Coarse Graining and Mesoscopic Simulations

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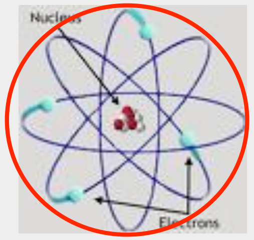
Contents:

- What are we doing and why?
- Inverse Monte-Carlo
- Langevin/Brownian dynamics
- Stochastic rotational dynamics
- Dissipative particle dynamics
- The Lowe-Andersen thermostat
- Local thermostats in MD.
- Case study: Free energy of confinement of a polymer
- Case study: The dynamics of mesoscopic bio-filaments
  (and how to do rigid constraints)

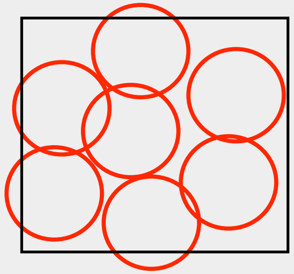
What is coarse graining?

Answer: grouping things together and treating them as one object

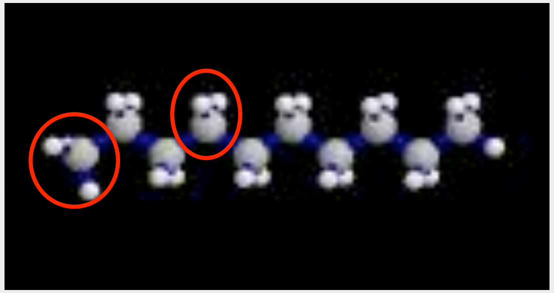
You are already familiar with the concept.



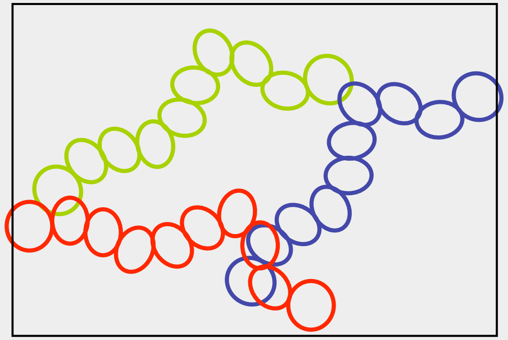
Quantum MD



Classical MD



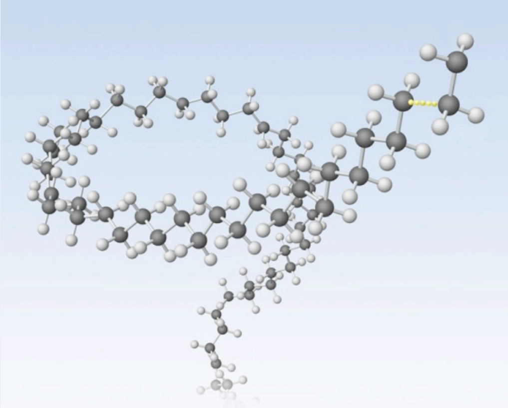
n-Alkane



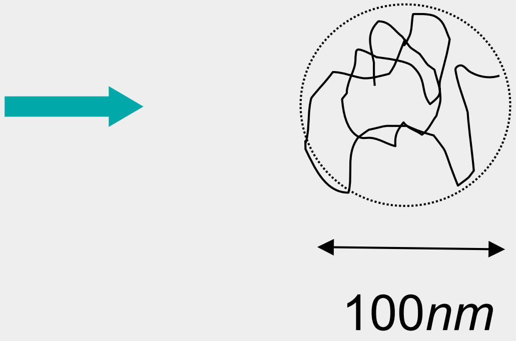
United atom model

What is mesocopic simulation?

Answer: extreme coarse graining to treat things on the mesoscopic scale (The scale ~ 100nm which is huge by atomic standards but where fluctuations are still relevant)

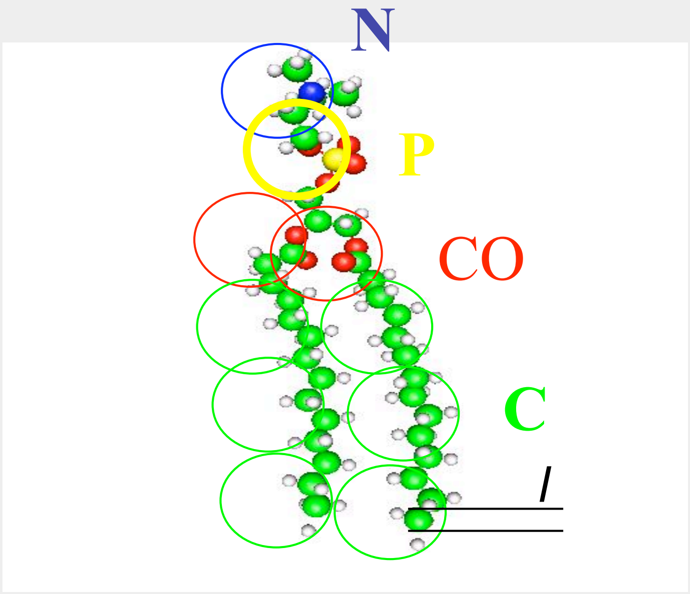


long polymer

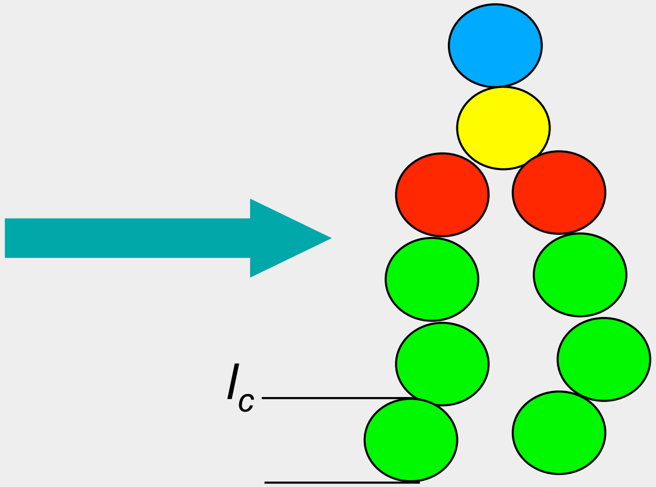


What are the benefits of coarse graining?

Why stop there? Eg. this lipid



All-atom model
118 atoms

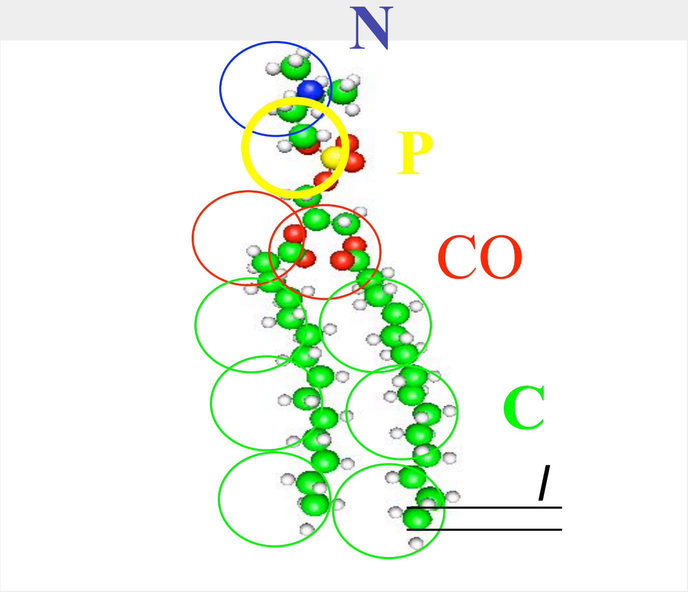


Coarse-grained model
10 sites

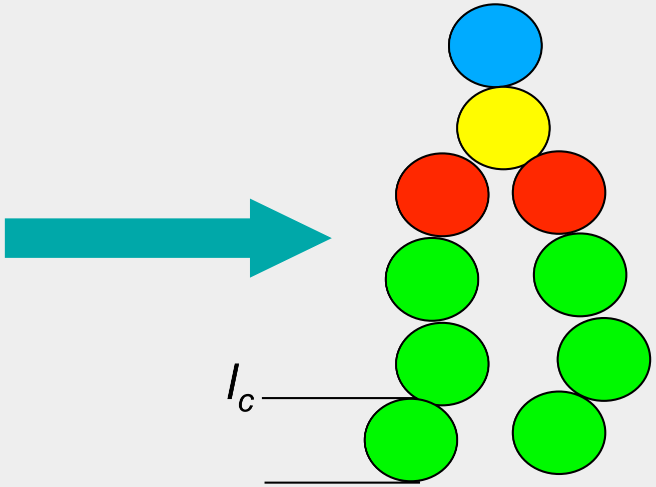
CPU per time step at least 100 times less (or even better)

What are the benefits of coarse graining?

Why stop there? Eg. this lipid



All-atom model
118 atoms



Coarse-grained model
10 sites

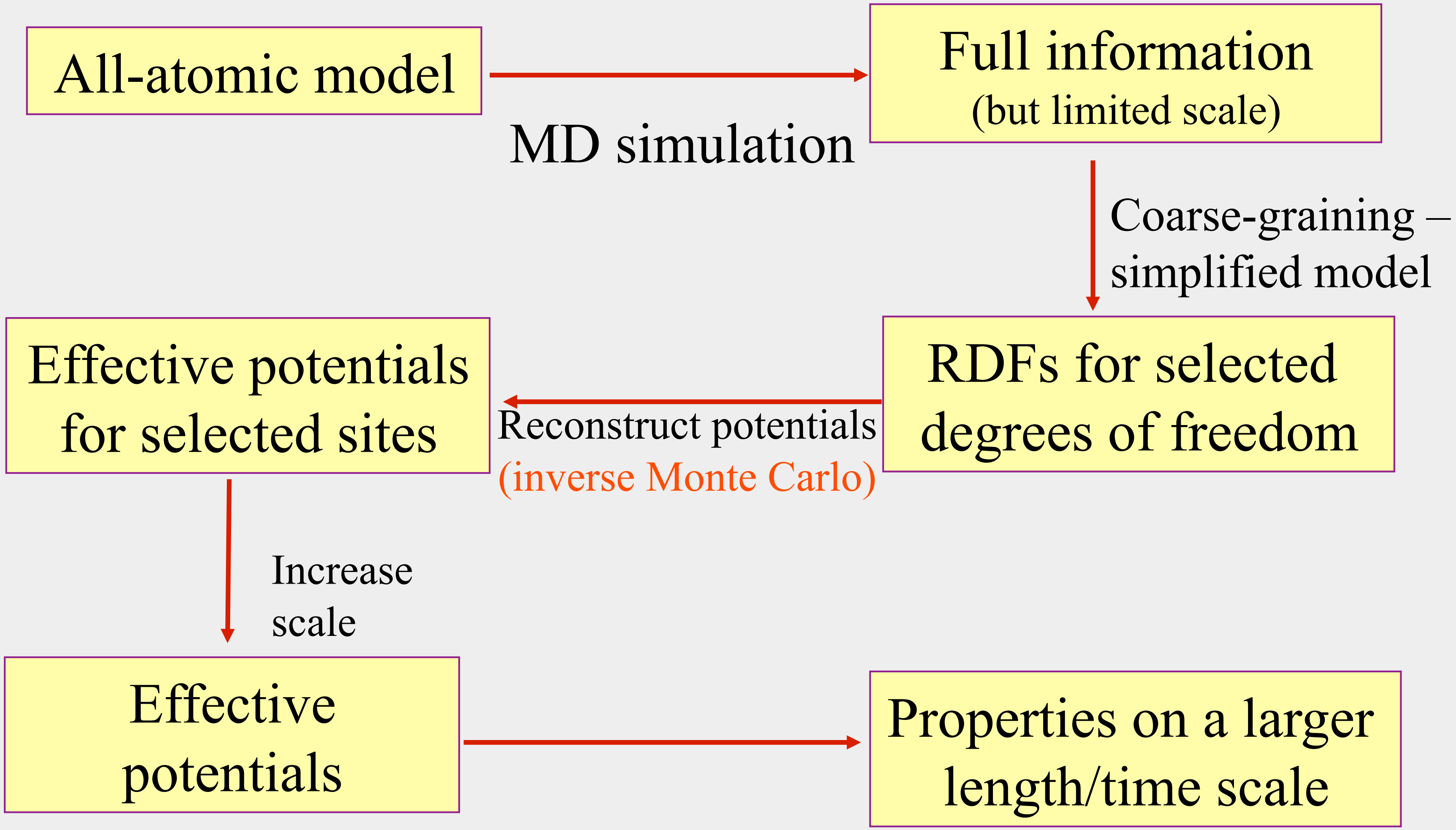
Maximum time-step

$$\Delta t_{\max} \sim l\sqrt{\frac{m}{kT}}$$

$$\Delta t_{\max} \sim l_c\sqrt{\frac{m_c}{kT}}$$

Longer time-steps possible

Coarse graining with inverse Monte Carlo



All-atomic model

MD simulation

Full information
(but limited scale)

Coarse-graining –
simplified model

RDFs for selected
degrees of freedom

Reconstruct potentials
(inverse Monte Carlo)

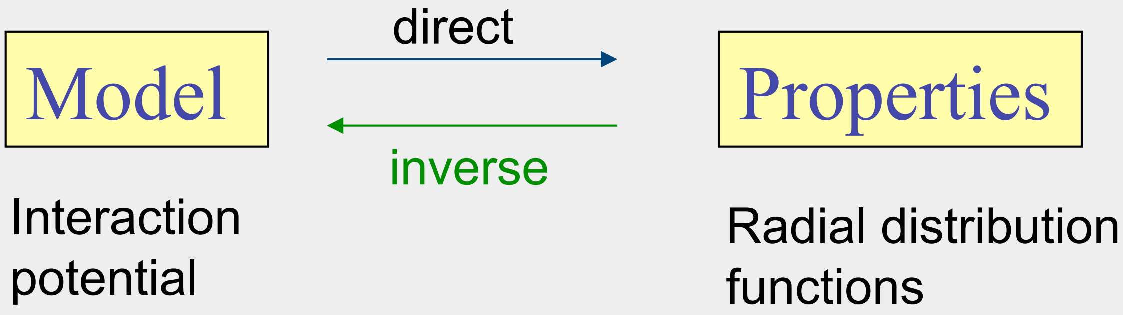
Effective potentials
for selected sites

Increase
scale

Effective
potentials

Properties on a larger
length/time scale

Inverse Monte Carlo



Model

direct

inverse

Properties

Interaction potential

Radial distribution functions

- Effective potentials for coarse-grained models from "lower level" simulations

- Effective potential = potential used to produce certain characteristics of the real system

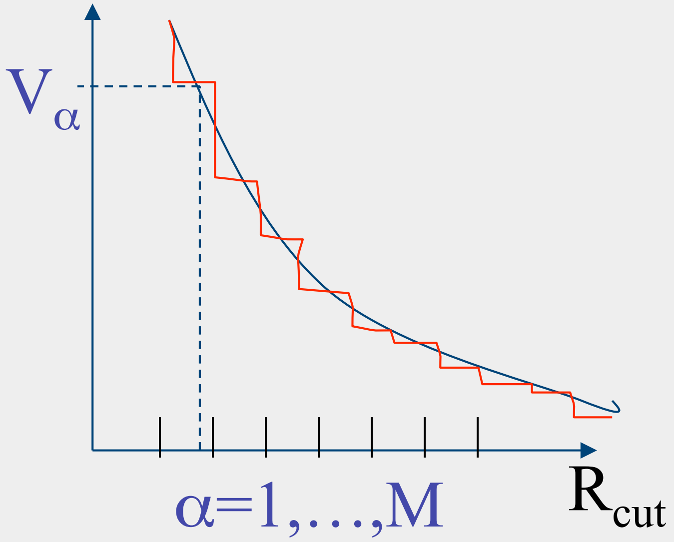
- Reconstruct effective potential from experimental RDF

Inverse Monte Carlo

(A.Lyubartsev and A.Laaksonen, Phys.Rev.A.,52,3730 (1995))

Consider Hamiltonian with pair interaction:

$$H = \sum_{i,j} V(r_{ij})$$



Make "grid approximation":

Hamiltonian can be rewritten as:

$$H = \sum_{\alpha} V_\alpha S_\alpha$$

Where $V_\alpha=V(R_{cut}\alpha/M)$ - potential within α-interval,
S_α - number of particle's pairs with distance between them within α-interval

S_α is an estimator of RDF:

$$g(r_\alpha) = \frac{1}{4\pi r_\alpha^2 \Delta r} \frac{V}{N^2/2} \langle S_\alpha \rangle$$

Inverse Monte Carlo

In the vicinity of an arbitrary point in the space of Hamiltonians one can write:

$$\Delta\langle S_\alpha\rangle = \sum_\gamma \frac{\partial\langle S_\alpha\rangle}{\partial V_\gamma}\Delta V_\gamma + O(\Delta V^2)$$

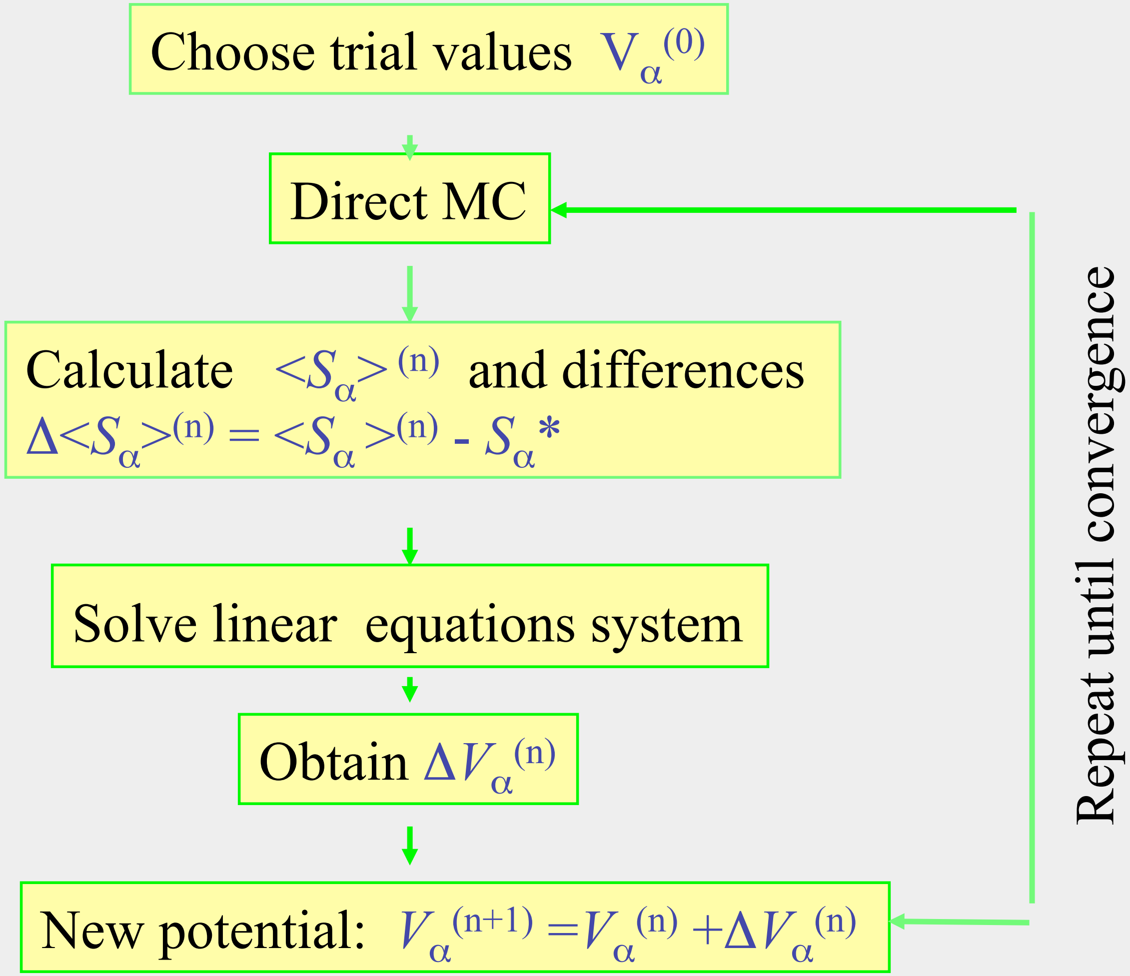
where

$$\frac{\partial\langle S_\alpha\rangle}{\partial V_\gamma} = \frac{\partial}{\partial V_\gamma}\left(\frac{\int dq S_\alpha(q)\exp\left(-\beta\sum_\lambda V_\lambda S_\lambda(q)\right)}{\int dq \exp\left(-\beta\sum_\lambda V_\lambda S_\lambda(q)\right)}\right) = -\beta\left(\langle S_\alpha S_\gamma\rangle - \langle S_\alpha\rangle\langle S_\gamma\rangle\right)$$

with

$$\beta = 1/kT,\quad q = \{\vec{r}_1,\ldots,\vec{r}_N\}$$

Inverse Monte Carlo



Choose trial values $V_\alpha^{(0)}$

Direct MC

Calculate $\langle S_\alpha \rangle^{(n)}$ and differences
$\Delta \langle S_\alpha \rangle^{(n)} = \langle S_\alpha \rangle^{(n)} - S_\alpha^*$

Solve linear equations system

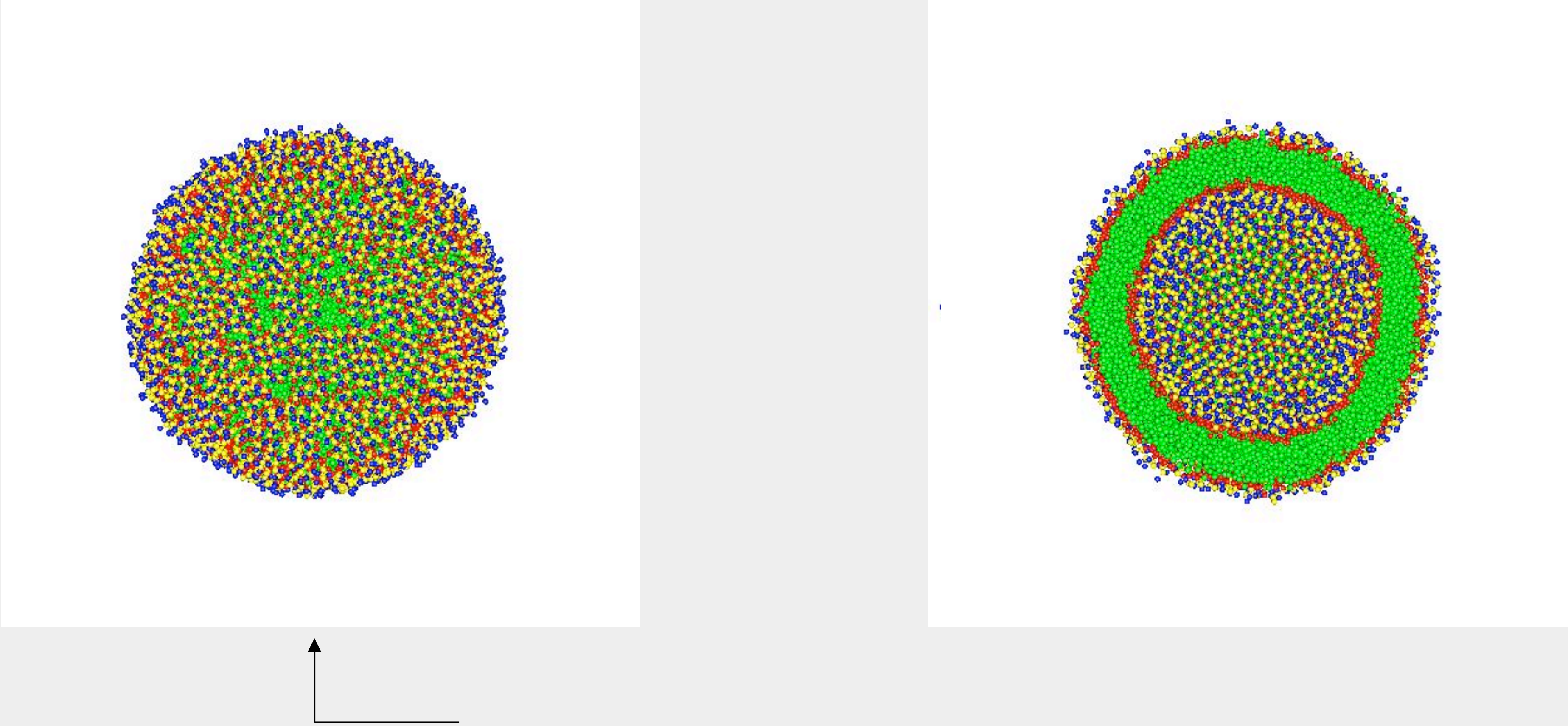
Obtain $\Delta V_\alpha^{(n)}$

New potential: $V_\alpha^{(n+1)} = V_\alpha^{(n)} + \Delta V_\alpha^{(n)}$

Repeat until convergence

Example: vesicle formation

Starting from a square plain piece of membrane, 325x325 Å, 3592 lipids:
(courtesy of Alexander Lyubartsev)



cut plane

The dispersed phase problem

Many important problems involve one boring species (usually a solvent) present in abundance and another intersting speices that is a large molecule or molecular structure.

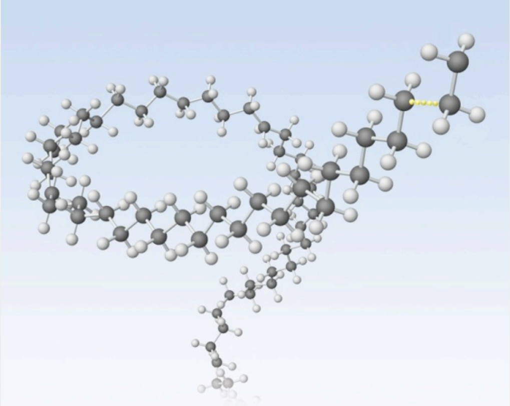
Examples

- Polymer solutions
- Colloidal suspensions
- Aggregates in solution

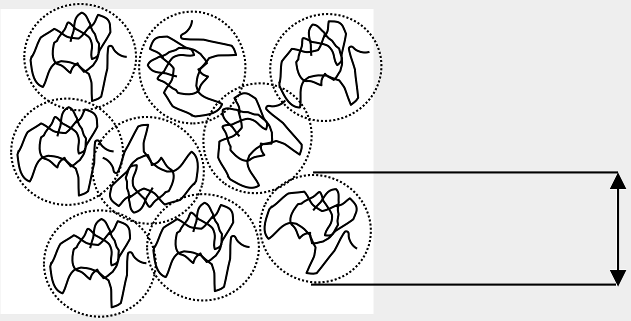
This is very problematic

The dispersed phase problem

Polymers are long molecules consisting of a large number N (up to many millions) of repeating units. For example polyethylene



Consider a polymer solution at the overlap concentration (where the polymers roughly occupy all space)



$L \sim N^{1/2} b$

where b is of the order of the monomer size

The dispersed phase problem

Volume fraction of momomers $\phi_m \sim \frac{1}{N^{1/2}}$

Volume fraction of solvent

(assuming solvent molecules similar in size to monomers) $\phi_s \sim \frac{N_s b^3}{N^{3/2} b^3} \sim 1 - \frac{1}{N^{1/2}} \sim 1$

Number of solvent molecules per polymer $N_s \sim N^{3/2}$

So, if N=10^6, not unreasonable, we need 10^9 solvent molecules per polymer

Time-scale

Configurations change on the time-scale it takes the polymer to diffuse a distance of its own size τ_D. From the diffusion equation root mean squared displacement Δ as a function of time t is

$$\Delta^2 = 6Dt$$

$$\rightarrow \quad \tau_D \sim \frac{L^2}{D}$$

Experimentally: b (polyethylene) = 5.10^{-10}m
b(DNA) = 5.10^{-8}m
So for N=10^6 l_p(polyethylene) = 5.10^{-7}m (1/2μ)
l_p(DNA) = 5.10^{-5}m (50μ)

Use Stokes-Einstein to estimate $D \sim \dfrac{kT}{6\pi\eta L}$

$$\left.\begin{array}{l}\text{k=Boltzmann's constant}\\ \text{T=Temperature}\\ \eta\text{=shear viscosity of solvent}\end{array}\right\} \begin{array}{l}\text{kT(room temp.)}\sim 4.10^{-14}\ \text{gcm}^2/\text{s}^2\\ \eta\text{(water)}\sim 0.01\ \text{g/cm s}\end{array}$$

So $\tau_D(\text{polyethylene}) \sim 1\,\text{s}\ (\sim 10^{12}\ \text{time-steps})$

$$\tau_D(dna) \sim 10^8\,\text{s}\ (\sim 10^{20}\ \text{time-steps})$$

Time-scale

Coarse graining required

Configurations change on the time-scale it takes the polymer to diffuse a distance of its own size τ_D. From the diffusion equation root mean squared displacement Δ as a function of time t is

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k=Boltzmann's constant
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η=shear viscosity of solvent

$\Big\}$ kT(room temp.)~4.10^{-14} gcm^2/s^2
η(water)~0.01 g/cm s

So $\tau_D(\text{polyethylene}) \sim 1\,\text{s}\,(\sim 10^{12}\ \text{time-steps})$

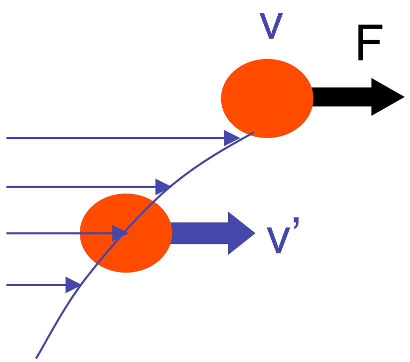
$$\tau_D(dna) \sim 10^8\,\text{s}\,(\sim 10^{20}\ \text{time-steps})$$

The ultimate solvent coarse graining

Throw it away and reduce the role of the solvent to:

1) Just including the thermal effects (i.e the fluctutations that jiggle the polymer around)

2) Including the thermal and fluid-like like behaviour of the solvent. This will include the “hyrodynamic interactions” between the monomers.



Hydrodynamic interactions

The Langevin Equation
(fluctuations only)

Solve a Langevin equation for the big phase:

Force on particle *i*

$$\boxed{m_i \frac{\partial \vec{v}_i}{\partial t}} = -\gamma \vec{v} + \vec{F}_R + \vec{F}_x$$

-γv is the friction force, here the friction coefficient is related to the monomer diffusion coeffiient by D=γkT

$\vec{F}_R$ is a random force with the property $\left\langle \vec{F}_R(t)\vec{F}_R(t') \right\rangle = 6kT\gamma\delta(t-t')$

$\vec{F}_x$ is the sum of all other forces

Many ways to solve this equation

Forbert HA, Chin SA. Phys Rev E 63, 016703 (2001)

It is basically a thermostat.

The Andersen thermostat

(fluctuations only)

Use an Andersen thermostat: A method that satisfies detailed balance (equilibium properties correct)

Integrate the equations of motion with a normal velocity Verlet algorithm

$$\vec{r}_i(t+\Delta t) = \vec{r}_i(t) + \Delta t \vec{v}_i(t) + \frac{\Delta t^2}{2m_i}\vec{F}(t)$$

$$\vec{v}_i(t+\Delta t) = \vec{v}_i(t) + \frac{\Delta t}{2m_i}\left(\vec{F}(t) + \vec{F}(t+\Delta t)\right)$$

Then with a probability $\Gamma\Delta$t (Γ is a “bath” collision probability) set

$$v_i(t+\Delta t) = \frac{kT}{m}\theta_i$$

Where θ_i is a Gaussian random number with zero mean and unit variance. (i.e. take a new velocity component from the correct Maxwellian)

Gives a velocity autocorrelation function C(t)=<v(0)v(t)>

$$C(t) = \frac{3kT}{m}\exp\left(-\Gamma t\right)$$

Identical to the Langevin equation with γ/m=Γ

Andersen vs Langevin

Question: Should I ever prefer a Langevin thermostat to an Andersen thermostat?

Answer: No. Because Andersen satisfies detailed balance you can use longer time-steps without producing significant errors in the equilibrium properties

(who cares that it is not a stochastic differential equation)

Brownian Dynamics

(fluctuations and hydrodynamics)

Use Brownian/Stokesian dynamics

Integrates over the inertial time in the Langevin equation and solve the corresponding Smoluchowski equation (a generalized diffusion equation). As such, only particle positions enter.

$$\vec{r}_i(t+\Delta t) = \vec{r}_i(t+\Delta t) + \Delta t \sum_j \frac{\vec{\vec{D}}_{ij} \cdot f_j(t)}{kT} + \delta\vec{r}_i^{\,G}$$

$\delta\vec{r}_i^{\,G}$ are "random" displacements that satisfy

$$\left\langle \delta\vec{r}_i^{\,G} \delta\vec{r}_j^{\,G} \right\rangle = 2\vec{\vec{D}}_{ij}\delta(t)$$

and $\vec{\vec{D}}_{ij}$ is the mobility tensor

D.L. Ermak and J.A. McCammon, J. Chem. Phys. 969, 1352 (1978)
"Computer simulations of liquids", M.P. Allen and D.J. Tildesley, (O.U. Press, 1987)

Brownian Dynamics

(fluctuations and hydrodynamics)

If the mobility tensor is approximated by

$$\vec{\vec{D}}_{ij} = \frac{kT}{6\pi\eta a}\,\vec{\vec{1}}; \qquad i = j$$

$$\vec{\vec{D}}_{ij} = 0; \qquad i \neq j$$

The algorithm is very simple. This corresponds to neglecting hydrodynamic interactions (HI)

Including HI requires the pair terms. A simple approximation based on the Oseen tensor (the flow generated by a point force) is.

$$\vec{\vec{D}}_{ij} = \frac{kT}{6\pi\eta a}\,\vec{\vec{1}}; \qquad i = j$$

$$\vec{\vec{D}}_{ij} = \frac{kT}{6\pi\eta r_{ij}}\left(\vec{\vec{1}} + \frac{\vec{r}_{ij}\vec{r}_{ij}}{r_{ij}^{2}}\right); \; i \neq j$$

For a more accurate descrition it is much more difficult but doable, see the work of Brady and co-workers.

A. J. Banchio and J. F. Brady J. Chem. Phys. 118, 10323 (2003)

Brownian Dynamics

(fluctuations and hydrodynamics)

Limitations:

- Computaionally demanding because of long range nature of mobility tensor
- Difficult to include boundaries
- Fundamentally only works if inertia can be completely neglected

So should I just neglect hydrodynamics: **NO**

(hydrodynamics are what make a fluid a fluid)

Simple explicit solvent methods

An alternative approach: Keep a solvent but make it as simple as possible (strive for an “ising fluid”).

What makes a fluid:

- Conservation of momentum
- Isotropy
- Gallilean Invariance
- The right relative time-scale

$$\tau_H = \frac{l^2}{\nu}$$

time it takes momentum to diffuse *l*

$$\tau_s = \frac{l}{C_s}$$

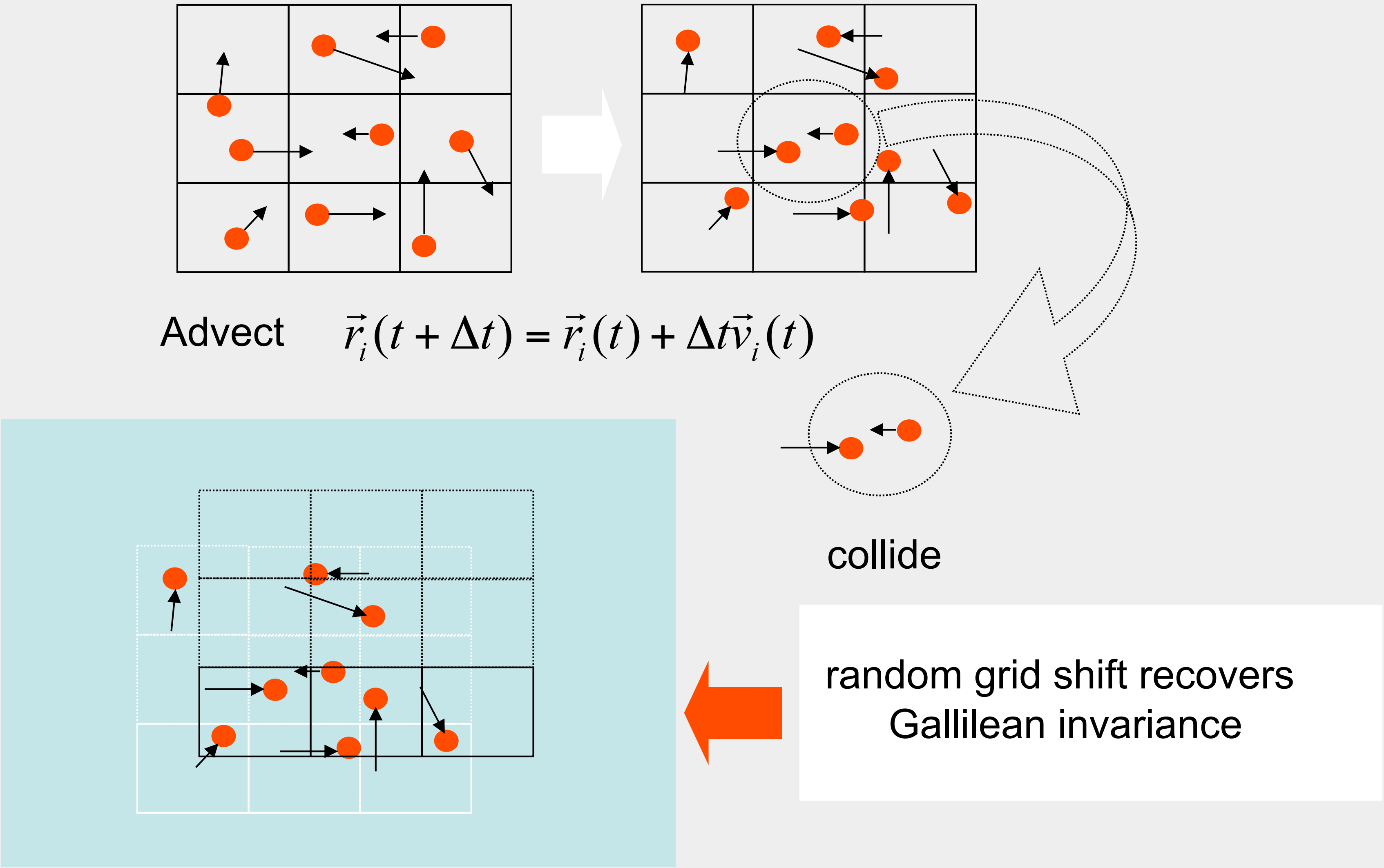
time it takes sound to travel *l*

$$\tau_D = \frac{l^2}{D}$$

time it takes to diffuse *l*

Stochastic Rotational dynamics

A. Malevanets and R. Kapral, J. Chem. Phys 110, 8605 (1999).



Advect $$\vec{r}_i(t+\Delta t) = \vec{r}_i(t) + \Delta t\,\vec{v}_i(t)$$

collide

random grid shift recovers
Gallilean invariance

Stochastic Rotational dynamics

Collide particles in same cell

$$\vec{v}_i' = \bar{v}(t) + R(v_i(t) - \bar{v}(t))$$

where the box centre of mass velocity is

$$\bar{v} = \frac{1}{N_{cell}} \sum_{cell} \bar{v}_i$$

basically rotates the relative velocity vector

with N_{cell} the number of particles in a given cell. R is the matrix for a rotation about a random axis

Advantages:

- Trendy
- Computationally simple
- Conserves mometum
- Conserves energy

Disadvantages

- Does not conserve angular momentum
- Introduces boxes
- Isotropy?
- Gallilean invariance jammed in by grid shift
- Conserves energy (need a thermostat for non-equilibrium simulations)

Stochastic Rotational dynamics

Equation of state: Ideal gas

Parametrically: exactly the same as all other ideal gas models
must fix

- number of particles per cell (cf ρ)
- degree of rotation per collision (cf Γ)
- number of cells traversed before velocity is decorrelated (cf Λ)

Time-scales

Transport coefficients: theoretical results accurate in the wrong range of parameters. For realistic parameters, must callibrate.

For an analysis see
J.T. Padding abd A.A. Louis, Phys. Rev. Lett. 93, 2201601 (2004)

Dissipative Particle Dynamics

part 1: the method

First introduced by Koelman and Hoogerbrugge as an “off-lattice lattice gas” method with discrete propagation and collision step.

P.J. Hoogerbrugge and J.M.V.A. Koelman, Europhys. Lett. 19, 155 (1992)
J.M.V.A. Koelman and P.J. Hoogerbrugge and , Europhys. Lett. 21, 363 (1993)

This formulation had no well defined equilibrium state (i.e. corresponded to no known statistical ensemble). This didn’t stop them and others using it though.

The formulation usually used now is due to Espanol and Warren.

P. Espanol and P.B. Warren, Europhys. Lett. 30, 191, (1995).

Particles move according to Newton’s equations of motion:

$$\frac{d\vec{r}_i}{dt} = \vec{v}; \frac{d\vec{p}_i}{dt} = \vec{f}_i$$

$$\left\{ \begin{array}{ll} \vec{r}_i & \text{position of particle } i \\ \vec{v}_i = \vec{p}_i / m_i & \text{velocity of particle } i \\ \vec{f}_i & \text{force on particle } i \\ m_i & \text{mass of particle } i \end{array} \right.$$

Dissipative Particle Dynamics

So what are the forces?

They are three fold and are each pairwise additive

$$\vec{f}_i = \sum_{j \neq i} \vec{f}_{ij}^{\,C} + \vec{f}_{ij}^{\,D} + \vec{f}_{ij}^{\,R}$$

The "conservative" force:

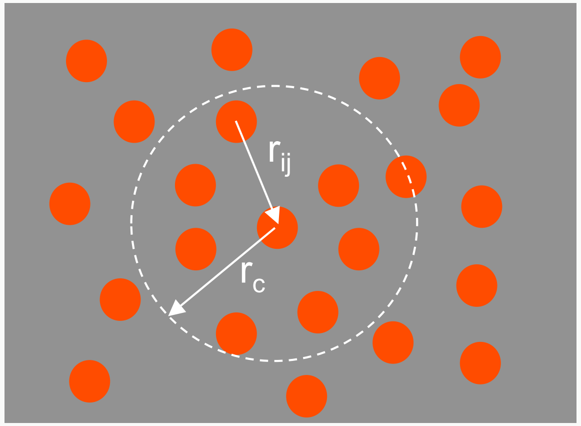
$$f_{ij}^{C} = a_{ij}\left(1 - \frac{r_{ij}}{r_c}\right)\frac{\vec{r}_{ij}}{r_{ij}} \qquad (r_{ij} < r_c)$$

$$f_{ij}^{C} = 0 \qquad (r_{ij} \geq r_c)$$

where; $\vec{r}_{ij} = \vec{r}_i - \vec{r}_j ; r_{ij} = \left|\vec{r}_{ij}\right|$

a_{ij} Is a "repulsion" parameter

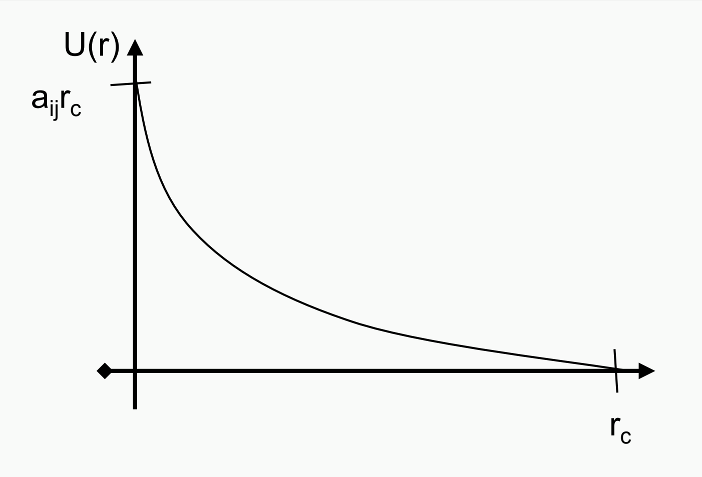
r_c Is an interaction cut-off range parameter



Dissipative Particle Dynamics

What is the Conservative force?
Simple: a repulsive potential with the form

$$U(r_{ij}) = a_{ij} r_c \left(1 - \frac{r_{ij}}{r_c}\right)^2$$



It is “soft” in that, compared to molecular dynamics it does not diverge to infinity at any point (there is no hard core repulsion.

The “dissipative” force

$$\vec{f}_{ij}^{\,D} = -\gamma\omega_d(r_{ij})\underbrace{\left(\hat{r}_{ij}\cdot\vec{v}_{ij}\right)}\hat{r}_{ij}$$

Component of relative
velocity along line of centres

$\vec{v}_{ij} = \vec{v}_i - \vec{v}_j$ is the relative velocity

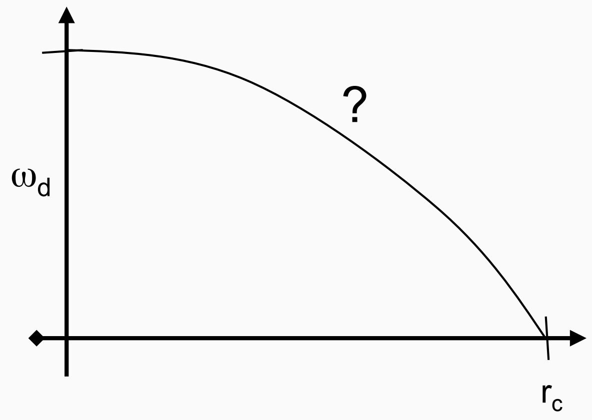
γ is a friction coefficient

ω_d is a distance dependent weight function that is zero for $r_{ij} > r_c$

Dissipative Particle Dynamics

What is the Dissipative force?

- A friction force that dissipates relative momentum (hence kinetic energy)
- A friction force that transports momentum between particles



The random force:

$$\vec{f}_{ij}^{\,R} = -\sigma \omega_r (r_{ij}) \theta_{ij} \hat{r}_{ij}$$

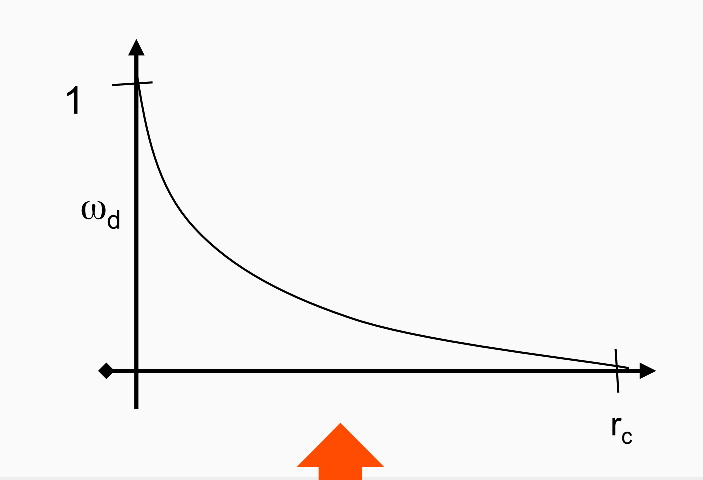
σ is a fluctuation amplitude

ω_r is a distance dependent weight function that is zero for $r_{ij} > r_c$

θ_{ij} is a Gaussian distributed random number with zero mean and unit variance

Fluctuation Dissipation

To have the correct canonical distribution function (constant NVT) the dissipative (cools the system) and random (heats the system) forces are related:



The weight functions are related

$$\omega_d(r_{ij}) = \left[\omega_r(r_{ij})\right]^2$$

As are the amplitudes

$$\sigma^2 = 2\gamma kT$$

For historical (convenient?) reasons ω_d is given the same form as the conservative force

$$\omega_d = \left(1 - \frac{r_{ij}}{r_c}\right)$$

DPD as Soft Particles and a Thermostat

Without the random and dissipative force, this would simply be molecular dynamics with a soft repulsive potential.

With the dissipative and random forces the system has a canonical distribution, so they act as a thermostat.

These two parts of the method are quite separate but the thermostat has a number of nice features.

Local
Conserves Momentum
Gallilean Invariant

Integrating the equations of motion

How to solve the DPD equations of motion is itself something of an issue. The nice property of molecular dynamics type algorithms (e.g. satisfying detailed balance) are lost because of the velocity dependent dissipative force. This is particularly true in the parametrically correct regime

Why is this important?

•Any of these algorithms are okay if the time-step is small enough

•The longer a time-step you can use, the less computational time your simulations need

How long a time step can I use?

•Beware to check more than that the temperature is correct

•The radial distribution function is a more sensitive test. The temperature can be okay while other equilibrium properties are severely inaccurate.
L-J.Chen, Z-Y Lu, H-J ian, Z-Li, and C-C Sun, J. Chem. Phys. 122, 104907 (2005)

Integrating the equations of motion

Euler-type algorithm

P. Espanol and P.B. Warren, Europhys. Lett. 30, 191, (1995).

$$\vec{r}_i(t+\Delta t) = \vec{r}_i(t) + \Delta t \vec{v}_i(t)$$
$$\vec{v}_i(t+\Delta t) = \vec{v}_i(t) + \Delta t \vec{f}_i(t)$$
$$\vec{f}_i(t+\Delta t) = \vec{f}_i(\vec{r}_i(t+\Delta t), \vec{v}_i(t+\Delta t))$$

And <u>note</u> that, because we are solving a stochastic differential equation

$$\vec{f}_{ij}^{R} = \frac{\sigma \omega_r(r_{ij}) \theta_{ij} \hat{r}_{ij}}{\sqrt{\Delta t}}$$

(Applies for all the following except the LA thermostat)

Integrating the equations of motion

Modified velocity Verlet algorithm

R.D. Groot and P.B. Warren, J. Chem. Phys. 107, 4423, (1997).

$$\vec{r}_i(t+\Delta t) = \vec{r}_i(t) + \Delta t \vec{v}_i(t) + \frac{1}{2}\Delta t^2 \vec{f}_i(t)$$

$$\vec{v}'_i(t+\Delta t) = \vec{v}_i(t) + \lambda \Delta t \vec{f}_i(t)$$

$$\vec{f}_i(t+\Delta t) = \vec{f}_i(\vec{r}_i(t+\Delta t), \vec{v}_i'(t+\Delta t))$$

$$\vec{v}_i(t+\Delta t) = \vec{v}_i(t) + \frac{1}{2}\Delta t(\vec{f}_i(t) + \vec{f}_i(t+\Delta t))$$

Here λ is an adjustable parameter in the range 0-1

- Still widely used
- Actually equivalent to the Euler-like scheme

Integrating the equations of motion

Self-consistent algorithm:

I Pagonabarraga, M.H.J. Hagen and D. Frenkel, Europhys. Lett. 42, 377, (1998).

$$\vec{r}_i(t+\Delta t) = \vec{r}_i(t) + \Delta t \vec{v}_i(t) + \frac{1}{2}\Delta t^2 \vec{f}_i(t)$$

$$\vec{v}_i\left(t+\frac{\Delta t}{2}\right) = \vec{v}_i\left(t-\frac{\Delta t}{2}\right) + \Delta t \vec{f}_i(t)$$

$$\vec{v}(t) = \frac{1}{2}\left(\vec{v}_i\left(t+\frac{\Delta t}{2}\right) + \vec{v}_i\left(t-\frac{\Delta t}{2}\right)\right)$$

Updating of velocities is performed iteratively

- Satisfies detailed balance (longer time-steps possible)
- Computationally more demanding

Which method should I use?

1) It depends on the conservative force (interaction potential). The time step must always be small enough such that the conservative equations of motion adequately conserve total energy. To check this, run the simulation without the thermostat and check total energy.

2) If this limits the time-step the methods that satisfy detailed balance lose their advantage.

3) If not, use the self-consistent or LAT methods. Never Euler or modified Verlet.

4) There are some much better methods that still do not strictly satisfy detailed balance (based on more sophisticated Langevin-type algorithms).
W.K. den Otter and J.H.R. Clarke, Europhys. Lett. 53, 426 (2001).
T. Shardlowe, SIAM J. Sci. Comput. (USA) 24, 1267 (2003).

5) For a review see
P. Nikunen, M. Karttunen and I. Vattulainen, Comp. Phys. Comm. 153, 407 (2003).

Alternatively, change the method

- The complications arise because the stochastic differential equation is difficult to solve without violating detailed balance (see Langevin vs Andersen thermostats)

In the same spirit let us modify the Andersen scheme such that

- Bath collisions exchange relative momentum between pair of particles by taking a new relative velocity from the Maxwellian distribution for relative velocities

- Impose the new relative velocity in such a way that linear and angular momentum is conserved.

- Following the same arguments as Andersen, detail balance is satisfied

Leads to the Lowe-Andersen thermostat

The Lowe-Andersen thermostat

Lowe-Andersen thermostat (LAT):

C.P.Lowe, Europhys. Lett. 47, 145, (1999).

$$\vec{r}_i(t+\Delta t) = \vec{r}_i(t) + \Delta t\vec{v}_i(t) + \frac{1}{2}\Delta t^2 f_i^C(t)$$

$$\vec{v}_i\big(t+\Delta t\big) = \vec{v}_i \qquad\qquad \Gamma\Delta t < \xi$$

$$\vec{v}_j\big(t+\Delta t\big) = \vec{v}_j \qquad\qquad \Gamma\Delta t < \xi$$

$$\text{“Bath” collision}\left\{\begin{aligned} &\vec{v}_i\big(t+\Delta t\big) = \vec{v}_i + \frac{\mu_{\mathrm{ij}}}{m_i}\left(\theta_{ij}\sqrt{\frac{kT}{\mu_{ij}}} - \big(\vec{v}_i - \vec{v}_j\big)\cdot\hat{r}_{ij}\right)\hat{r}_{ij} \qquad \Gamma\Delta t \geq \xi \\ &\vec{v}_j\big(t+\Delta t\big) = \vec{v}_j - \frac{\mu_{\mathrm{ij}}}{m_j}\left(\theta_{ij}\sqrt{\frac{kT}{\mu_{ij}}} - \big(\vec{v}_i - \vec{v}_j\big)\cdot\hat{r}_{ij}\right)\hat{r}_{ij} \qquad \Gamma\Delta t \geq \xi \end{aligned}\right.$$

Here Γ is a bath collision frequency (plays a similar role to γ/m in DPD)

- Bath collisions are processed for all pairs with $r_{ij}<r_c$
- The current value of the velocity is always used in the bath collision (hence the lack of an explicit time on the R.H.S.)
- The quantity ξ is a random number uniformly distributed in the range 0-1
- The quantity μ_{ij} is the reduced mass for particles *i* and *j*, $\mu_{ij}=m_i\, m_j/(m_i+m_j)$

The Lowe-Andersen vs DPD

(as a thermostat)

- Conserve linear momentum (BOTH)
- Conserve angular momentum (BOTH)
- Gallilean invariant (BOTH)
- Local (BOTH)
- Simple integration scheme satisfies detailed balance (LA YES, DPD NO)

The Lowe-Andersen vs DPD

(as a thermostat)

Disadvantage?: It does not use weight functions w_d and w_r (or alternatively you could say it uses a hat shaped weight functions)

But, no-one has ever shown these are useful or what form they should best take. The form $\omega_r=(1-r_{ij}/r_c)$ is only used for convenience (work for someone?)

They could be introduced using a distance dependent collision probability
In the limit of small time-steps LAT and DPD are actually equivalent!
E.A.J.F. Peters, Europhys. Lett. 66, 311 (2004).

Word of warning: in the LAT, bath collisions must be processed in a random order

- Is the DPD thermostat ever better than the Lowe-Andersen thermostat?

In simple terms: you can take a longer time-step with LA than with DPD without screwing things up.and there are no disadvantages so….

NO

Can I use these thermostats in normal MD?

Yes and in fact they have a number of advantages:

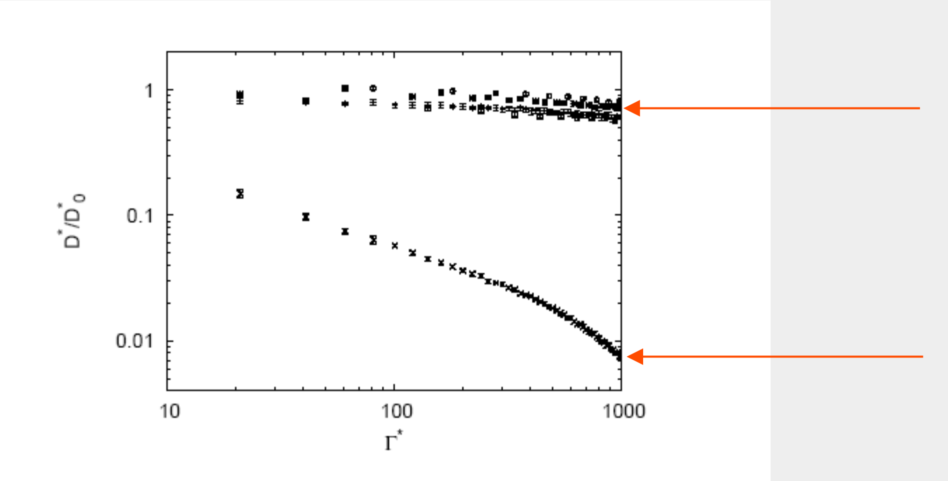
1) Because they are Gallilean invariant they do not see translational motion as an increase in temperature. Nose-Hoover (which is not Gallilean invariant does)

T. Soddemann , B. Dünweg and K. Kremer, Phys. Rev. E 68, 046702 (2003)

2) Because they preserve hydrodynamic behavior, even in equilibrium they disturb the dynamics of the system much less than methods that do not (the Andersen thermostat for example)

Can I use these thermostats in normal MD?

Example: a well know disadvantage of the Andersen thermostat is that at high thermostating rates diffusion in the system is suppressed (leading to inefficient sampling of phase space)



Lowe-Andersen

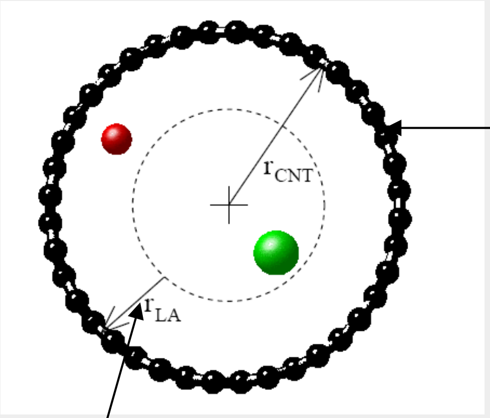
Andersen

whereas for the Lowe-Andersen thermostat it is not.

E. A. Koopman and C.P. Lowe, J. Chem. Phys. 124, 204103 (2006)

Can I use these thermostats in normal MD?

3) Where is heat actually dissipated? At the boundaries of the system. Because these thermostats are local (whereas Nose-Hoover is global) one can enforce local heat dissipation.



Carbon nanotube modelled by “frozen” carbon structure

Heat exchange of diffusants with the nanotube modelled by local thermostating during diffusant-microtubule interactions

S. Jakobtorweihen,M. G. Verbeek, C. P. Lowe, F. J. Keil, and B. Smit Phys. Rev. Lett. 95, 044501 (2005)

DPD Summary

•The dissipative and random forces combine to act as a thermostat (Fullfilling the same function as Nose-Hoover or Andersen thermostats in MD)

•As a thermostat it has a number of advantages over some commonly used MD thermostats

•The conservative force corresponds to a simple soft repulsive harmonic potential between particles, but in principle it could be anything
(The DPD thermostat can also be used in MD
T. Soddemann, B. Dunweg and K. Kremer, Phys. Rev. E68, 046702 (2003))

•The equations of motion are awkward to integrate accurately with large time-steps. Chose your algorithm and test it with care.

•The Lowe-Andersen thermostat has the same features as the DPD thermostat but is computationally more efficient as it allows longer time-steps.

Dissipative particle dynamics

part 2: why this form for the conservative force?

In principle the conservative force can be anything you like, what are the reasons for this choice? Some common statements;

"It is the effective interaction between blobs of fluid"
No it isn't, at least not unless you are very careful about what you mean by effective.

"A soft potential that allows longer time-steps"
Maybe, but relative to what?

Factually: it is not a Lennard-Jones (or molecular-like) potential.
It is the simplest soft potential with a force that vanishes at some distance r_c

As with any soft potential it has a simple equation of state in the fluid regime and at high densities.

The equation of state of a DPD Fluid

For a single component fluid with pairwise additive spherically symmetric interparticle potentails the pressure *P* in terms of the radial distribution function *g(r)* is

$$P = \rho kT + \frac{2\pi}{3}\rho^2 \int_0^{r_c} r f^C(r) g(r) r^2 dr$$

where ρ is the density. For a soft potential with range r_c at high densities, $\rho \gg 3/(4\pi r_c^3)$ g(r)~1 so

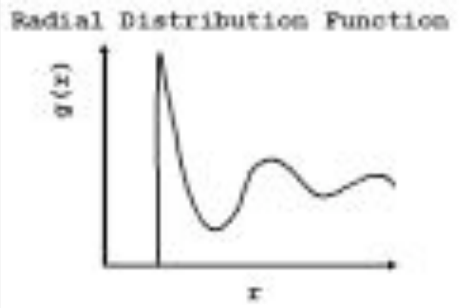
$$\frac{P}{\rho kT} = 1 + \frac{2\pi}{3kT}\rho \int_0^{r_c} r f^C(r) r^2 dr = 1 + \frac{\alpha}{kT}\rho$$

Where α is a constant. For DPD $\alpha = .101 a_{ij} r_c^4$

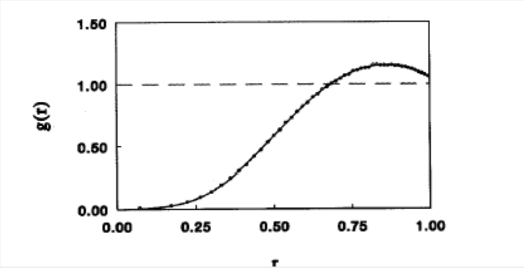
Note though that :

•If ρ is too high or *kT* too low the DPD fluid will freeze making the method useless.

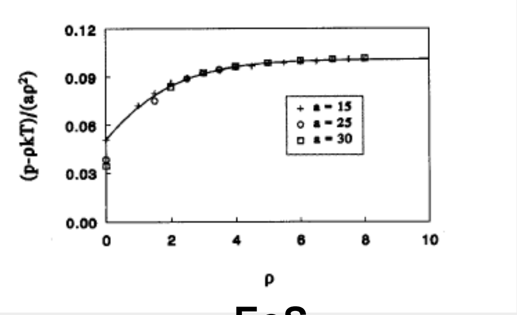
•And α/kT is not the the true second Virial coefficient so this does not hold at low densities



g(r) real fluid



g(r) DPD fluid



EoS

Mapping a DPD Fluid to a real fluid

R.D. Groot and P.B. Warren, J. Chem. Phys. 107, 4423, (1997).

Match the dimensionless compressibility κ for a DPD fluid to that of real fluid

$$\kappa^{-1} = \frac{1}{kT}\frac{\partial p}{\partial \rho}$$

For a (high density) DPD fluid, from the equation of state

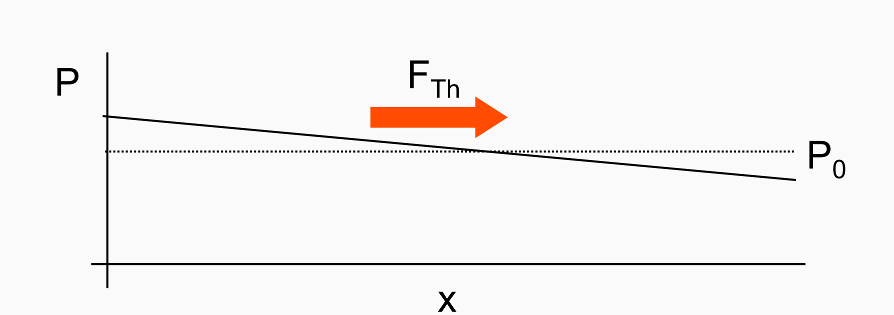
$$\kappa^{-1} = 1 + \frac{2\alpha}{kT}\rho$$

For water κ^{-1}~16 so in DPD $a_{ij}=75kT/\rho r_c^4$
Once the density is fixed, this fixes the repulsion parameter.

You can use a similar procedure to map the dimensionless compressibility of other fluids.

What’s right and what’s wrong

By setting the dimensionless compressibility correctly we will get the correct thermodynamic driving forces F_{Th} for small pressure gradients (the chemical potential gradient is also correct)



Technically, we reproduce the structure factor at long wavelengths correctly.

But, other things are completely wrong, eg the compressibility factor $P/\rho kT$

And this assumes on DPD particle is <u>one</u> water molecule. If it represents *n* water molecules the $\rho(real)=n\rho(model)$ so a_{ij} must be $na_{ij}(n=1)$. That is the repulsion parameter is scaled with *n* and if $n>1$ the fluid freezes.
R.D. Groot and K.L. Rabone, Biophys. J. 81, 725 (2001).

DPD for a given equation of state

I. Paganabarraga and D. Frenkel, J. Chem. Phys 155, 5015 (2001)

The basic idea is to “input” an equation of state.
To do so a local “density” is defined

$$\rho_i = \frac{1}{[\omega]} \sum_j w(r_{ij})$$

where w is a weight function that vanishes for $r_{ij}>r_c$
The conservative force is the the derivative of the free-energy
(as a function of ρ) w.r.t. the particle positions

$$F_i^C = \sum_j \left(\psi_i' + \psi_j'\right) \frac{\omega\ (r_{ij})'}{[\omega]}$$

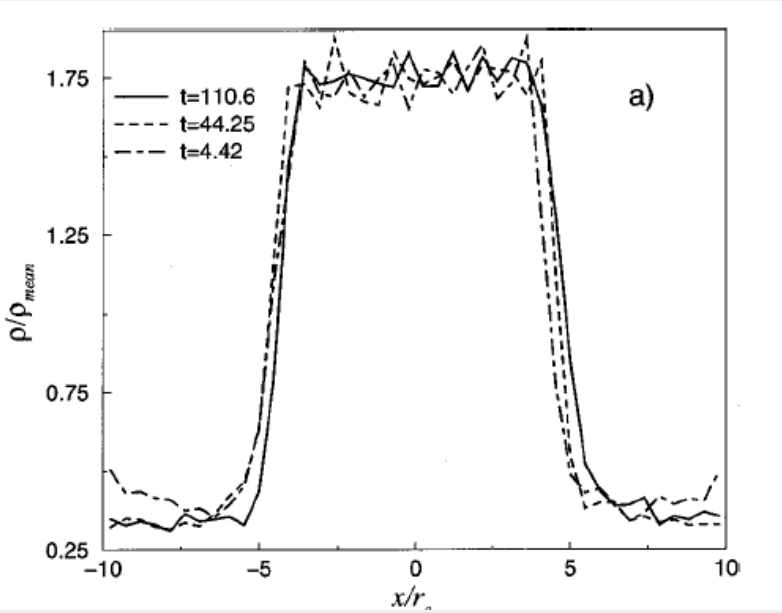
Where ψ_i is the excess free energy per partilce as calculated from the EoS
Is the density really the density?
Is it a free energy or a potential energy?

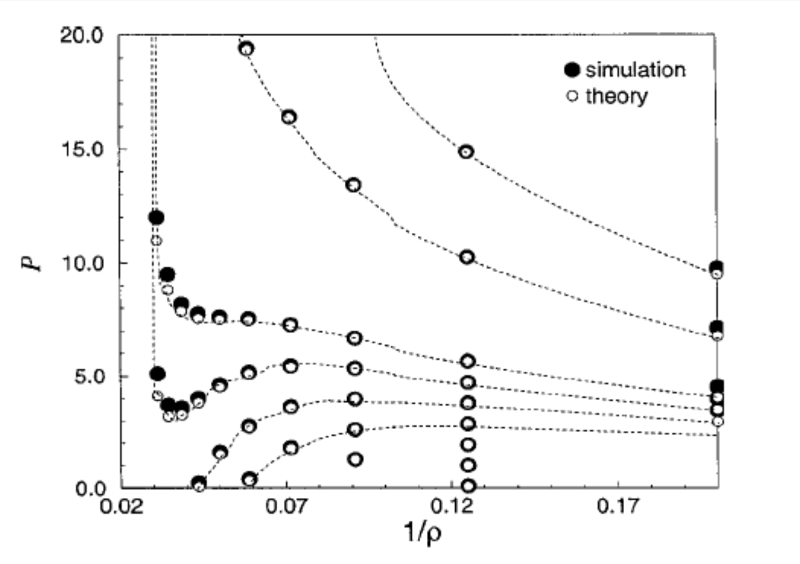
DPD for a given equation of state

Eg a van der Waals fluid

$$P = \frac{\rho k T}{1 - B\rho} - A\rho^2$$

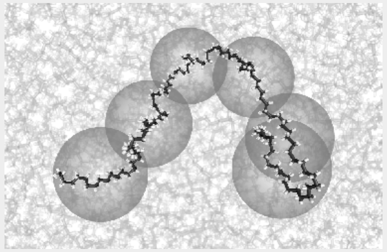
where A and B are parameters (related to the critical properties of the fluid). Simplest EoS that gives a gas liquid transition.





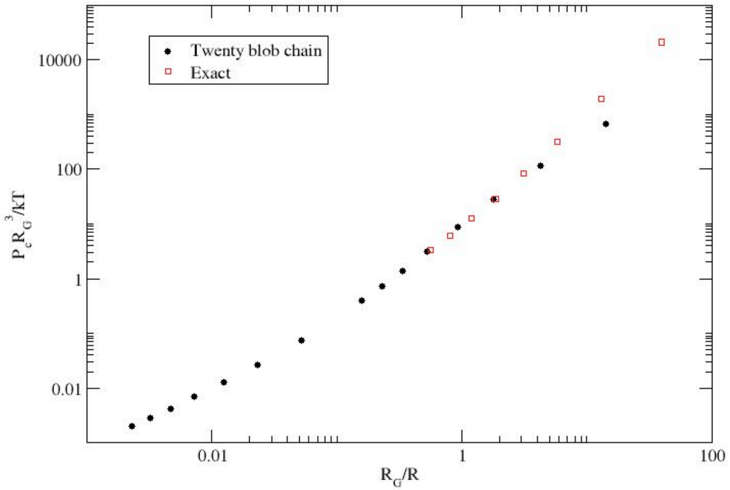
Case Study

Free energy of a spherically confined polymer



Effective potentials: potential between blobs is the (theoretical) effecive potential between long polymers

Works up to a point:
For higher degrees
of confinement
you need more blobs



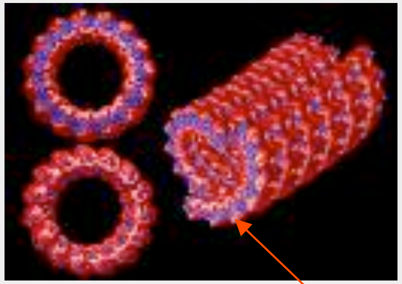
- **In Mesocopic modelling we have always thrown information out. The onus is on the user to justify what is in what is out and whether it matters.**

Case Study: The dynamics of biofilaments

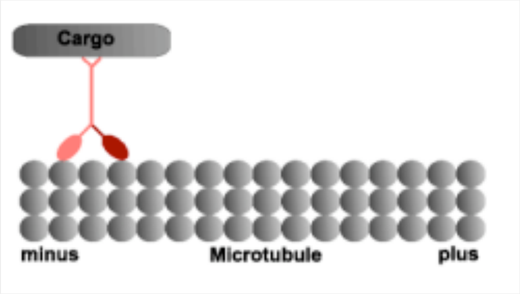
M. C. Lagomarsino, I. Pagoabarraga and C.P. Lowe
Phys. Rev. Lett. 94, 148104 (2004).
M. C. Lagomarsino, F.Capuani and C.P. Lowe, J. Theor. Biol. 224, 205 (2003)

Nature uses a lot of mesoscopic filaments for structure and transport

Example, microtubules (which act as tracks for molecular motors)



Globular protien

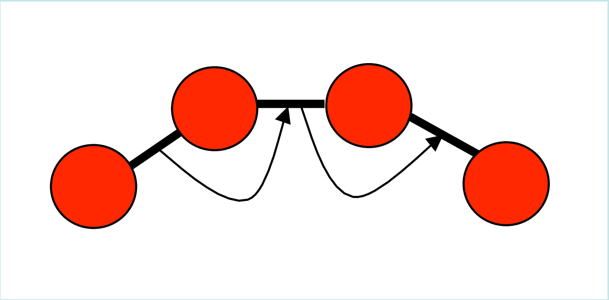


We want to simulate the dynamics of these things in solutions.
Without coarse graining – forget it

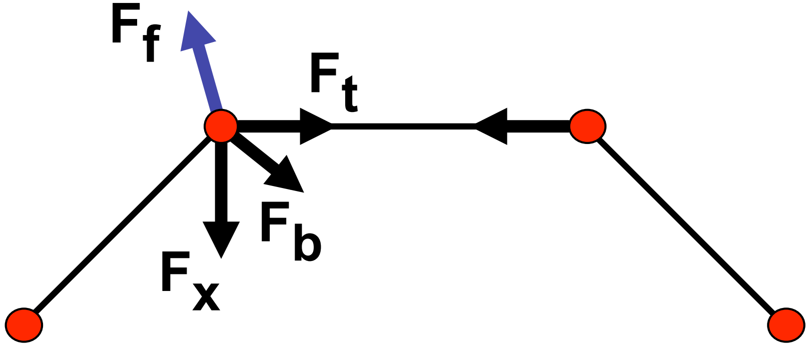
Case Study: The dynamics of biofilaments

$$U = \frac{\kappa}{2}\int_0^L \frac{ds}{R(s)^2}$$

Effective potential: The bending energy is that of an ideal elastic filament



Mesoscopic model



F_b - bending force (from the bending energy for a filament with stiffness κ that we described earlier)

F_t - Tension force (satisfies constraint of no relative displacement along the line of the links)

F_f - Fluid force (from the model discussed earlier, with F the sum of all non hydrodynamic forces)

F_x - External force

Solve equations of motion using a Langevin Equation!!

Imposing rigid constraints

Note that this is a quite generic problem:
- MD (fixing bond lengths to integrate out fast vibrational degrees of freedom)
- robotics
- computer animation

Step 1) Write the new positions in terms of the unconstrained positions (*nc*) and the as yet unknown constraint forces

$$\mathbf{r}_i(t+\Delta) = \mathbf{r}_i^{nc}(t+\Delta) + \frac{\Delta^2}{2m_i}\mathbf{F}_i^c(t)$$

Step 2) Constraint forces are equal and opposite, directed along current connector vector (conserve linear and angular momentum). Write in terms of scalar multipliers

$$\mathbf{F}_{ij}^c(t) = \frac{2\lambda_{ij}}{\Delta^2}\left[\mathbf{r}_i(t) - \mathbf{r}_j(t)\right]$$

Imposing rigid constraints

so

$$\mathbf{r}_{ij}(t+\Delta)^2 = l_{ij}^2 = \left[\mathbf{r}_{ij}^{nc}(t+\Delta) + \sum_{i\to k}\frac{\lambda_{ik}}{m_i}\mathbf{r}_{ik}(t) - \sum_{j\to k}\frac{\lambda_{jk}}{m_j}\mathbf{r}_{jk}(t)\right]^2$$

Step 3) Linearize (violations of the constraints are small)

$$l_{ij}^2 = \mathbf{r}_{ij}^{nc}(t+\Delta)^2 + 2\mathbf{r}_{ij}^{nc}(t+\Delta)\cdot\sum_{i\to k}\frac{\lambda_{ik}}{m_i}\mathbf{r}_{ik}(t) - 2\mathbf{r}_{ij}^{nc}(t+\Delta)\cdot\sum_{j\to k}\frac{\lambda_{jk}}{m_j}\mathbf{r}_{jk}(t)$$

Or in matrix form…

$$\mathrm{M}\lambda = \delta$$

Imposing rigid constraints

Matrix inversion is an order n^3 process so solve iteratively using SHAKE

Simply satisfy successive linearized constraints even though satisfying one violates others

$$\lambda_{ij} = \frac{\tilde{\mathbf{r}}_{ij}^2 - l_{ij}^2}{\left(m_i^{-1} + m_j^{-1}\right)\mathbf{r}_{ij} \cdot \tilde{\mathbf{r}}_{ij}}$$

$$\mathbf{r}_i(t+dt) = \tilde{\mathbf{r}}_i(t+dt) + \frac{1}{m_i}\lambda ij\mathbf{r}_{ij}(t)$$
$$\mathbf{r}_j(t+dt) = \tilde{\mathbf{r}}_j(t+dt) - \frac{1}{m_j}\lambda ij\mathbf{r}_{ij}(t)$$

Or

Imposing rigid constraints

For a linear chain matrix is tri-diagonal with elements

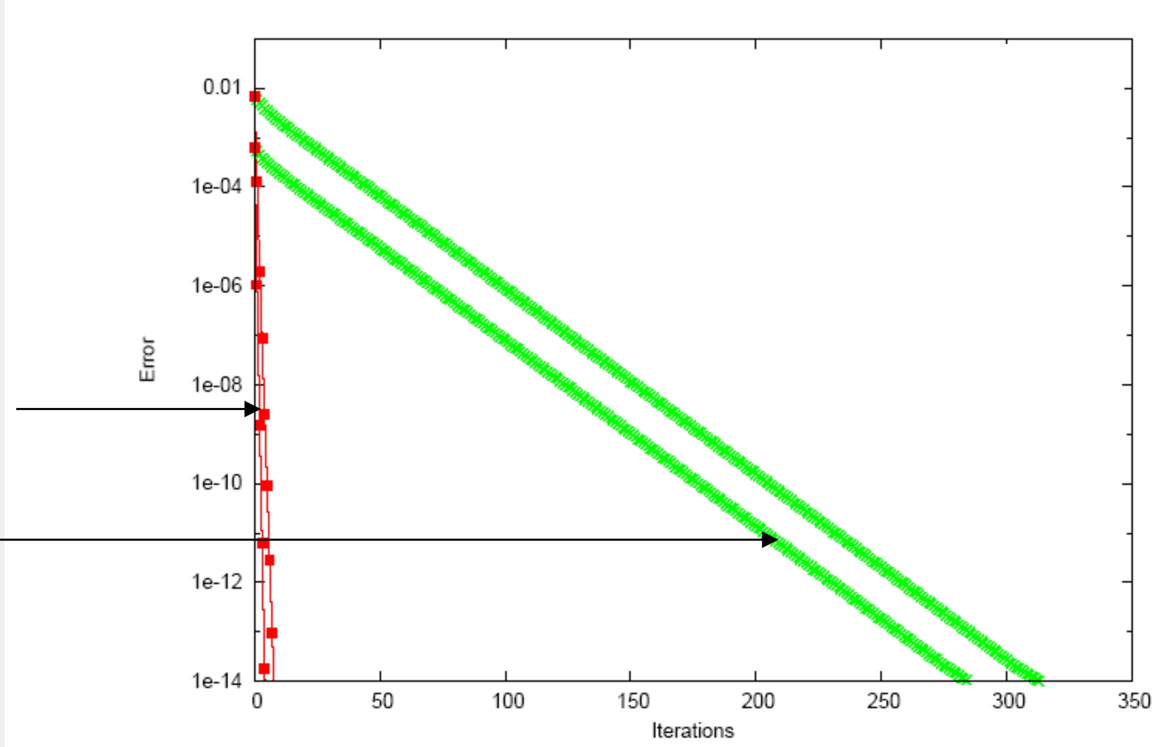
$$
\begin{aligned}
\mathrm{M}_{i,i-1} &= \frac{-2}{m_i}\mathbf{r}_{i-1,i}(t)\cdot\mathbf{r}^{nc}_{i,i+1}(t+\Delta) \\
\mathrm{M}_{i,i} &= \frac{2}{\mu_{i,i+1}}\mathbf{r}_{i,i+1}(t)\cdot\mathbf{r}^{nc}_{i,i+1}(t+\Delta) \\
\mathrm{M}_{i,i+1} &= \frac{-2}{m_{i+1}}\mathbf{r}_{i+1,i+2}(t)\cdot\mathbf{r}^{nc}_{i,i+1}(t+\Delta)
\end{aligned}
$$

And inverting a tri-diagonal matrix in order n operations is trivial (for rings and branches the matrix can be diagonalized in order n operation to make the problem equivalent to the linear chain)

Imposing rigid constraints

this method is termed “Matrix inverted linearized constrains – SHAKE”

A.G. Bailey and C.P. Lowe, J. Comp. Phys. **227**, 8949 (2008).

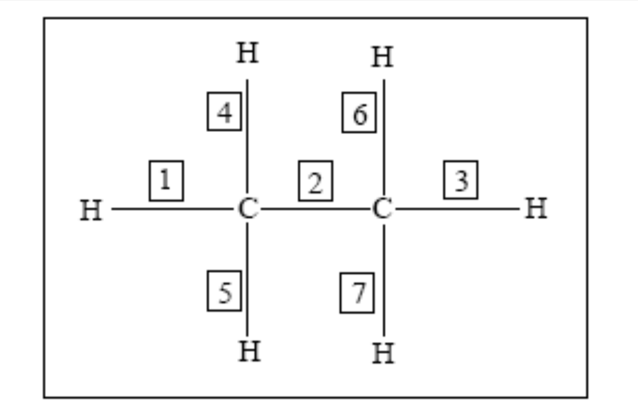


Milc SHAKE

SHAKE

Hybridizing MILC SHAKE and SHAKE

e.g. All atom molecule of alkanes

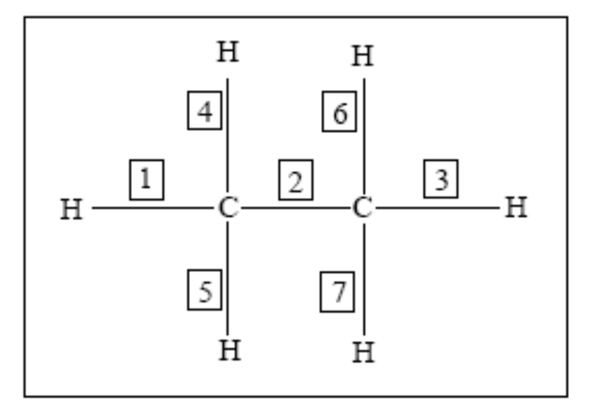


Using this labeling scheme the Jacobean is

$$\mathbf{J} = 2\left(\begin{array}{ccccccc}
\frac{\tilde{\mathbf{r}}_1\cdot\mathbf{r}_1}{\mu_1} & \frac{-\tilde{\mathbf{r}}_1\cdot\mathbf{r}_2}{m_c} & 0 & \frac{-\tilde{\mathbf{r}}_1\cdot\mathbf{r}_4}{m_c} & \frac{-\tilde{\mathbf{r}}_1\cdot\mathbf{r}_5}{m_c} & 0 & 0 \\
\frac{-\tilde{\mathbf{r}}_2\cdot\mathbf{r}_1}{m_c} & \frac{\tilde{\mathbf{r}}_2\cdot\mathbf{r}_2}{\mu_2} & \frac{-\tilde{\mathbf{r}}_2\cdot\mathbf{r}_3}{m_c} & \frac{\tilde{\mathbf{r}}_2\cdot\mathbf{r}_4}{m_c} & \frac{\tilde{\mathbf{r}}_2\cdot\mathbf{r}_5}{m_c} & \frac{-\tilde{\mathbf{r}}_2\cdot\mathbf{r}_6}{m_c} & \frac{-\tilde{\mathbf{r}}_2\cdot\mathbf{r}_7}{m_c} \\
0 & \frac{-\tilde{\mathbf{r}}_3\cdot\mathbf{r}_2}{m_c} & \frac{\tilde{\mathbf{r}}_3\cdot\mathbf{r}_3}{\mu_3} & 0 & 0 & \frac{\tilde{\mathbf{r}}_3\cdot\mathbf{r}_6}{m_c} & \frac{\tilde{\mathbf{r}}_3\cdot\mathbf{r}_7}{m_c} \\
\hline
\frac{-\tilde{\mathbf{r}}_4\cdot\mathbf{r}_1}{m_c} & \frac{-\tilde{\mathbf{r}}_4\cdot\mathbf{r}_2}{m_c} & 0 & \frac{\tilde{\mathbf{r}}_4\cdot\mathbf{r}_4}{\mu_4} & \frac{\tilde{\mathbf{r}}_4\cdot\mathbf{r}_5}{m_c} & 0 & 0 \\
\frac{-\tilde{\mathbf{r}}_5\cdot\mathbf{r}_1}{m_c} & \frac{\tilde{\mathbf{r}}_5\cdot\mathbf{r}_2}{m_c} & 0 & \frac{\tilde{\mathbf{r}}_5\cdot\mathbf{r}_4}{m_c} & \frac{\tilde{\mathbf{r}}_5\cdot\mathbf{r}_5}{\mu_5} & 0 & 0 \\
0 & \frac{-\tilde{\mathbf{r}}_6\cdot\mathbf{r}_2}{m_c} & \frac{\tilde{\mathbf{r}}_6\cdot\mathbf{r}_3}{m_c} & 0 & 0 & \frac{\tilde{\mathbf{r}}_6\cdot\mathbf{r}_6}{\mu_6} & \frac{\tilde{\mathbf{r}}_6\cdot\mathbf{r}_7}{m_c} \\
0 & \frac{-\tilde{\mathbf{r}}_7\cdot\mathbf{r}_2}{m_c} & \frac{\tilde{\mathbf{r}}_7\cdot\mathbf{r}_3}{m_c} & 0 & 0 & \frac{\tilde{\mathbf{r}}_7\cdot\mathbf{r}_6}{m_c} & \frac{\tilde{\mathbf{r}}_7\cdot\mathbf{r}_7}{\mu_7}
\end{array}\right)$$

Hybridizing MILC SHAKE and SHAKE

e.g. All atom molecule of alkanes

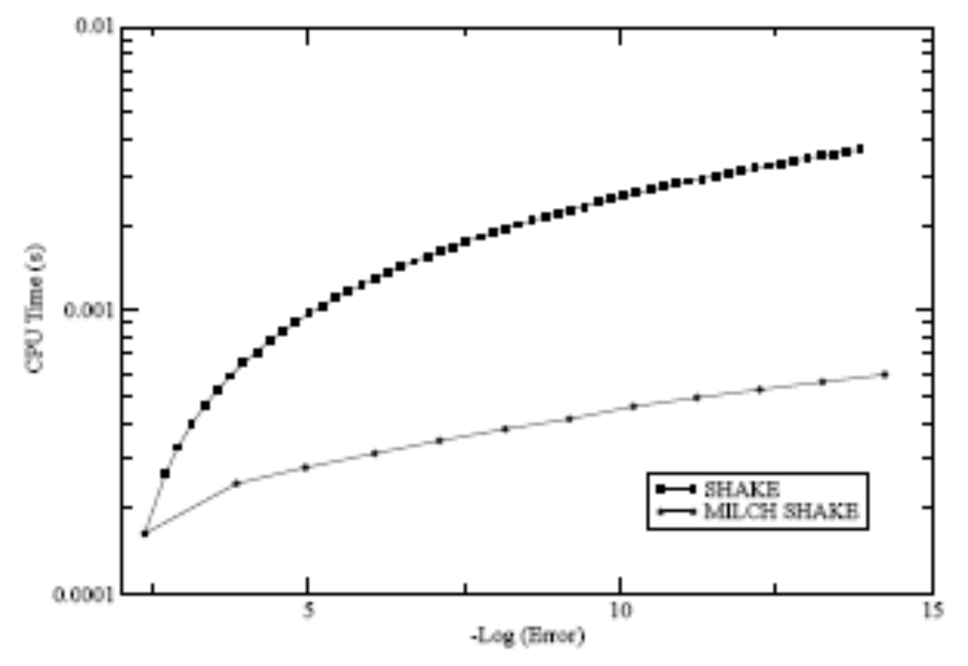


Using this labeling scheme the approximate Jacobean is

$$\mathbf{J} \approx 2 \left(\begin{array}{ccccccc} \frac{\tilde{\mathbf{r}}_1 \cdot \mathbf{r}_1}{\mu_1} & \frac{-\tilde{\mathbf{r}}_1 \cdot \mathbf{r}_2}{m_c} & 0 & 0 & 0 & 0 & 0 \\ \frac{-\tilde{\mathbf{r}}_2 \cdot \mathbf{r}_1}{m_c} & \frac{\tilde{\mathbf{r}}_2 \cdot \mathbf{r}_2}{\mu_2} & \frac{-\tilde{\mathbf{r}}_2 \cdot \mathbf{r}_3}{m_c} & 0 & 0 & 0 & 0 \\ 0 & \frac{-\tilde{\mathbf{r}}_3 \cdot \mathbf{r}_2}{m_c} & \frac{\tilde{\mathbf{r}}_3 \cdot \mathbf{r}_3}{\mu_3} & 0 & 0 & 0 & 0 \\ \hline 0 & 0 & 0 & \frac{\tilde{\mathbf{r}}_4 \cdot \mathbf{r}_4}{\mu_4} & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & \frac{\tilde{\mathbf{r}}_5 \cdot \mathbf{r}_5}{\mu_5} & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 & \frac{\tilde{\mathbf{r}}_6 \cdot \mathbf{r}_6}{\mu_6} & 0 \\ 0 & 0 & 0 & 0 & 0 & 0 & \frac{\tilde{\mathbf{r}}_7 \cdot \mathbf{r}_7}{\mu_7} \end{array} \right).$$

Performance of the MILCH SHAKE algorithm

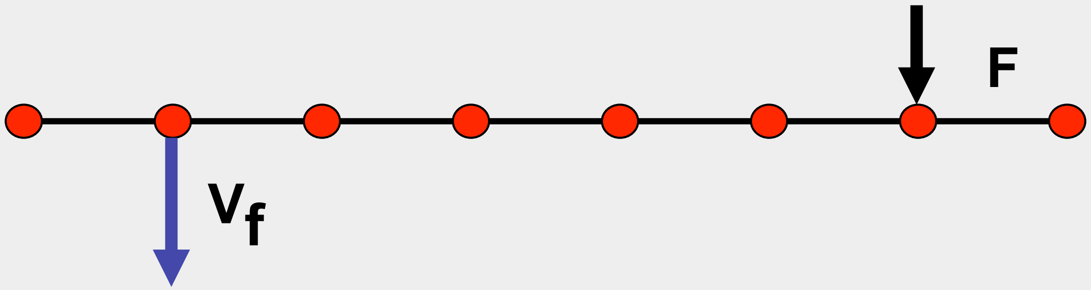
A.G. Bailey and C.P. Lowe, J. Comp. Chem. **30**, 2485 (2009)



Eg. For hexane

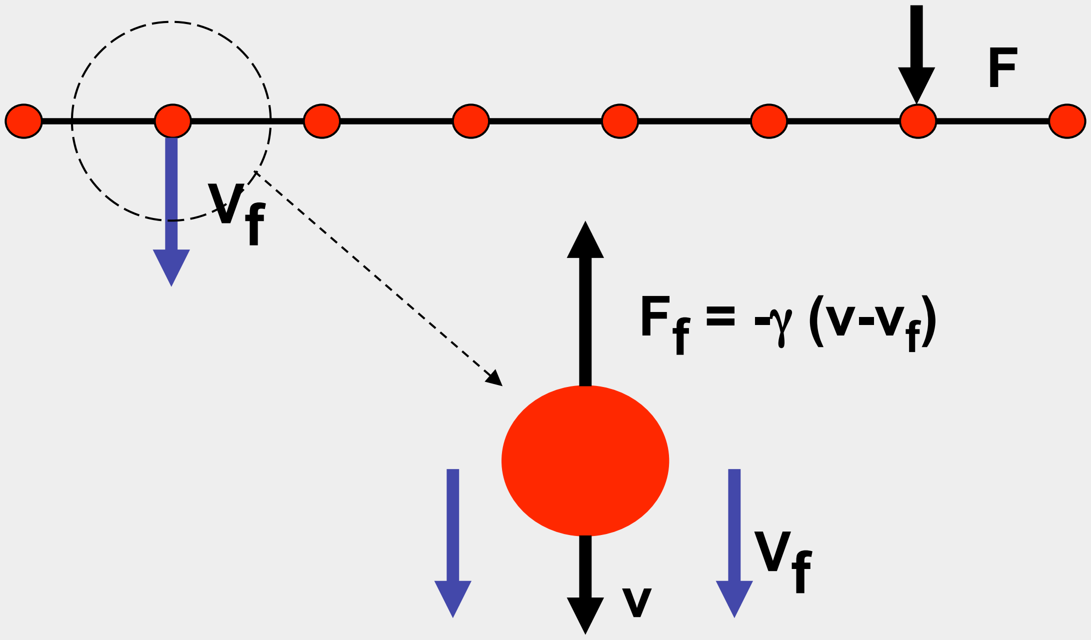
The fluid force

A simple model, a chain of rigidly connected point particles with a friction coefficient γ



Why might this not give a complete picture?

A simple model, a chain of rigidly connected point particles with a friction coefficient γ subject to an external force F



The Oseen tensor gives the solution to the fluid flow equations (on a small scale) for a point force acting on a fluid. This gives the velocity of the fluid due to the force on another bead as

$$\vec{v}_f(\vec{r}\,) = \frac{1}{8\pi\eta}\left(\frac{\vec{F}}{r} + \left(\vec{F}\cdot\vec{r}\,\right)\frac{\vec{r}}{r^3}\right)$$

These equations are linear so solutions just add

$$\vec{F}_{if}(\vec{r}_i) = -\gamma\vec{v}_i + \frac{\gamma}{8\pi\eta}\sum_{i\neq j}\left(\frac{\vec{F}_j}{r_{ij}} + \left(\vec{F}_j\cdot\vec{r}_{ij}\right)\frac{\vec{r}}{r_{ij}^3}\right)$$

Stokesian dynamics without the the fluctuations

Approximate the solution as an integral. For a uniform perpendicular force.

$$F_f(s) = \gamma\left(v - \frac{F}{8\pi\eta b}\ln\left(\frac{s(1-s)}{b^2}\right)\right)$$

- s = the distance along a rod of unit length
- b = is the bead separation

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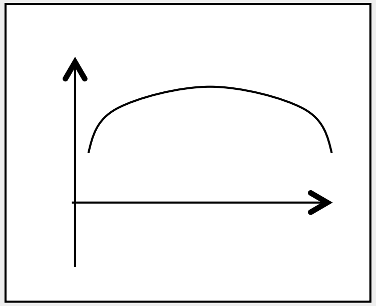
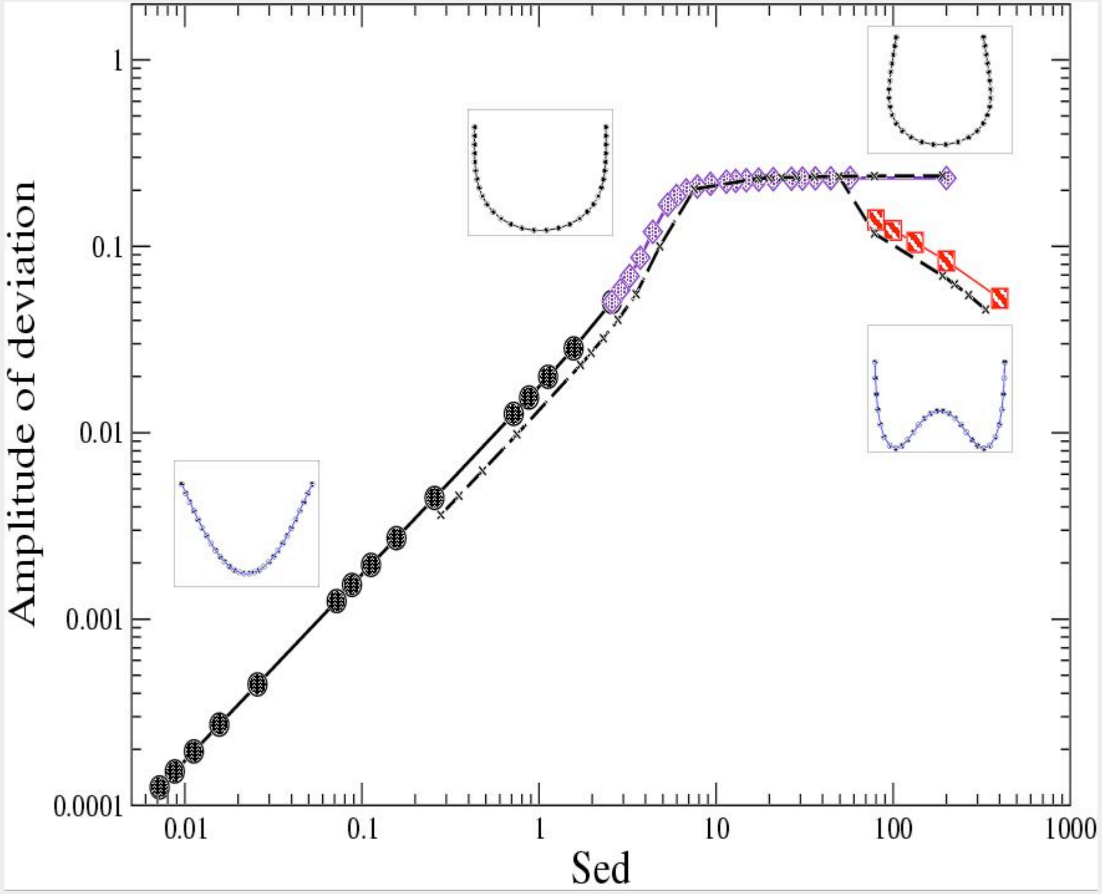


- s = the distance along a rod of unit length
- b = is the bead separation

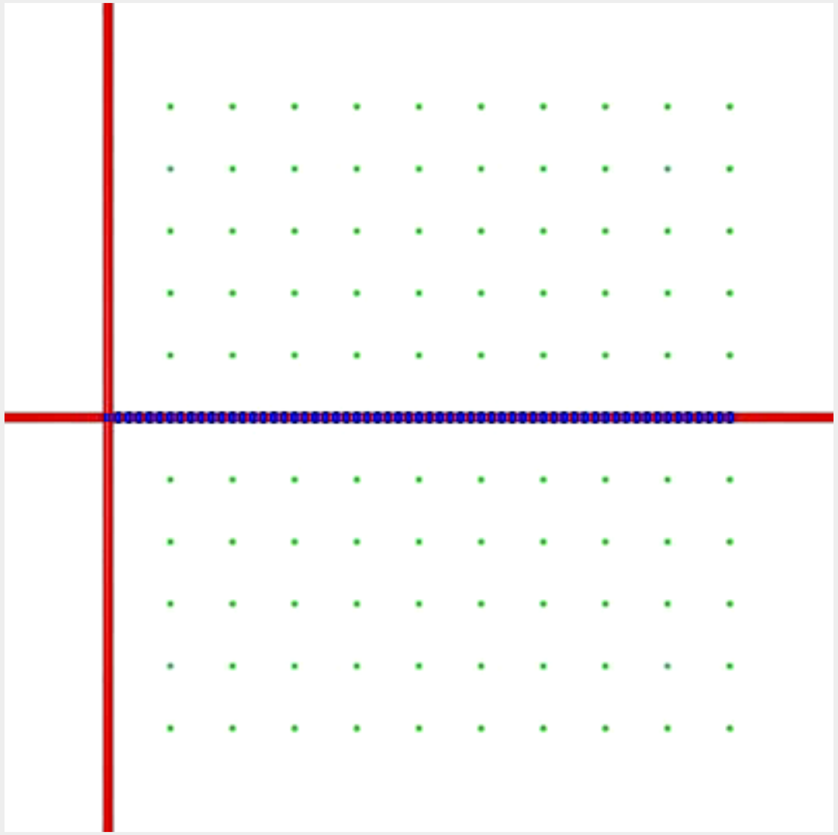
If the velocity is uniform the friction is higher at the end than in the middle

- **Constructing the mesoscopic model gives us a theory**

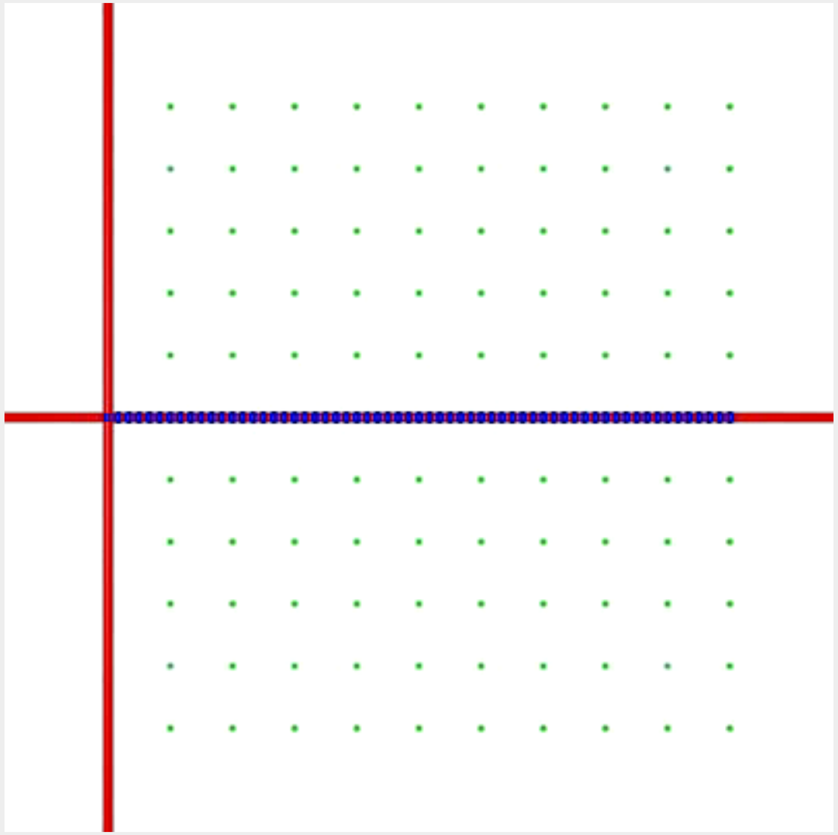
What happens with uniform force acting downwards?



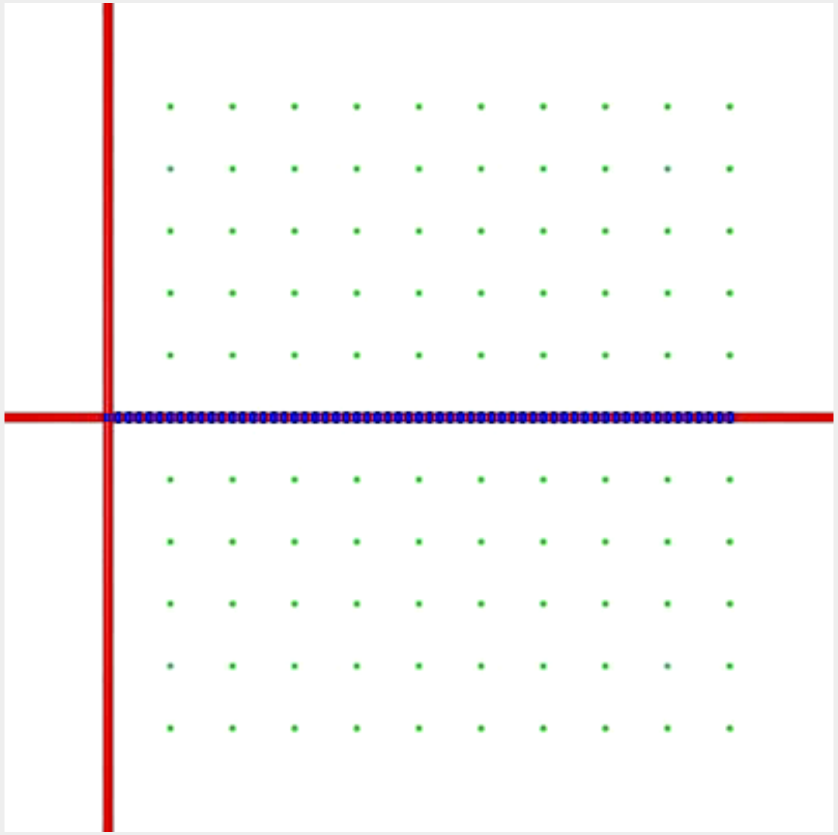
Sed = B= FL^2/κ = ratio of bending to hydrodynamic forces
If the filament is long enough, the bending modulus small enough or the force high enough, the filament bends significantly.



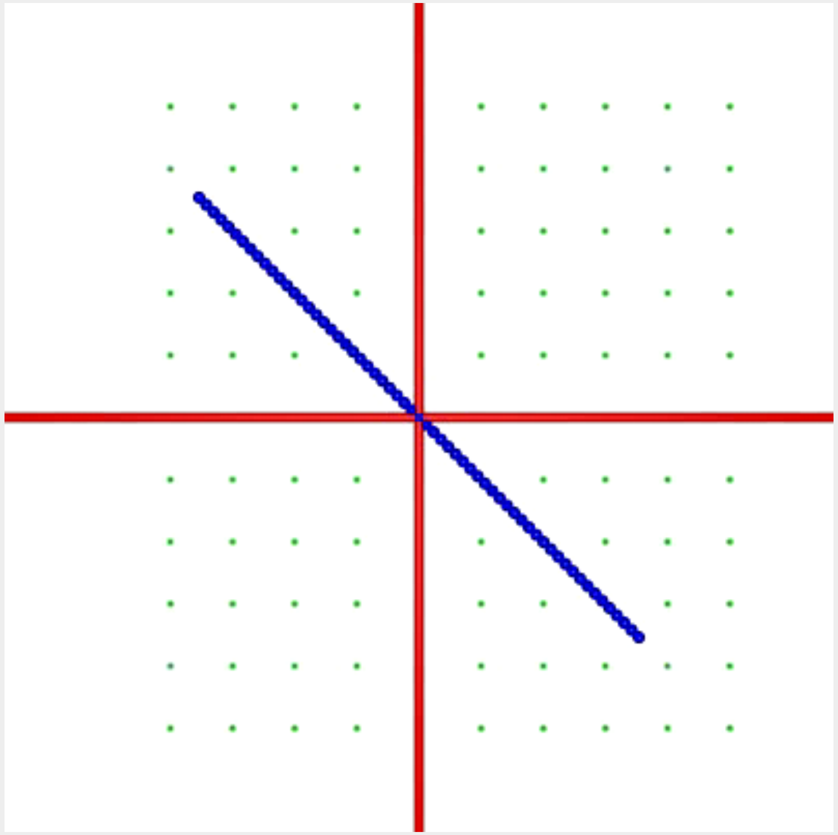
B = 300



B = 3000

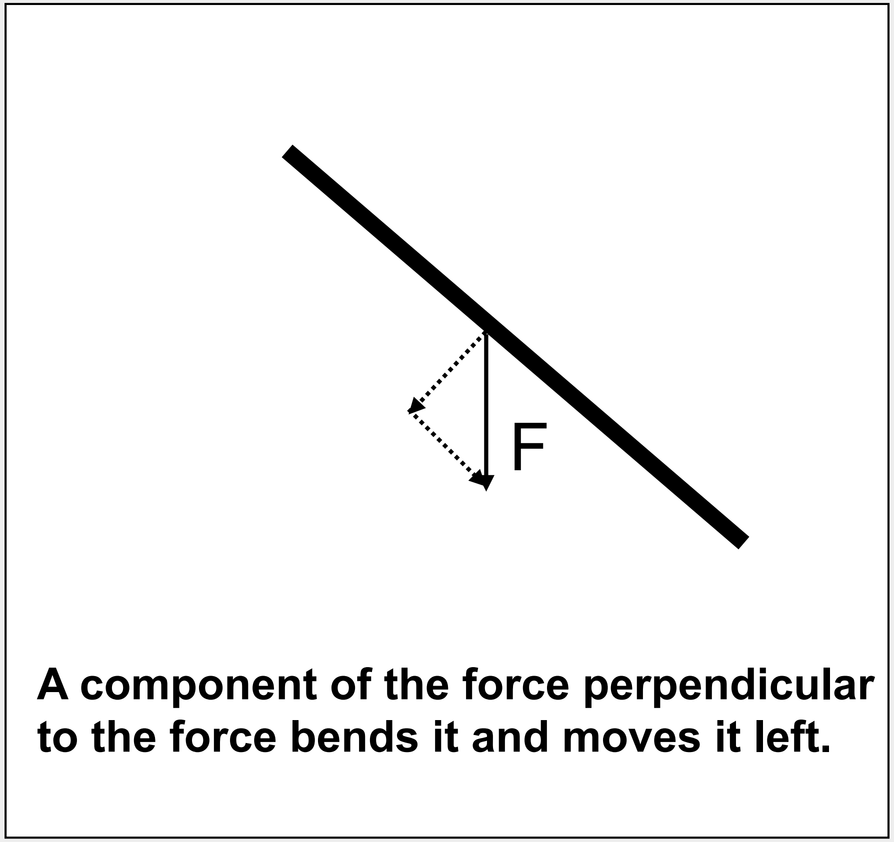


B = 15000

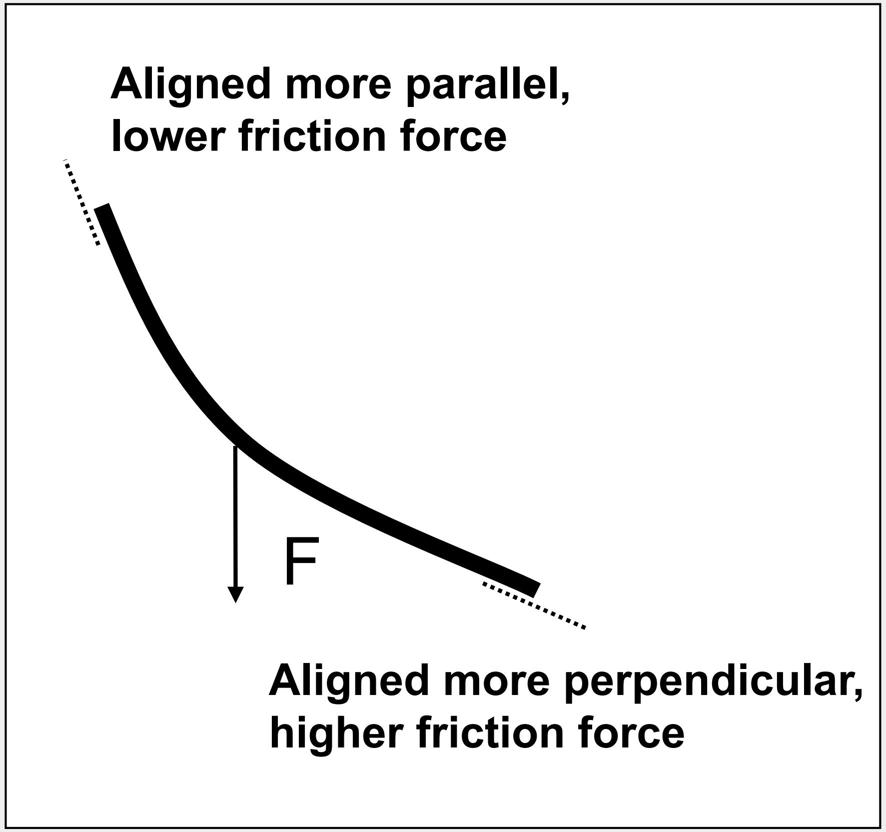


B = 1, filament aligned at 45^0

Why?



A component of the force perpendicular to the force bends it and moves it left.

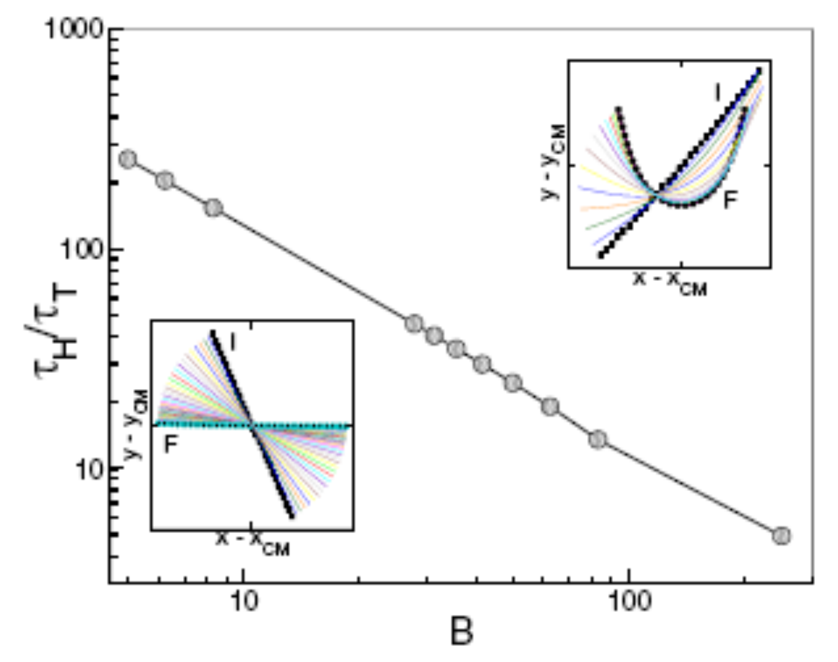


Aligned more parallel, lower friction force

Aligned more perpendicular, higher friction force

So a torque acts on the fibre to rotate it towards the prependicular

How long does it take to reorientate?



From this we can;

- work out what conditions are necessary in the real world to see the effect
- work out when the approximation of neglecting diffusion and dipole orientation is sensible.

Is this practically relevant?

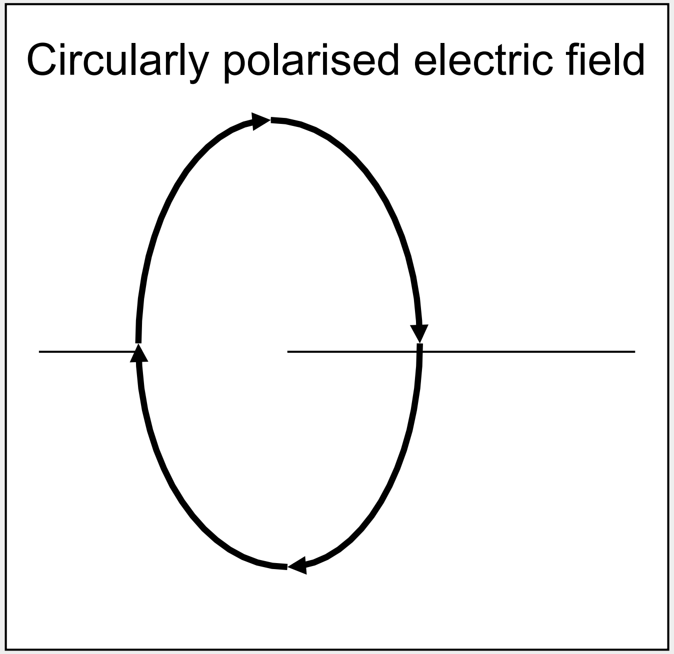
- For a microtubule the bending modulus is known
- and we estimate, B ~ 1 requires F~1 pN for a 10 micron
- microtubule. This is reasonable on the micrometer scale.

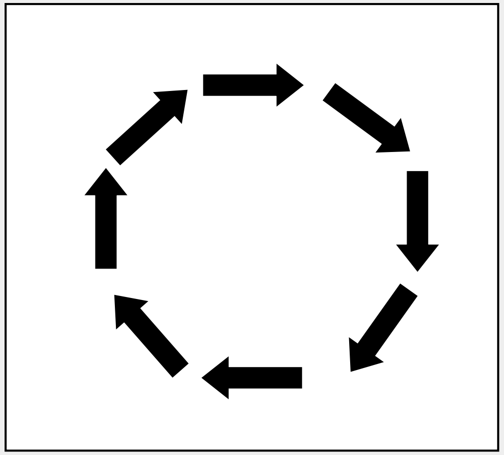
- For sedimentation (external force is gravity) , no.
  Gravity is not strong enough. You'd need a ultracentrifuge

- Microtubules are barely charged and the charge is known, we estimate
  an electric field of 100 V/m for B ~ 200 (L=30 microns). So it
  should be doable.

But this only orientate the filament in a plane (perpendicular to the force direction)

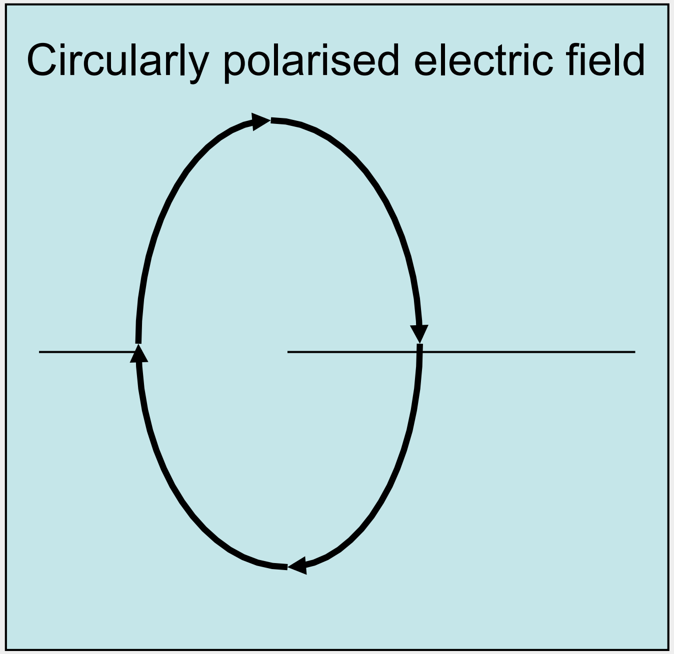
What if we apply a force in a direction that rotates?



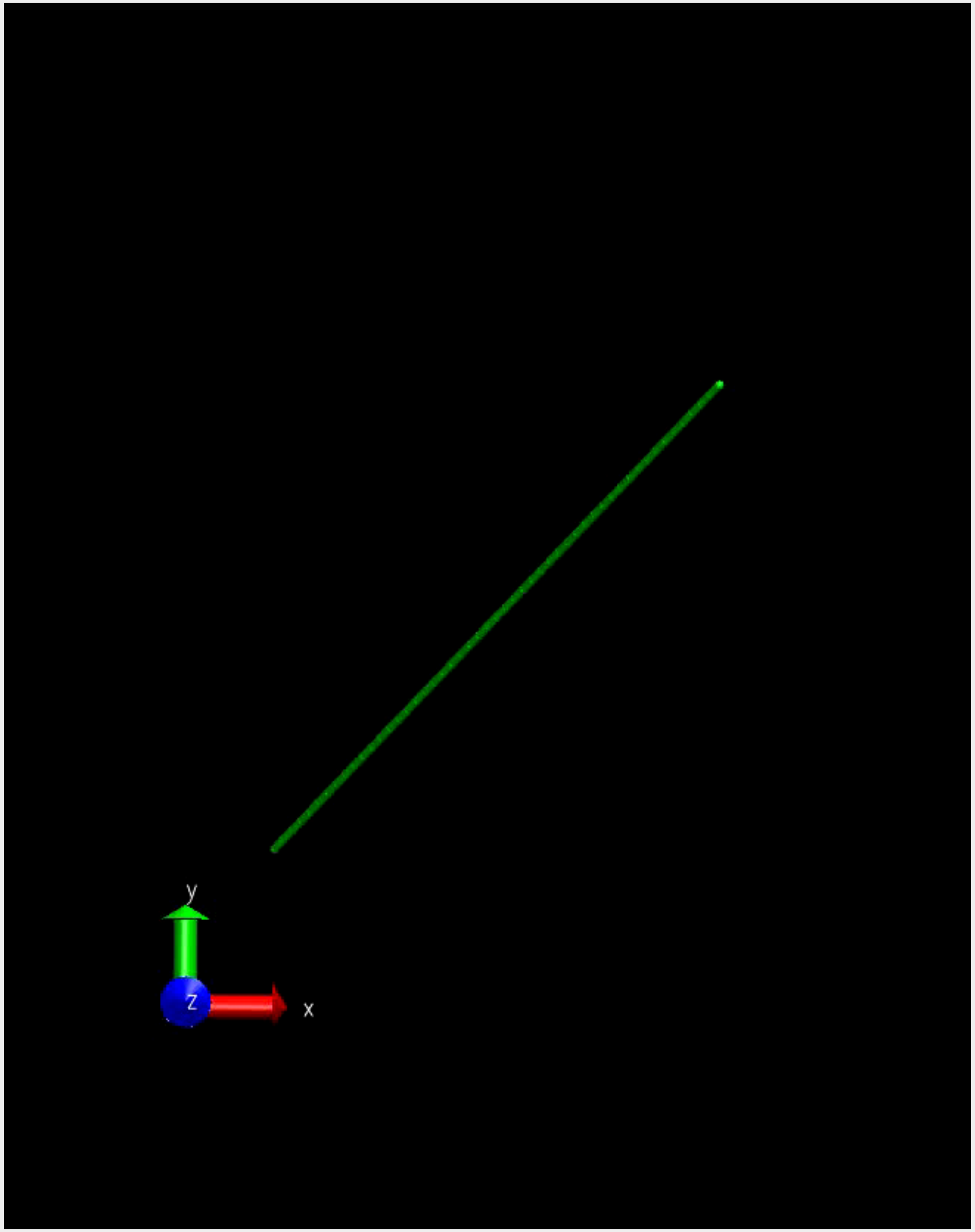


Electric field as a function of time

Dimensional Analysis
30μ Microtubule in water,
Field= 100 V/m
Frequecy 1 Hz
Movie time~real time



Circularly polarised electric field



Dimensional Analysis
30m Microtubule in water,
Field= 100 V/m
Frequecy 1 Hz
Movie time~real time

Circularly polarised electric field