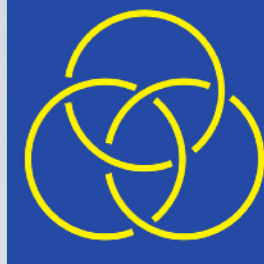


EUTOPIA Tutorial on Molecular Dynamics Simulations and LAMMPS

Davide Michieletto, University of Edinburgh

What are MD Simulations?



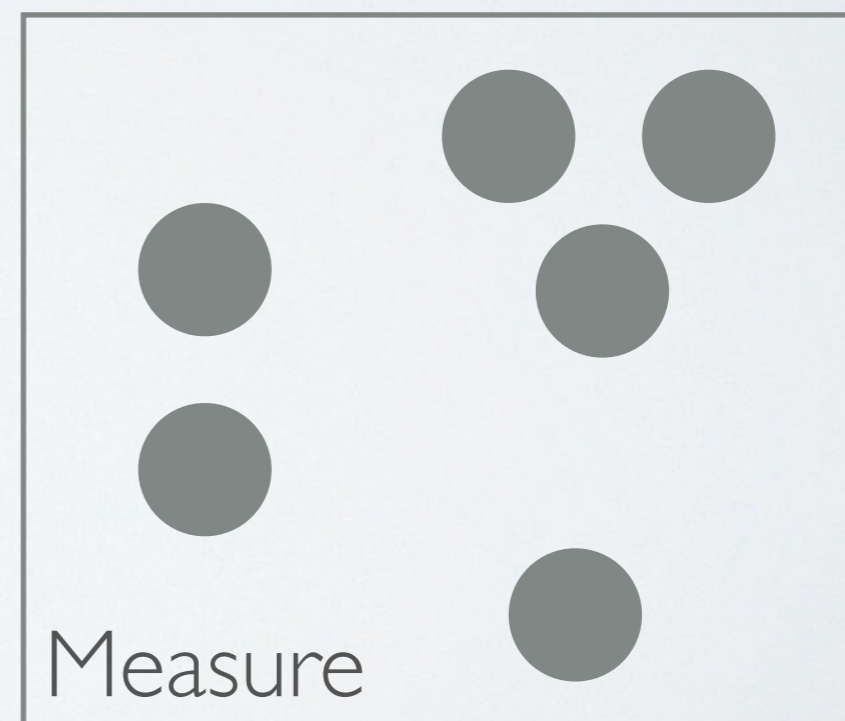
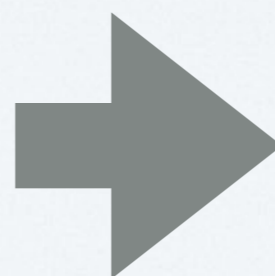
“It is a bit like performing an experiment ...”

Understanding Molecular Simulation, Frenkel and Smit

1. Prepare your sample
2. Select a model (how they interact)
3. Integrate Newton's equations of motion
4. Measure observable of interest



Evolve



Preparing the Sample



To fully specify your system state you have to define

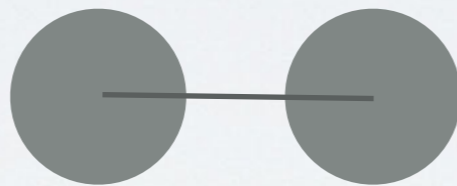
For each of the N atoms

1. Positions (x, y, z)
2. Velocity (v_x, v_y, v_z)

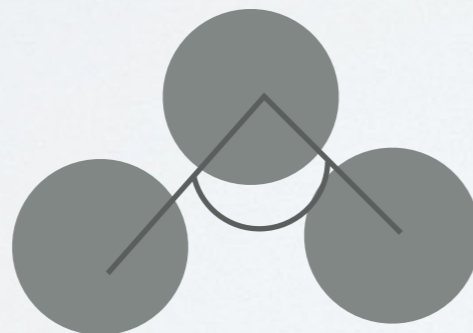
For each pair

- pair interactions, e.g. excluded volume or native contacts

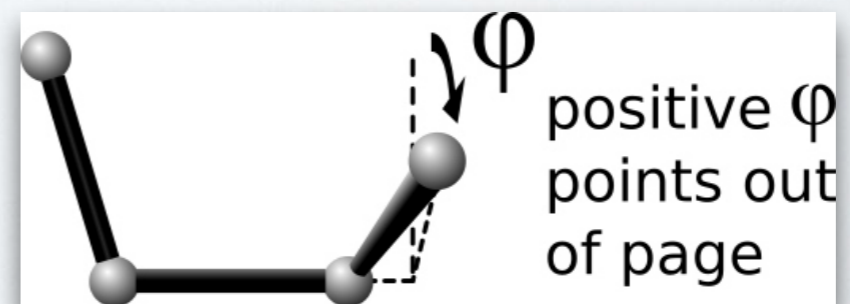
For connected pairs
- Bonds



For triplets
- Angles

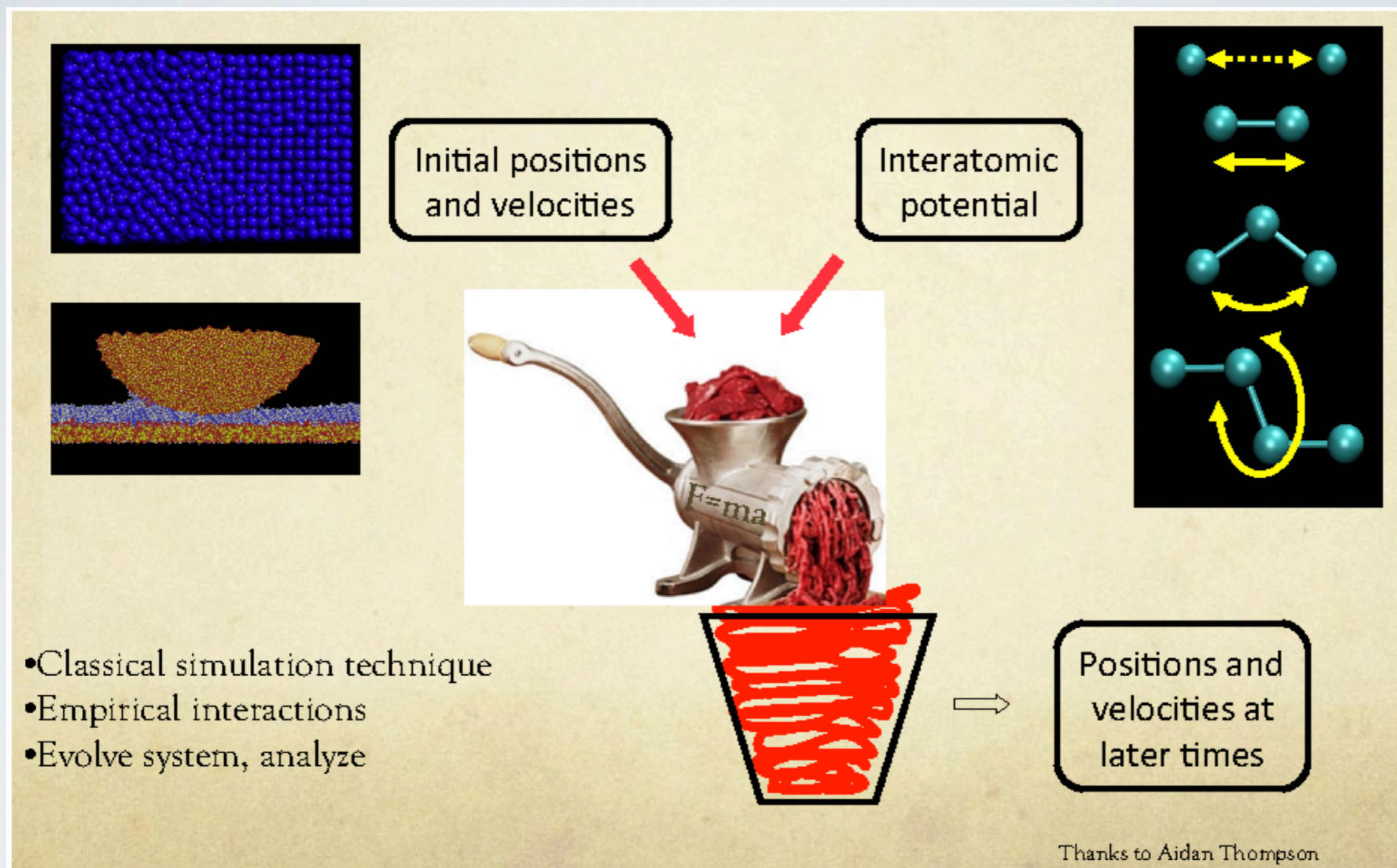
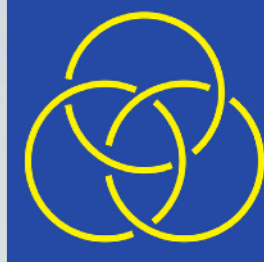


For quadruplets
- Dihedrals



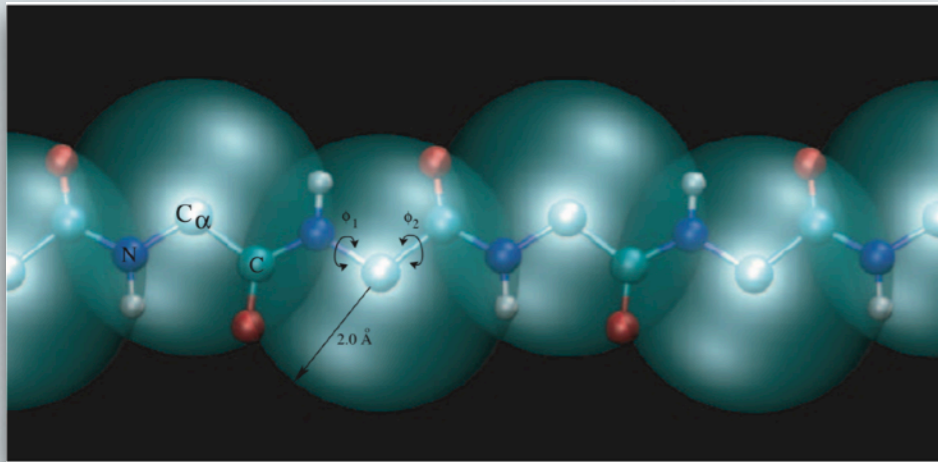
Loosely termed “topology”

What are MD Simulations?

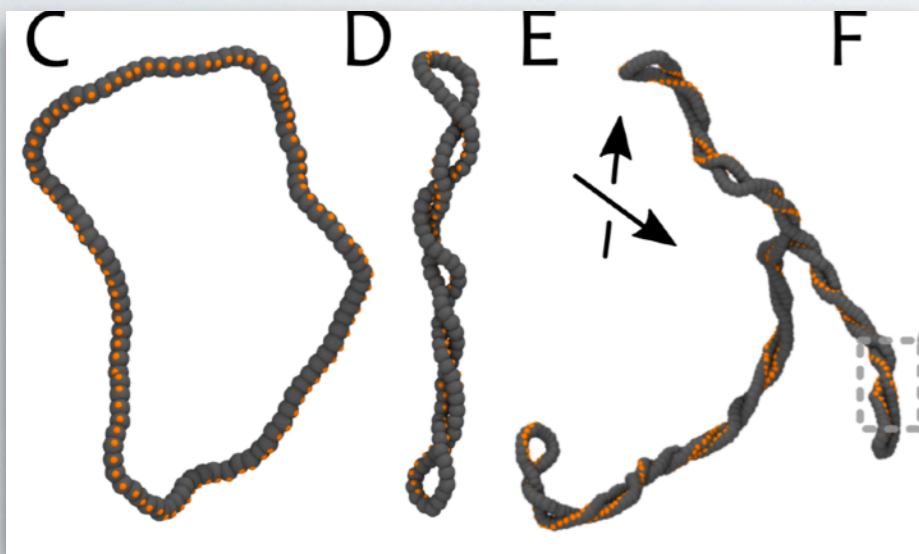


Things you can do

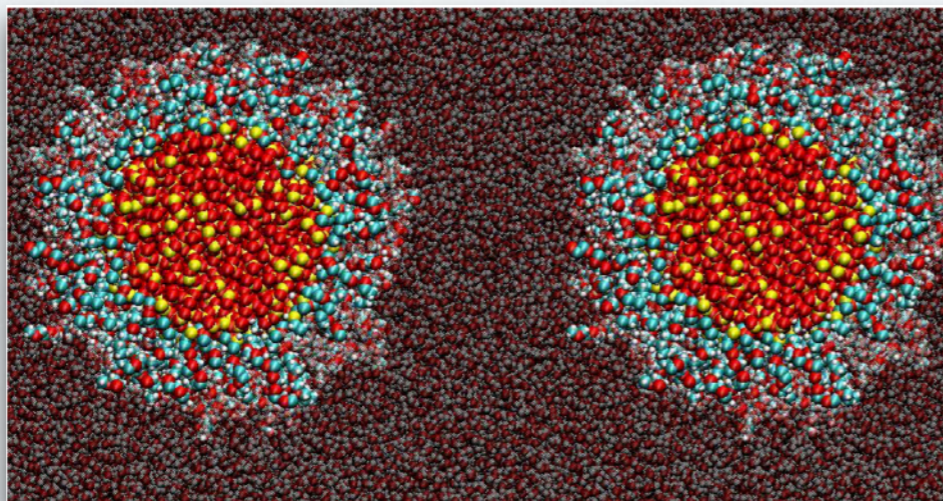
Protein models Coluzza Plos One



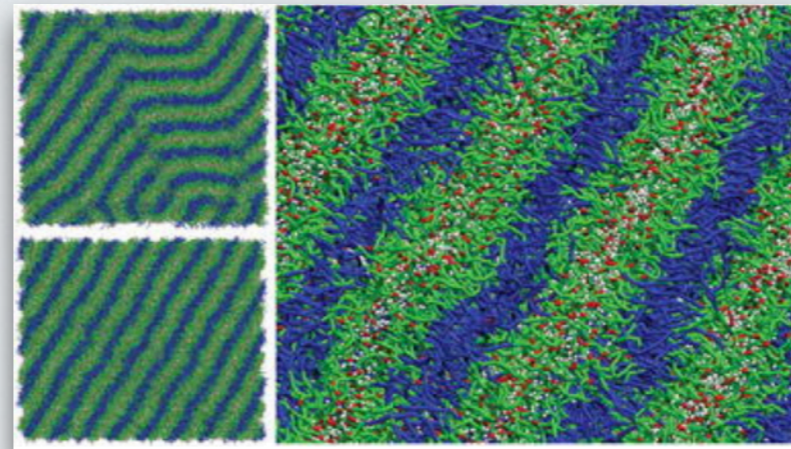
DNA models Smrek et al



PEO
Silica
Particles
In water

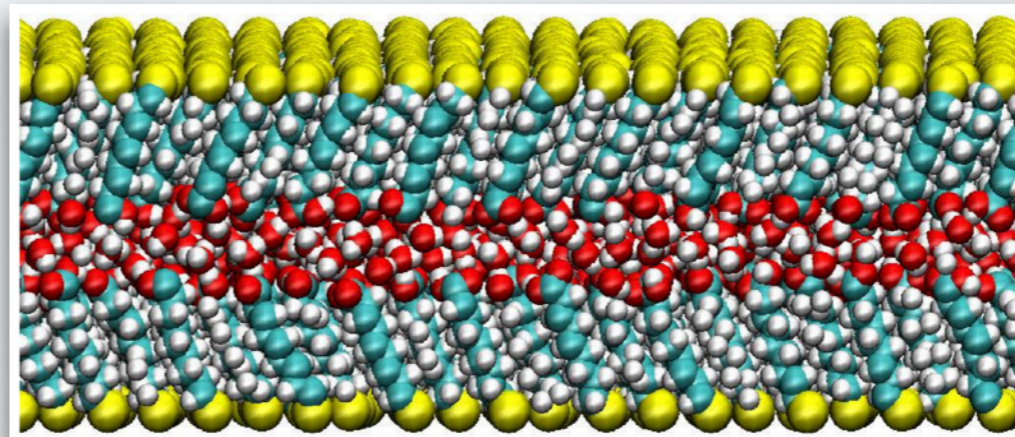


Self assembly/polymers

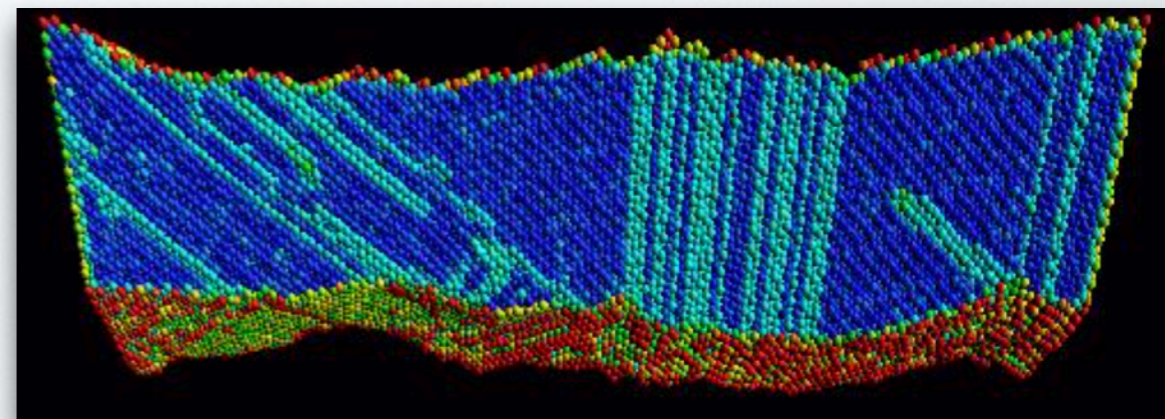


M Klein Science 2008

Water/Lipids



Granular/Hard materials



Min Zhou Cu nanowire



Select an Ensemble



Specify the ensemble

Microcanonical ensemble: Number, Volume and Energy conserved

Velocity (and hence temperature) can change, total energy is fixed

No exchange of heat or energy with environment and happening in vacuum

$$k_B T(t) = \sum_{i=1}^N \frac{m v_{i,\alpha}^2(t)}{N_f} \quad \alpha = x, y, z$$

N_f is the number of degrees of freedom

Canonical ensemble: Number, Volume and Temperature conserved

Distribution of velocities is preserved globally by a thermostat (see later)



In molecular dynamics simulations it is typical to use “dimensionless” units. These are so-called Lennard-Jones units:

Distance. σ / σ^*

This means:

1. decide your s^* [1 nm, 10 cm, 10 km...]
2. Express all distances in units of this length
3. Use s^* to map to real units.

Energy. $\epsilon / k_B T$

Mass. m / m^*

Units - Time



NOTE. Until you are mapping to real units, everything with a * is 1. Hence τ_{LJ} is also 1.

$$\text{LJ Time. } F = ma \rightarrow \frac{k_B T}{\sigma^*} = m^* \sigma^* / \tau_{LJ}^2 \quad \tau_{LJ} = \sigma^* \sqrt{\frac{m^*}{k_B T}}$$

Time to move a bead ballistically

$$\text{Inertial Time. } ma = -\gamma v \rightarrow \tau_{in} = \frac{m^*}{\gamma}$$

Time to decorrelate velocity

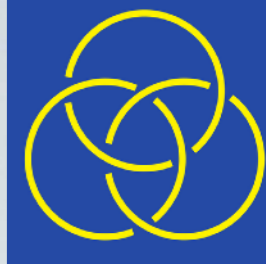
For $t > \tau_{in}$ Brownian dynamics is a good approximation

$$\text{Brown. Time. } ma = (2\gamma k_B T)^{1/2} \eta \rightarrow D = \frac{k_B T}{\gamma} \rightarrow \tau_B = \frac{\sigma^2}{D} = \frac{3\pi\eta_s \sigma^3}{k_B T}$$

Time for a bead to diffuse its own size

In LAMMPS (Brownian Dynamics mode) you can set $1/\gamma = \text{damp}$. γ is a friction term that depends on environment too.

Specify Interactions



I. Pair interactions (between any two pair of atoms in the system)

Lennard Jones

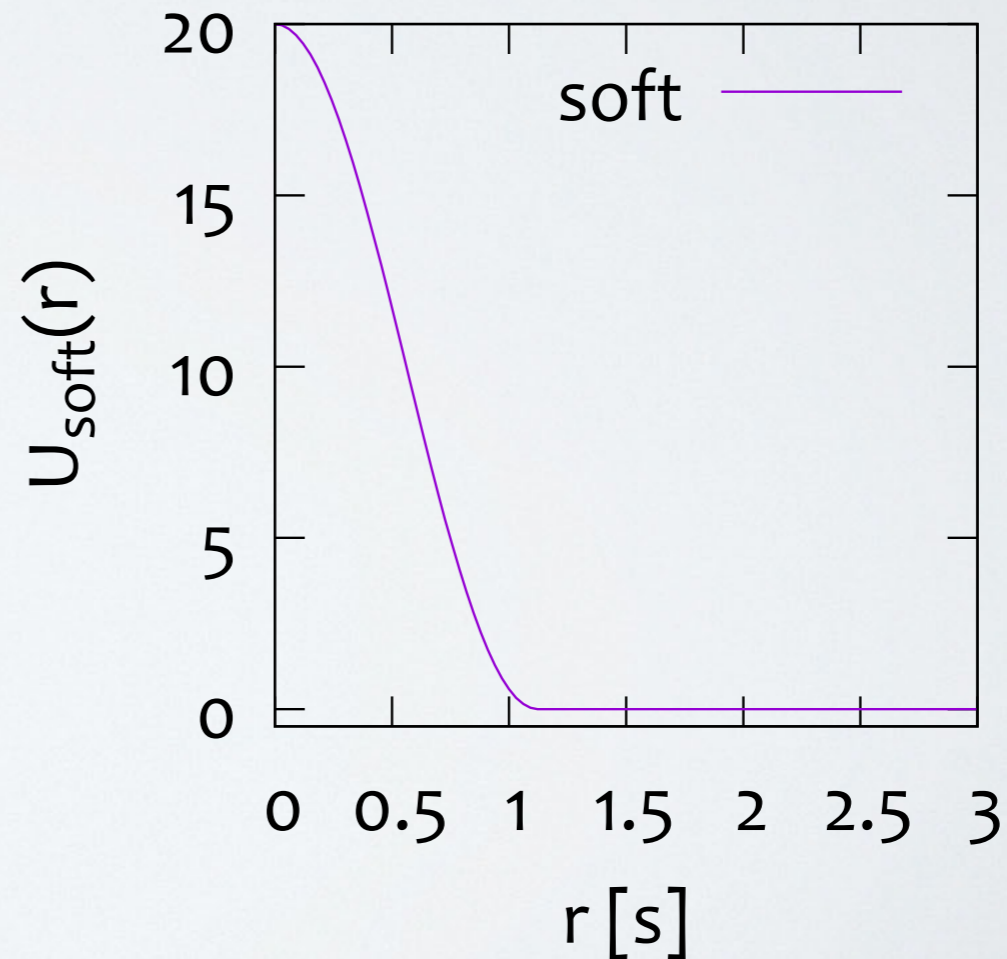
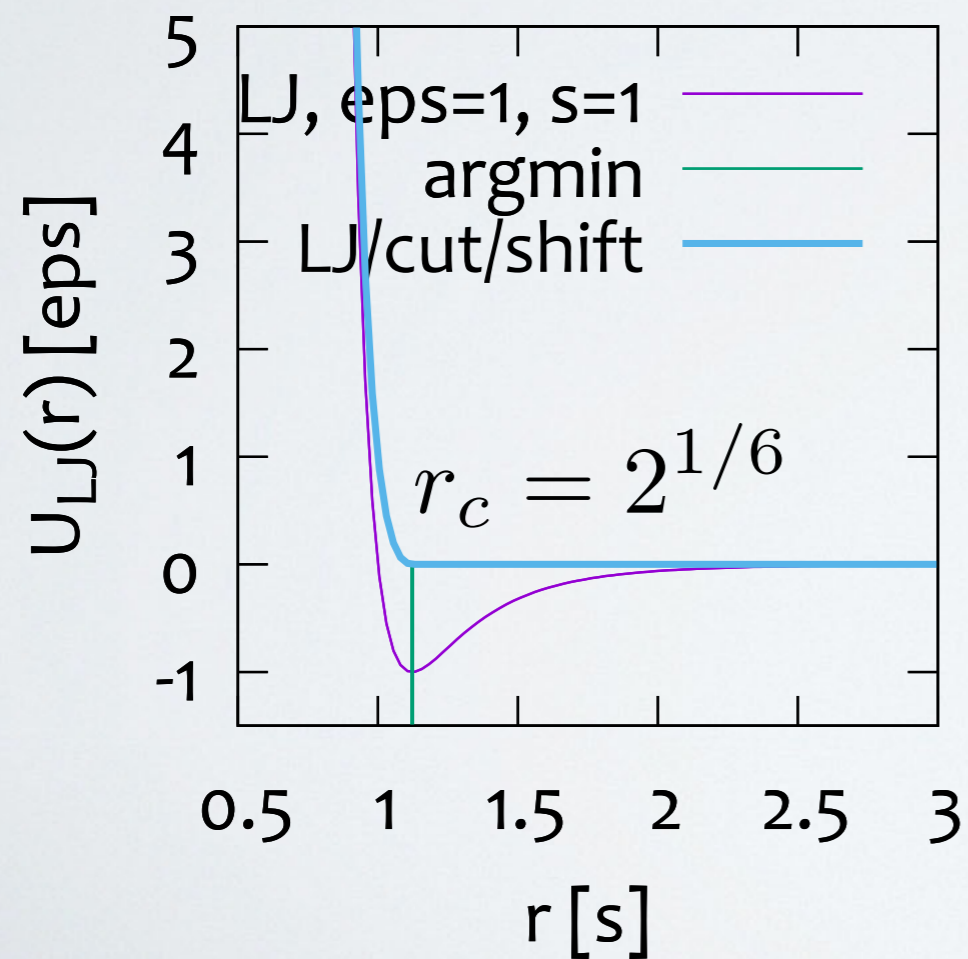
Soft

● $U_{LJ}(r) = 4\epsilon \left[\left(\frac{\sigma}{r}\right)^{12} - \left(\frac{\sigma}{r}\right)^6 \right]$

$$U_{soft}(r) = A \left[1 + \cos \left(\frac{\pi r}{r_c} \right) \right]$$

● $U_{LJ}(r) = 4\epsilon \left[\left(\frac{\sigma}{r}\right)^{12} - \left(\frac{\sigma}{r}\right)^6 + \frac{1}{4} \right]$

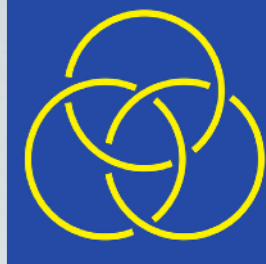
$$r < r_c$$



Uncrossable Repulsive or Partly Attractive

Crossable Only Repulsive

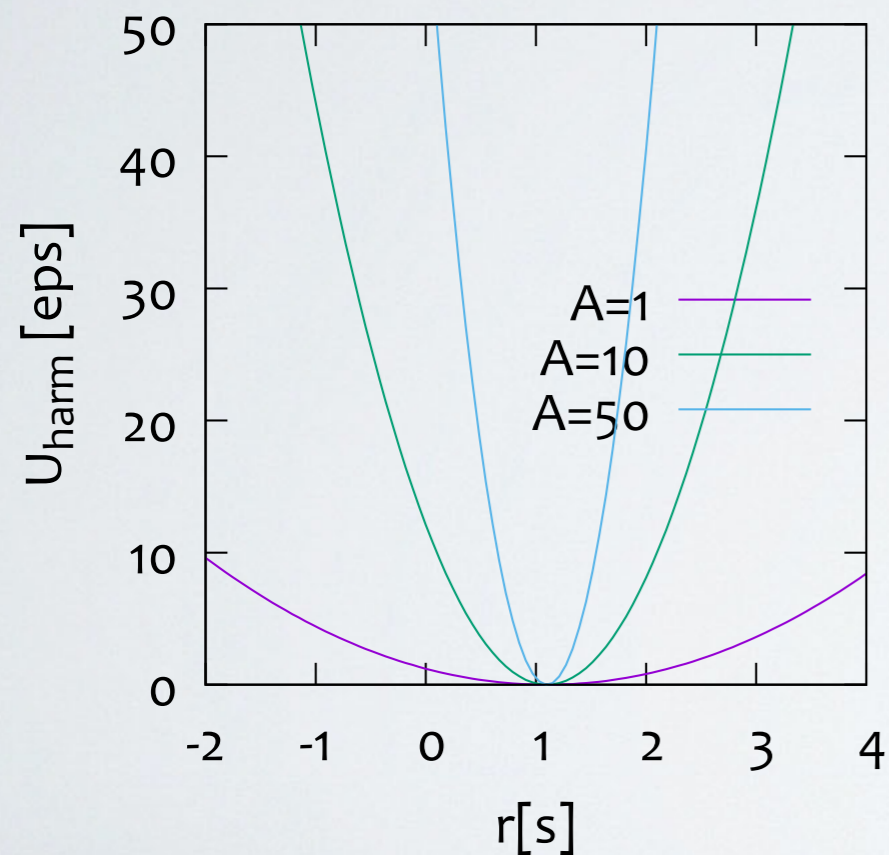
Specify Interactions



2. Bonded interactions (between bonded pairs of atoms)

Harmonic

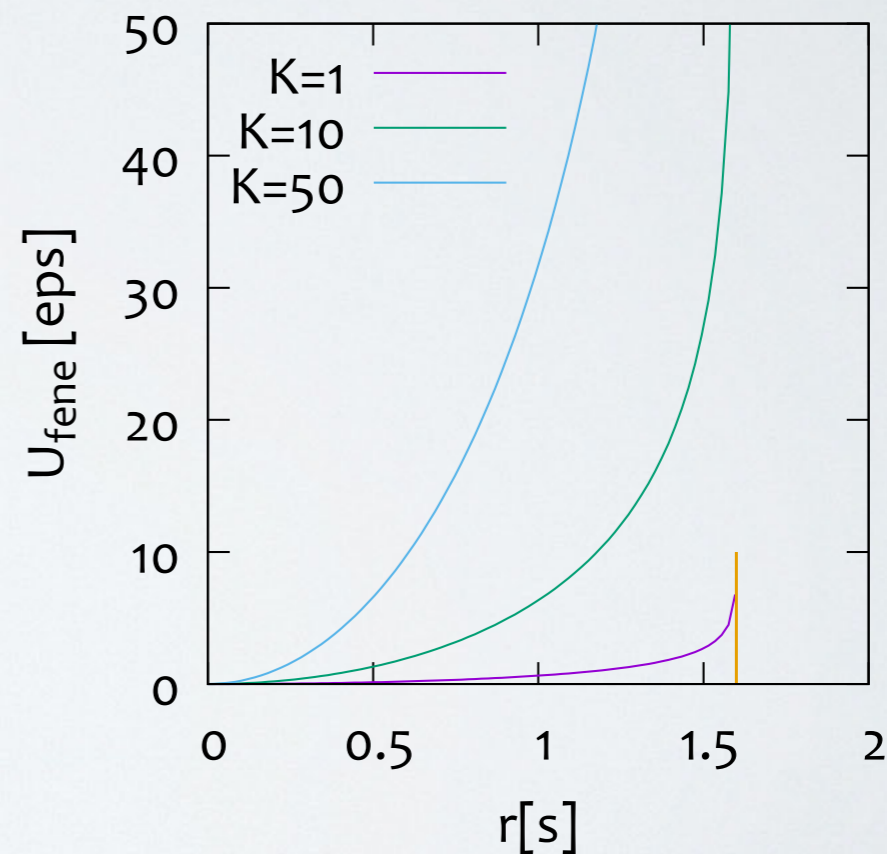
$$U_{harm}(r) = A(r - r_0)^2$$



Does not diverge Minimum at r_0

FENE = Finitely Extensible Non-linear Elastic

$$U_{fene}(r) = -0.5KR_0^2 \log \left[1 - \left(\frac{r}{R_0} \right)^2 \right]$$



Diverges at R_0 Minimum at 0

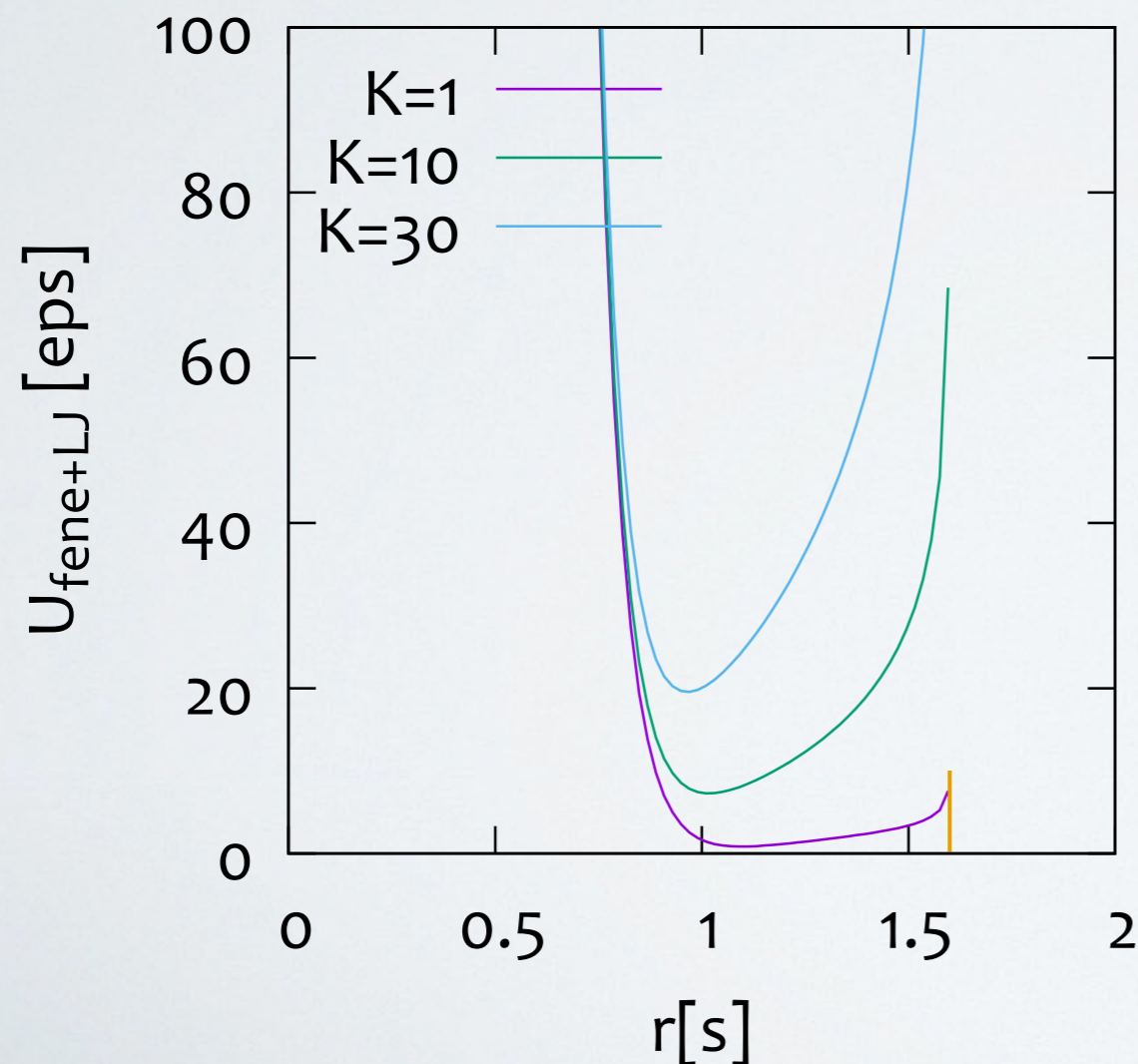
Specify Interactions



2. Bonded interactions (between bonded pairs of atoms)

FENE + LJ

$$U_{fene+LJ}(r) = -0.5K R_0^2 \log \left[1 - \left(\frac{r}{R_0} \right)^2 \right] + 4\epsilon \left[\left(\frac{\sigma}{r} \right)^{12} - \left(\frac{\sigma}{r} \right)^6 + 1/4 \right]$$



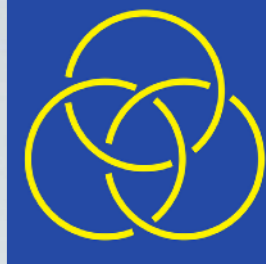
Diverges at R_0

Minimum at $\sim 1 \setminus \sigma$

Diverges as $r \rightarrow 0$

Bonded beads cannot be stretched by more than 0.6 their size and cannot overlap \rightarrow Truly uncrossable polymer

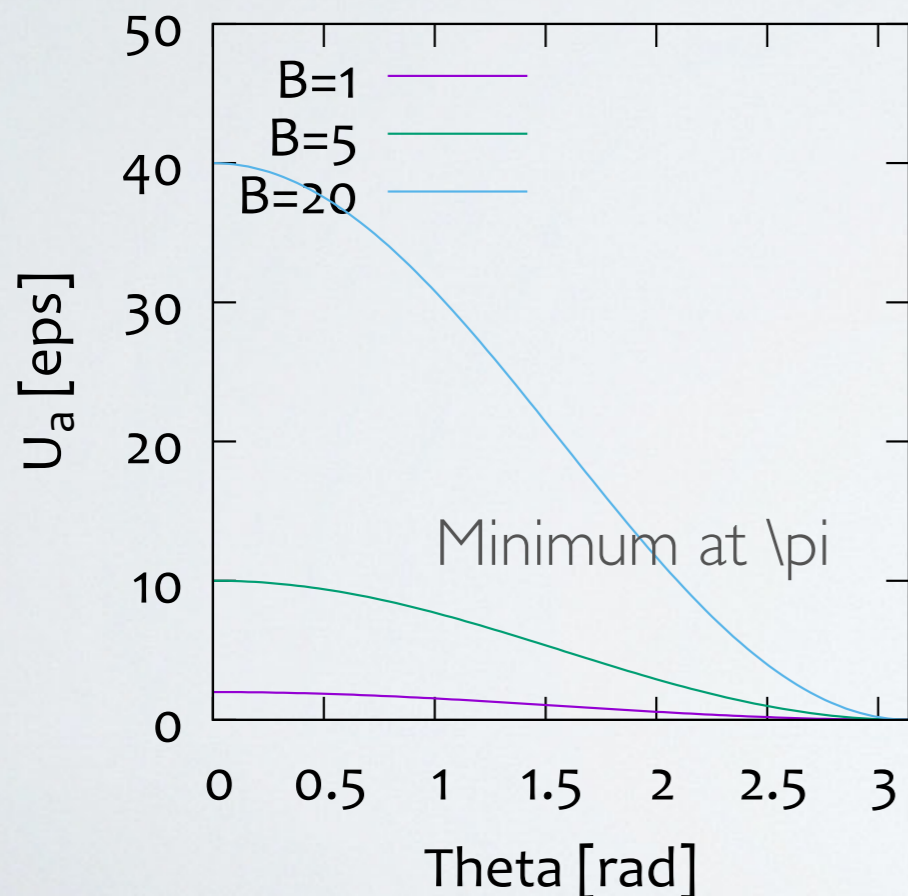
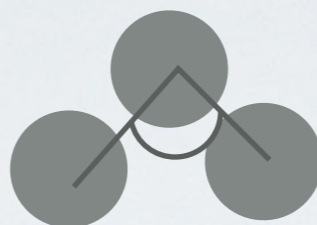
Specify Interactions



3. Angle interactions (between triplets of atoms)

Cosine

$$U_a(\theta) = B(1 + \cos \theta)$$



Elastic modulus "B" [energy]

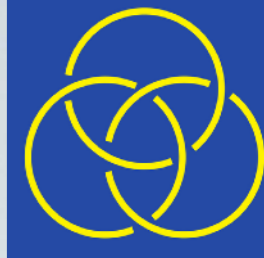
$$B = \frac{k_B T l_p}{\sigma}$$

Where l_p is the persistence length** of a polymer

Persistence length = length at which tangent-tangent correlation decorrelates, i.e.

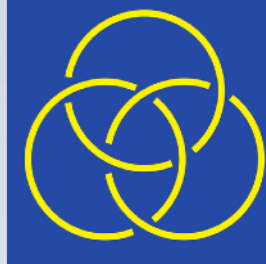
$$\langle \mathbf{t}_i \cdot \mathbf{t}_{i+l} \rangle_i = e^{-l/l_p}$$

Specify Interactions

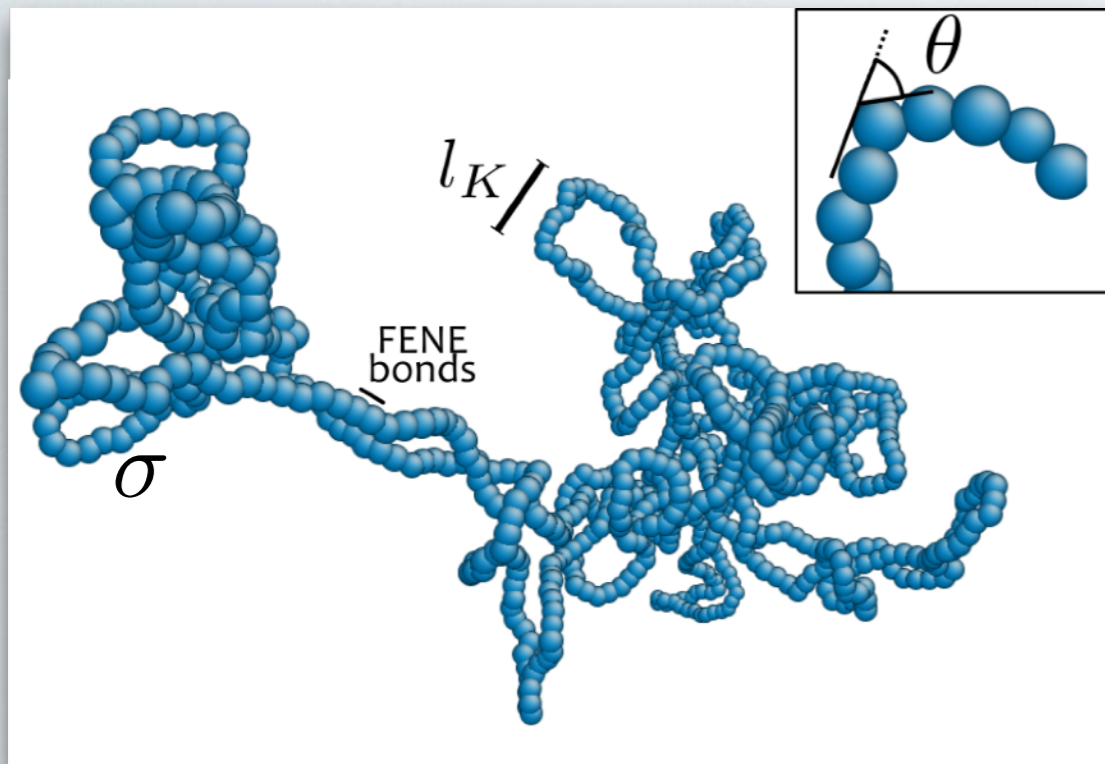


4. Dihedral (exercise for the avid student)

Almost there!!



- You set the interaction topology (pairs, bonds, angles,...),
- Decided how these interactions are tuned by potentials
- Specified the ensemble (NVE for now)



$$\frac{U_{LJ}}{k_B T} = 4 \left[\left(\frac{\sigma}{r} \right)^{12} - \left(\frac{\sigma}{r} \right)^6 \right]$$

$$\frac{U_{FENE}}{k_B T} = -\frac{K R_0^2}{2} \log \left[1 - \left(\frac{r}{R_0} \right)^2 \right]$$

$$U_{bend} = \frac{k_B T l_K}{2\sigma} (1 + \cos \theta)$$

Now what?

Integration of Equations



We need to integrate the eq. of motion. What integrator scheme to use?

1. Newton Eq. are time reversible so the integrator should be it too
2. Fast
3. Must preserve volume in phase space (and thus energy)
4. Little energy drift

Not good: Euler

Not time reversible + energy drift

Popular solution: Verlet algorithm (sum of Taylor exp of $r(t+dt)$ and $r(t-dt)$)

$$r(t + \Delta t) = 2r(t) - r(t - \Delta t) + \frac{f(t)}{m} \Delta t^2$$

$$v(t) = \frac{r(t + \Delta t) - r(t - \Delta t)}{2\Delta t} + O(\Delta t^2)$$

Velocities are computed after positions ...



How's the CPU used?

80% to compute forces

15% to build neighbour lists

5% everything else

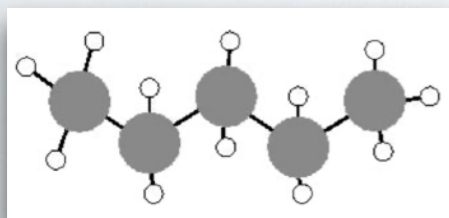
How to make it faster or more efficient?

1. LAMMPS can automatically run in parallel with no extra work and can run on GPUs
2. Smart coarse-graining. What is the minimum level of details to answer my specific question?
3. Use shortest cutoff you can justify

Example

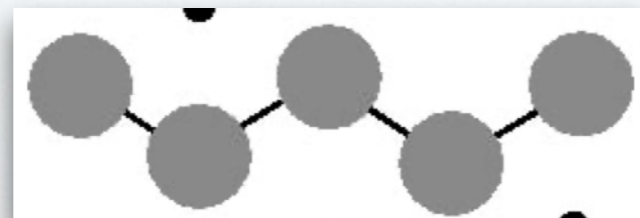
All Atom

dt=1 fsec
d= 0.1 nm
Cut-off = 1nm



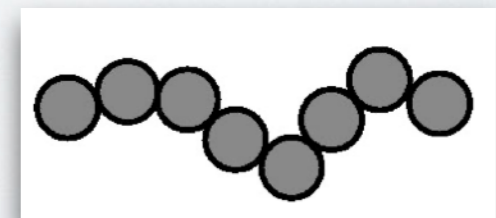
United-Atom

9x fewer interactions
20-30x faster



Bead spring

2-3 C atoms per bead
Even faster ..





<https://www2.ph.ed.ac.uk/~dmichiel/Lab.html>

Google: “dmichiel Lab”

Download: Tutorial0-nve

Thermostats



In NVE simulations you may want to keep temperature fixed, so you need a “thermostat”

Recall that the temperature is a collective feature defined as

$$k_B T(t) = \sum_{i=1}^N \frac{m v_{i,\alpha}^2(t)}{N_f} \quad \alpha = x, y, z$$

(i.e. there is no Temperature for 1 particle)

For N particles, the relative variance of the Temperature $\sim 1/N$

Andersen Thermostat: To keep a Maxwellian distribution of velocities at constant temperature, one can introduce a heat bath by adding stochastic forces acting on random particles (and otherwise NVE)



For particles in a solvent (water) it is best to use Langevin dynamics.

$$ma = -\gamma v - \nabla U + \sqrt{2\gamma k_B T} \eta$$

η Stochastic uncorrelated noise

$$\gamma = 3\pi\eta_s\sigma \quad \text{Friction}$$

The (big) particles are travelling within a solvent (friction) and (small) solvent particles are bumping into the (big) particles.

At times larger than the inertial time $\tau_i = m/\gamma$
this is Brownian motion

$$v = -\frac{\nabla U}{\gamma} + \sqrt{2D}\eta \quad D = k_B T / \gamma$$



<https://www2.ph.ed.ac.uk/~dmichiel/Lab.html>

Google: “dmichiel Lab”

Download: Tutorial0-nvt

Useful resources



LAMMPS documentation/tutorials/presentations

<https://lammmps.sandia.gov/tutorials.html>

Series of tutorials on MD simulations of polymers/knots/links

<https://www2.ph.ed.ac.uk/~dmichiel/Lab.html>

Recent hands-on notes for LAMMPS and Brownian active particles

<https://arxiv.org/pdf/2102.10399.pdf>

Your brain! :)

Don't be afraid, just open source codes and try to understand/fiddle with them...
what's the worst it can happen?

Cite appropriately



It takes a lot of work to come up with all this so...

If (using LAMMPS) {Plimpton Journal of Computational Physics 1995}

If (using bead-spring w FENE) {Kremer, Grest Macromolecules 1990}

If (using standard fix_bond_swap){Sides et al, J Polymer Science B 2004}

If you are interested to use/edit the codes from the tutorial,
feel free to take them and use/edit them
or get in touch as we may have cleaner/better solutions

Future events

Once a month
(last Thursday and Friday)

Python/GROMACS

Atomistic simulations

Topological Analysis

oxDNA

AFM tracing

...



Eutopia Academy for students and post-docs on tools in computational biophysics

Organizers: Davide Michieletto, Samuela Pasquali, Pawel Dabrowski-Tumanski

The Academy will be held on-line, each last Thursday and Friday of the month, February-June 2021. The link to the on-line event will be provided to all registered participants. The registration form will be sent via Eutopia mailing list before each event. Alternatively, please ask directly the organizers.

The plan of the Academy:

25-26 February 2021 – Molecular Dynamics and LAMMPS:

- Basics of MD, theory and simulations in LAMMPS (including simulation of knotted polymers);
- Visualization in VMD
- Simple analysis with C++ codes
- Tricks and tweaks for LAMMPS

Lecturer: Davide Michieletto

25-26 March 2021 – Analysis of the MD results:

- Introduction to Python
- Python-based analysis of trajectories
- Structure and trajectory visualization
- Troubleshooting

Lecturer: Marco Giuliani, Samuela Pasquali, Pawel Dabrowski-Tumanski

29-30 April 2021 – All atom simulations:

- Running all atom simulations
- Analyzing the DNA elasticity
- Emulating AFM images

27-28 May 2021 – Topological analysis:

- KnotPlot
- Topoly
- KymoKnot

eutopia.unitn.eu

