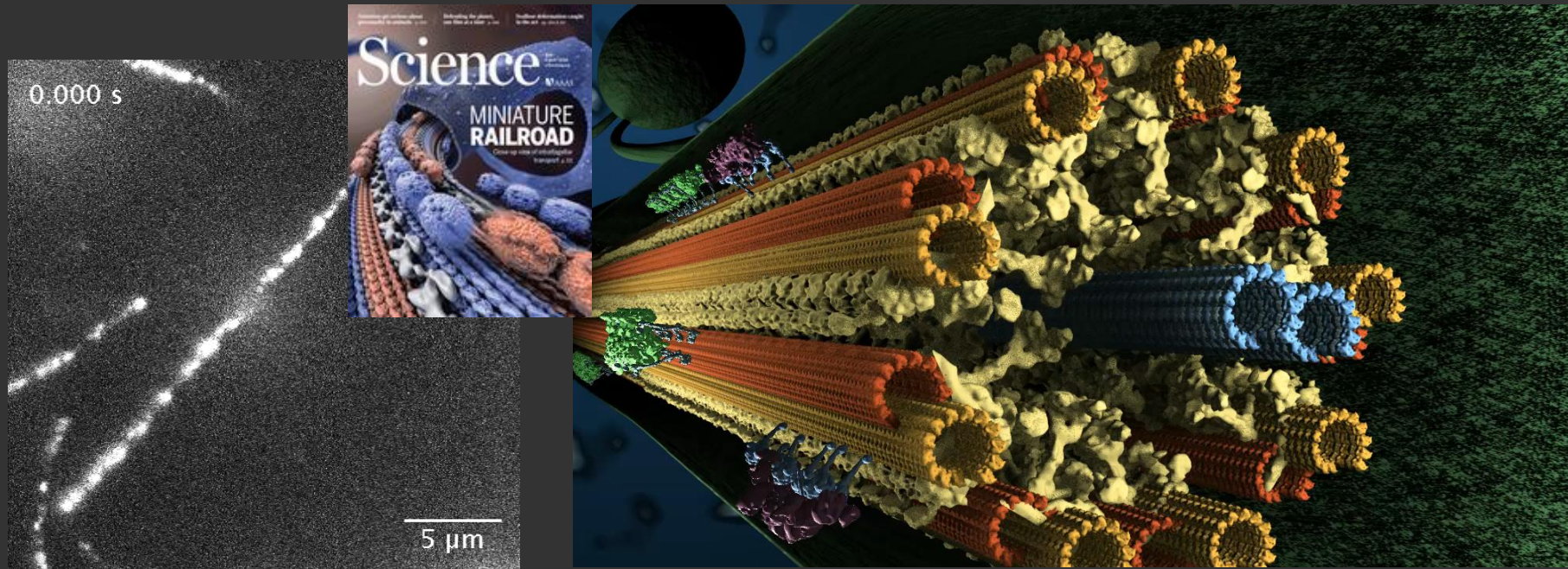


200nm

Cryo-ET Nicastro lab
Axoneme

Constructing the Axoneme: An Animation

TIRF microscopy of GFP labelled IFT trains in *Chlamydomonas* flagella attached to a coverslip. After 8 sec the movement is stopped by glutaraldehyde fixation.

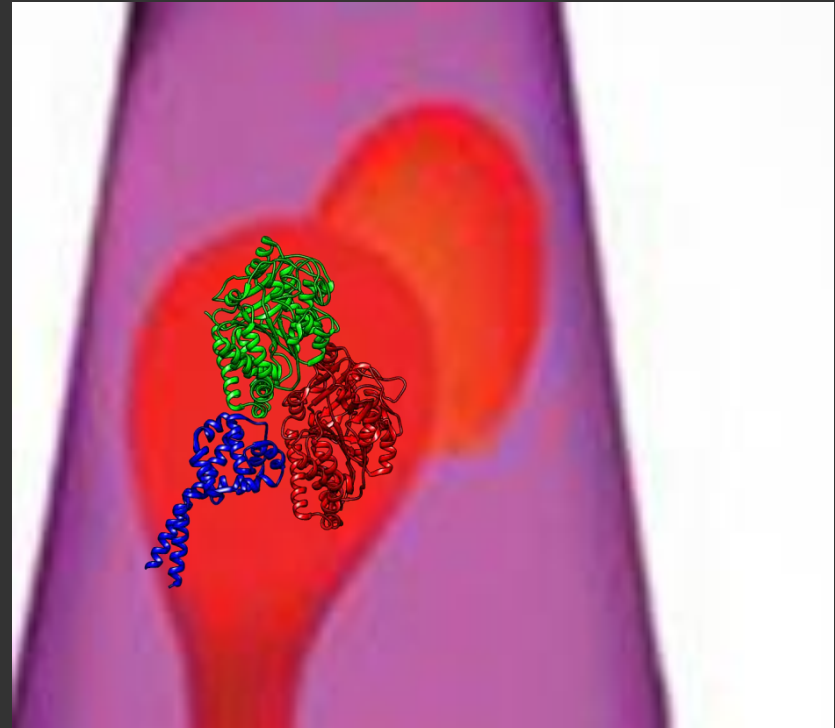


Animation by Bara Malkova for Pigino group

<https://www.mpi-cbg.de/en/research-groups/current-groups/gaia-pigino/gallery/>

Nicastro axoneme movie: <https://www.youtube.com/watch?v=9nZYlyFGm50>

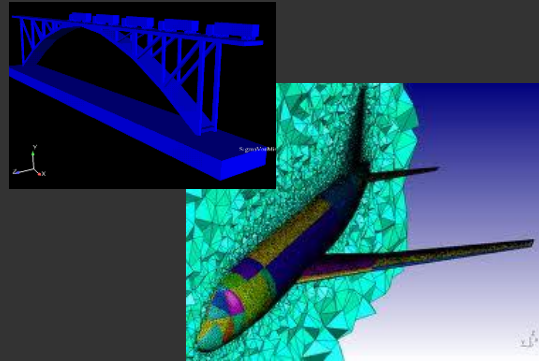
A New Mechanics for Soft Matter: FFEA



Fluctuating Finite Element Analysis (FFEA): proteins are continuum viscoelastic solids experiencing thermal noise

Fluctuating-Finite Element Analysis (FFEA)

FEA describes the shape of a complex object using a 3D mesh.



To model protein dynamics, FFEA includes a thermal noise term.

Change of momentum

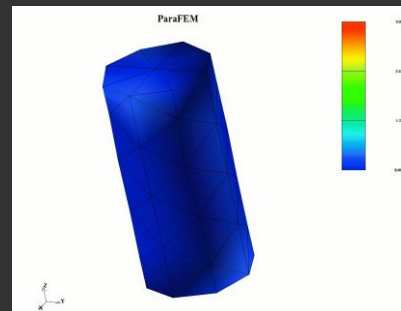
$$\rho \frac{D\mathbf{u}}{Dt} = \nabla \cdot (\boldsymbol{\sigma}^e + \boldsymbol{\sigma}^v + \boldsymbol{\sigma}^t)$$

Thermal noise
New in FFEA

Viscous dissipation
“Liquid”-like

Elastic stresses
“Solid”-like

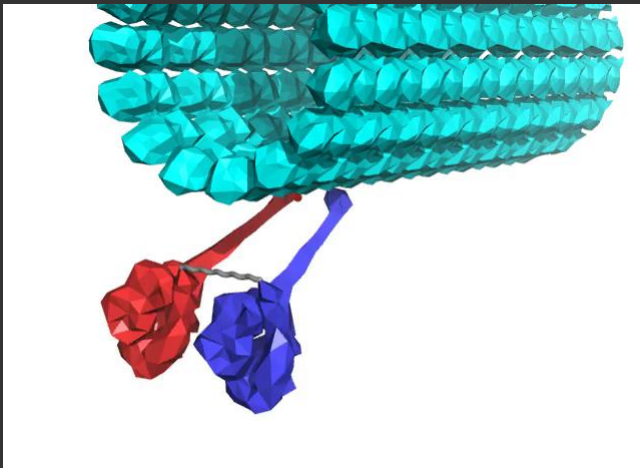
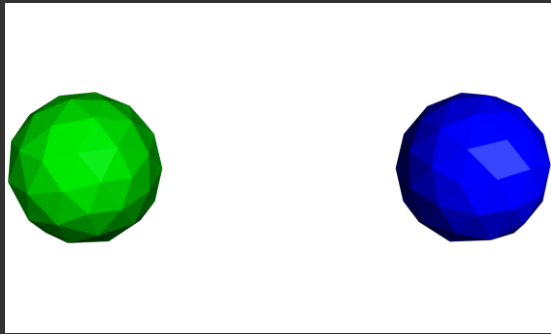
A fluctuating
“jelly” model of
a protein



FFEA is a new *continuum* method for bio-simulation appropriate for length-scales between 10 and 500nm (and larger)

FFEA Simulation Workflow

Volumetric Mesh generation from cryo-ET is non-trivial!



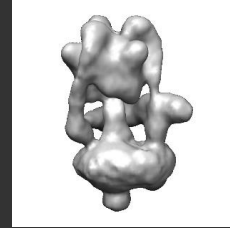
EMDB/PDB file



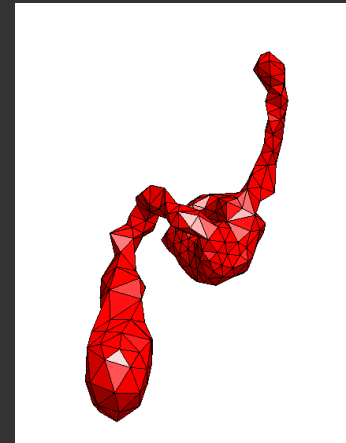
50nm



30nm



Generate mesh

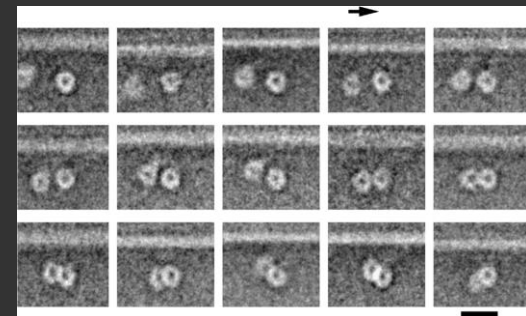


Assign material parameters & protein-protein interactions

FFEA

Analyse trajectory

Richardson *et al*, Proteins, 2014



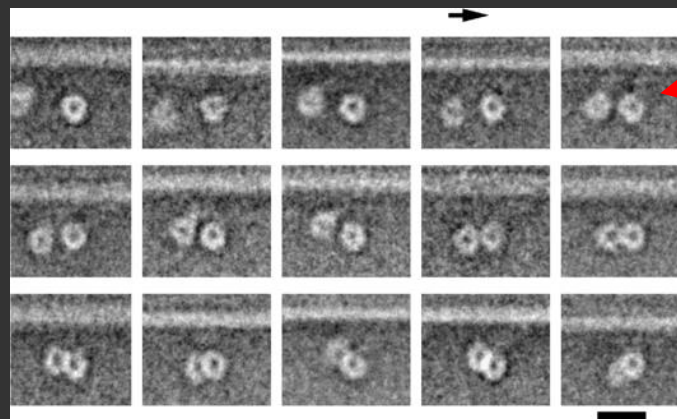
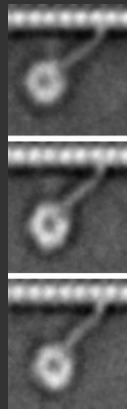
Imai *et al* Nat Comm 2015

Cryo-EM of Cytoplasmic Dynein

Cryo-EM of truncated cytoplasmic dynein shows the static conformations that dynein adopts while walking.



X-ray crystal structure
Kon et al NSMB 2011/Nature 2012

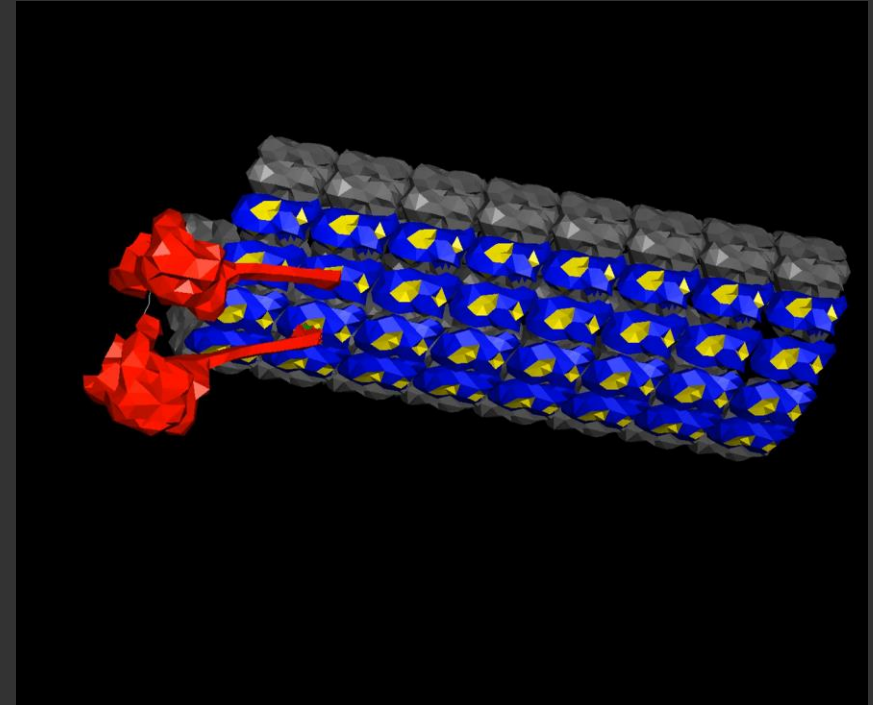
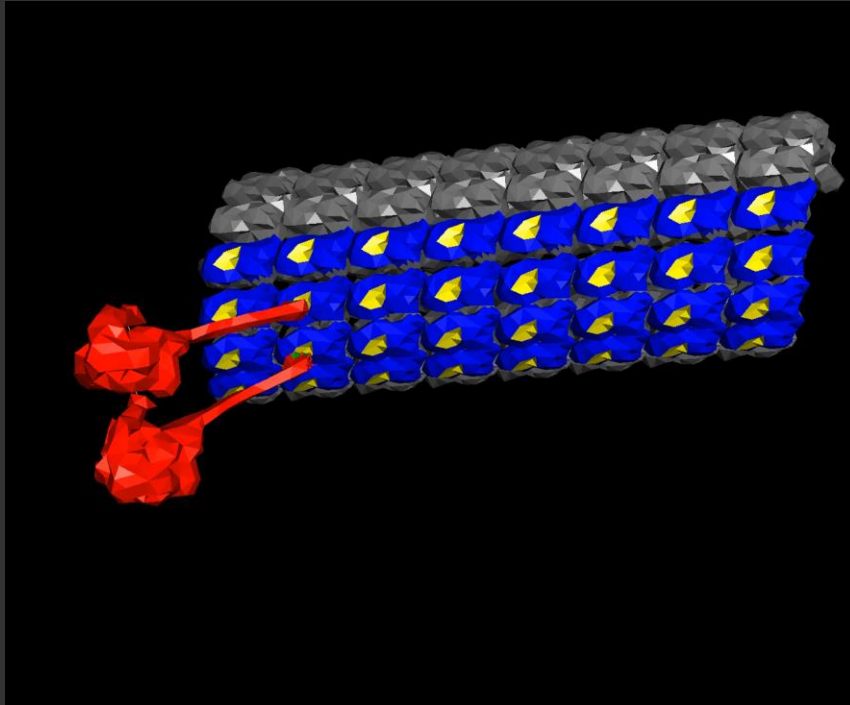


Dimers dissociate
during walking

Imai *et al* Nat Comm 2015

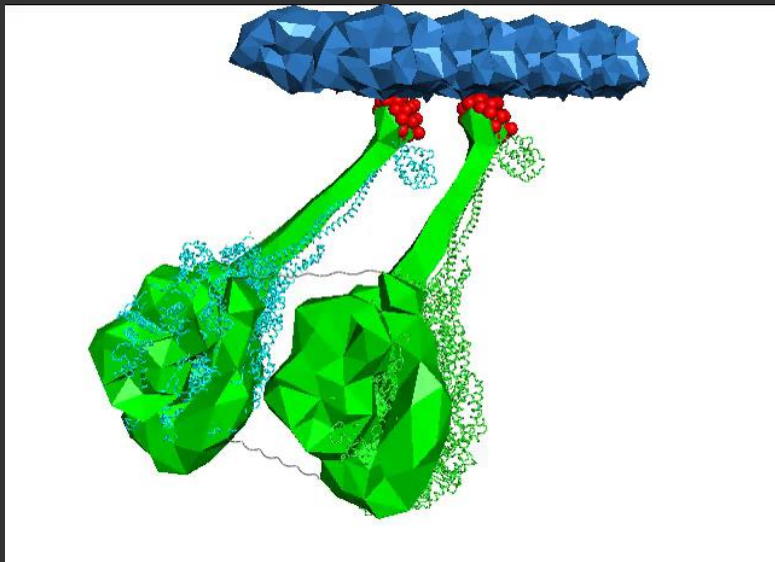
Can we use FFEA to turn these static picture into a mechanical model of dynein walking?

Apply a weakly attractive potential (blue) and strongly attractive (yellow) for the specific motor binding sites
FFEA over $\sim\mu\text{s}$ timescales



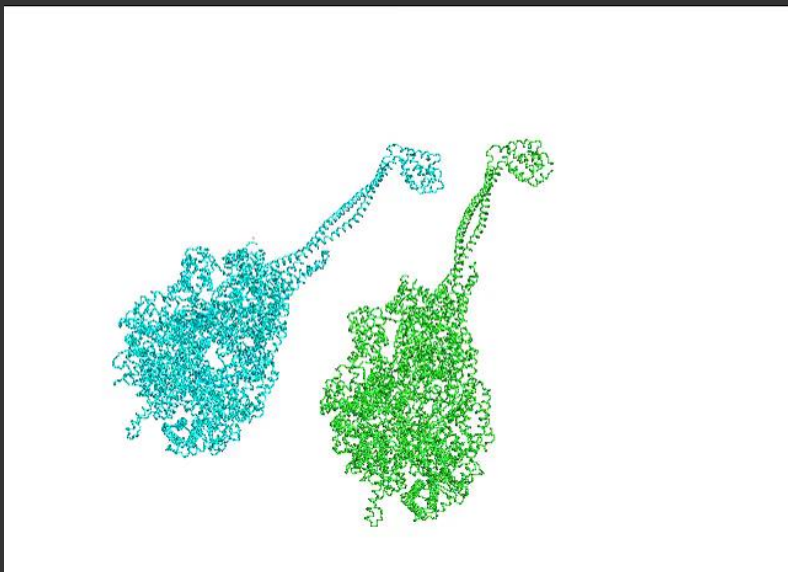
FFEA shows motor processivity is only achievable with a weak non-specific potential

From FFEA to Atomistic Models



FFEA models can be mapped back onto atomistic co-ordinates

Can make point mutations/add ligands etc, re-parameterise, assess effect on mesoscale!!

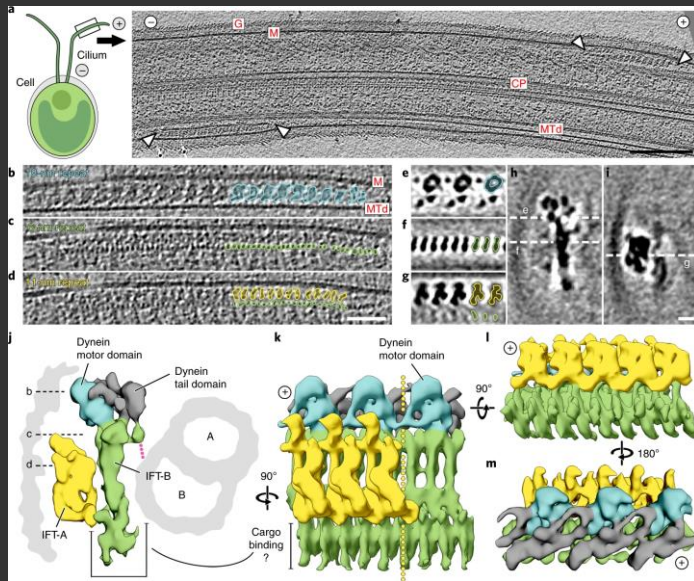


*Atomistic MD of dynein monomer:
980 265 atoms, 53 443 in dynein
See Kamiya et al, PEDS, 2016
(Dimer 1 636 455 total, 106,886 in dynein)*

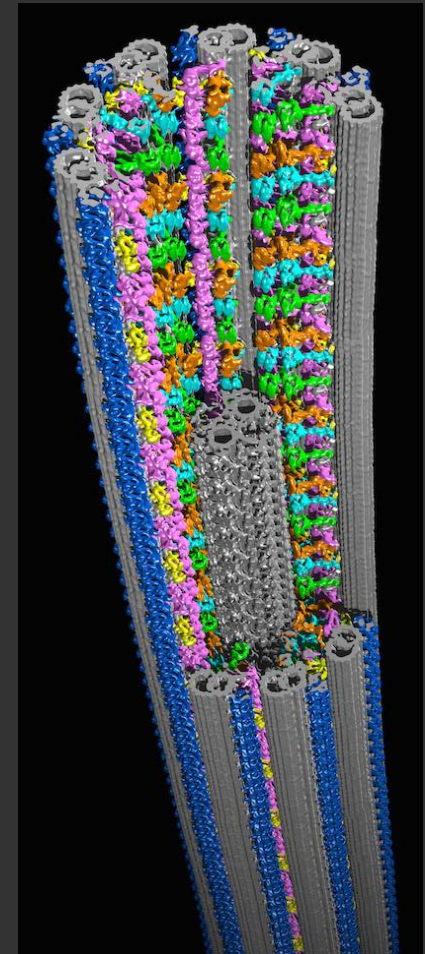
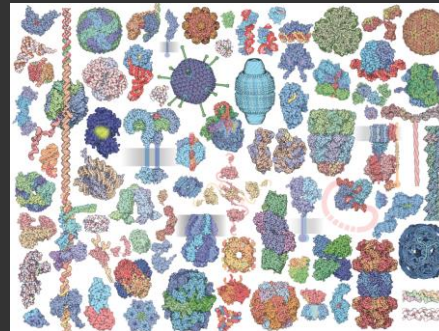
From cryo-ET to FFEA models

How can we construct hierarchical dynamic models of subcellular structures?

Pigino lab: NCB 2018



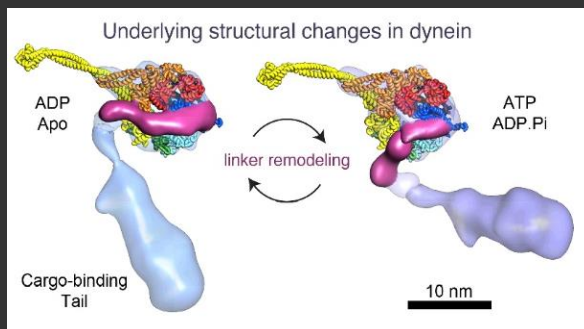
Identify molecular components



Assign multiple conformers



Automatic mesh generation



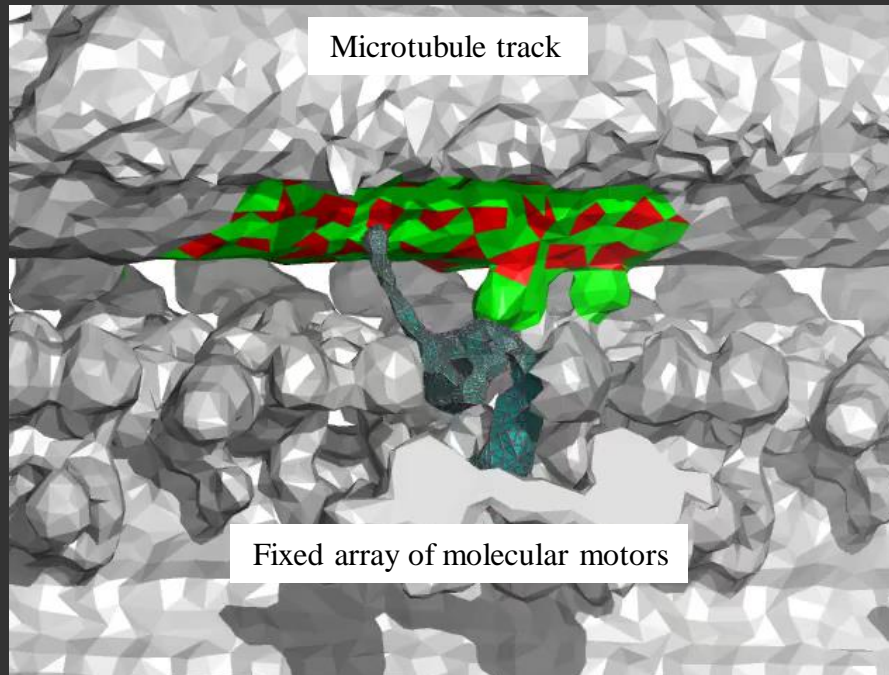
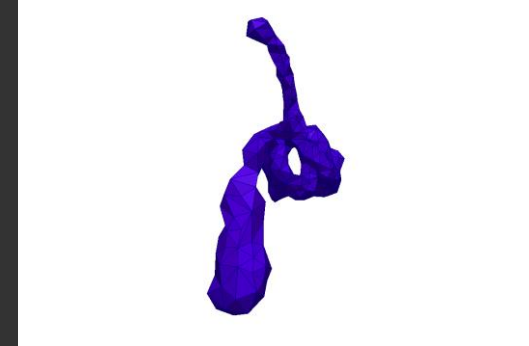
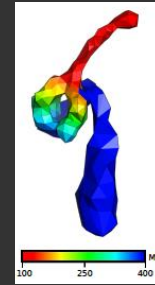
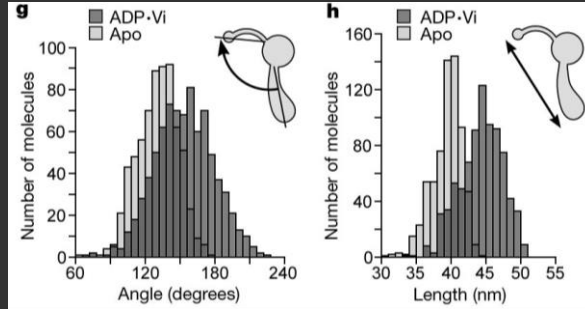
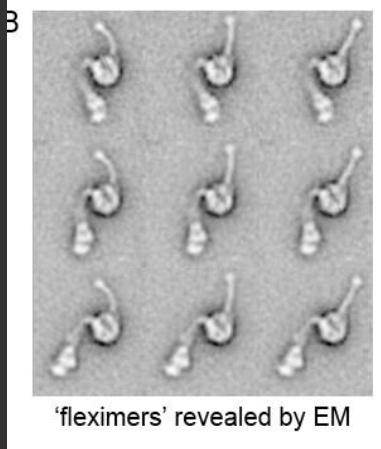
Roberts *et al*, *Structure* (2012), 20 1670

Nicastro lab

Assign material parameters:

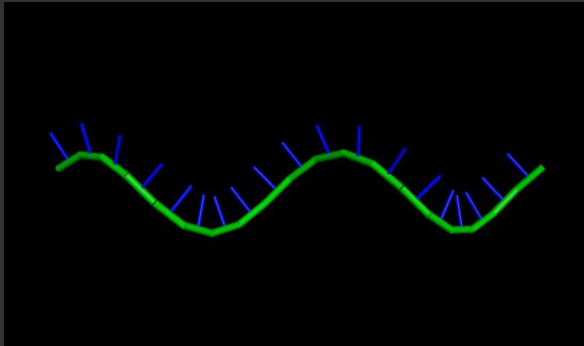
- i) Experimental data ii) MD simulations

(Hanson, Methods 2020; Richardson QRB 2020)

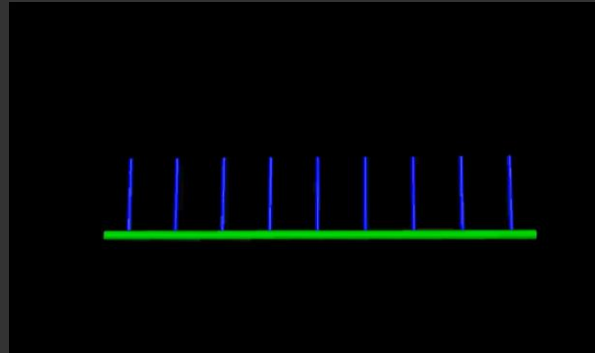


FFEA with Rods

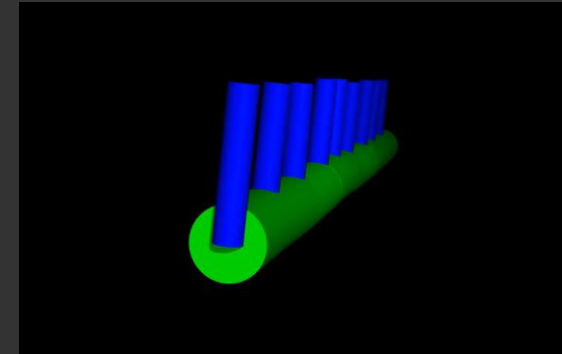
Twist



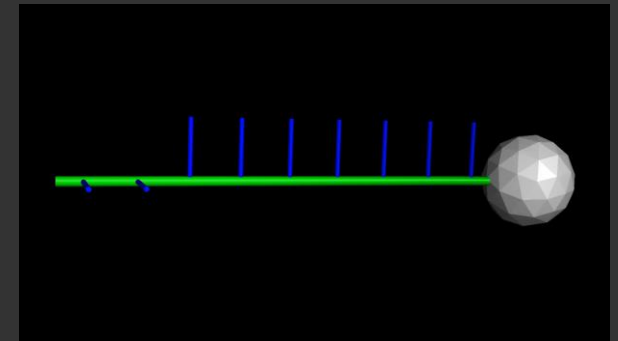
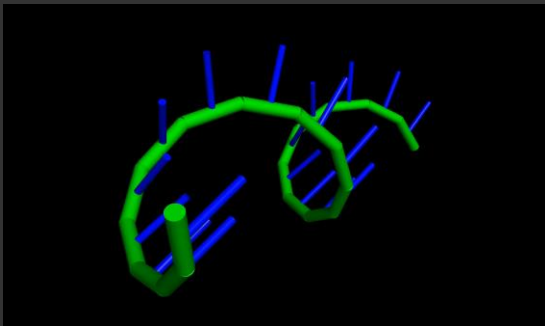
Hinge



Wobble



Rods+blobs

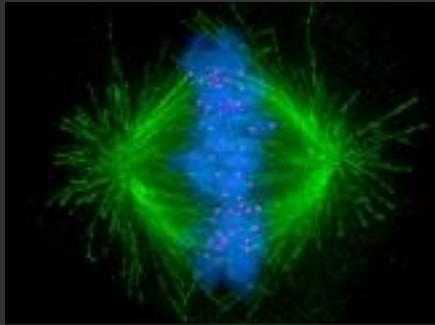


Long objects are inefficient for tetrahedral meshing

Welch et al Soft Matter 2020 “KOBRA: a fluctuating elastic rod model for slender biological macromolecules”

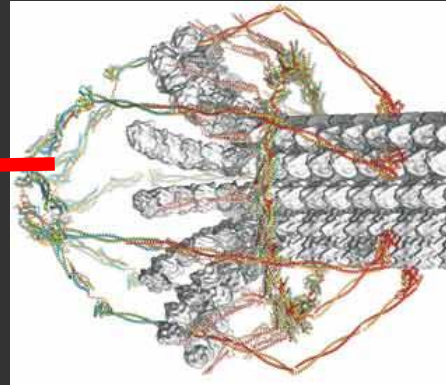
We are also intending to include 2D sheets (e.g. for membrane modelling)

Simulations of the Kinetochore Lateral Attachment with FFEA



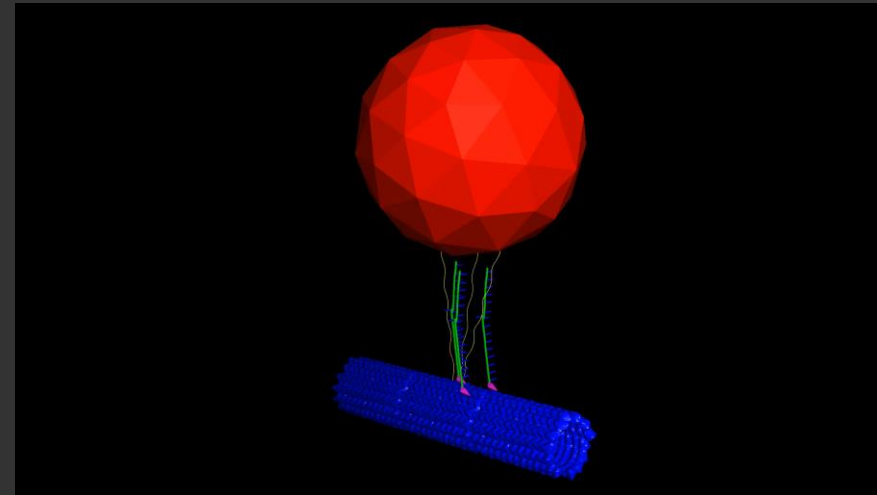
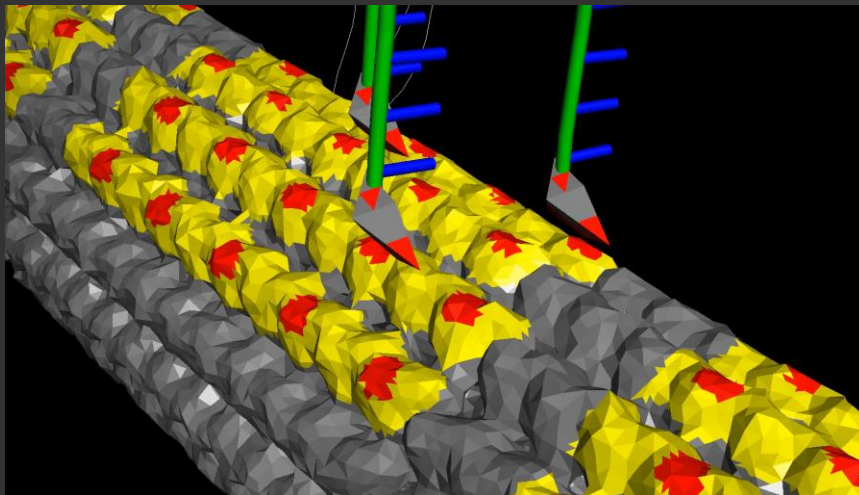
Microtubules green,
chromosomes (DNA) in blue
(Eva nogales)

DNA



The Kinetochore

Jenni & Harrison, Science, 2018



Modelling Philosophy

Experiment



Simulation

Data Analysis

<http://ffea.bitbucket.io/>
Solernou et al, PLoS Comp. Bio 2018

FFEA Funding ~ EPSRC/BBSRC

