



A brief survey of the LAMMPS particle simulation code: introduction, case studies, and future development

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Acknowledgements

Steve Plimpton (1426)

Aidan Thompson (1425)

Many other contributors to LAMMPS

(see: <http://lammps.sandia.gov/authors.html>)



Discussion outline

1. **MD basics**
2. **Why use LAMMPS?**
3. **Live demo #1**
4. **Basic information about LAMMPS**
5. **Live demo #2**
6. **Six very useful LAMMPS commands**
7. **Live demo #3**
8. **Vignettes of some LAMMPS research**
9. **Future areas of LAMMPS development**
10. **How to add a new feature to LAMMPS**
11. **Homework assignment**



Review of MD basics

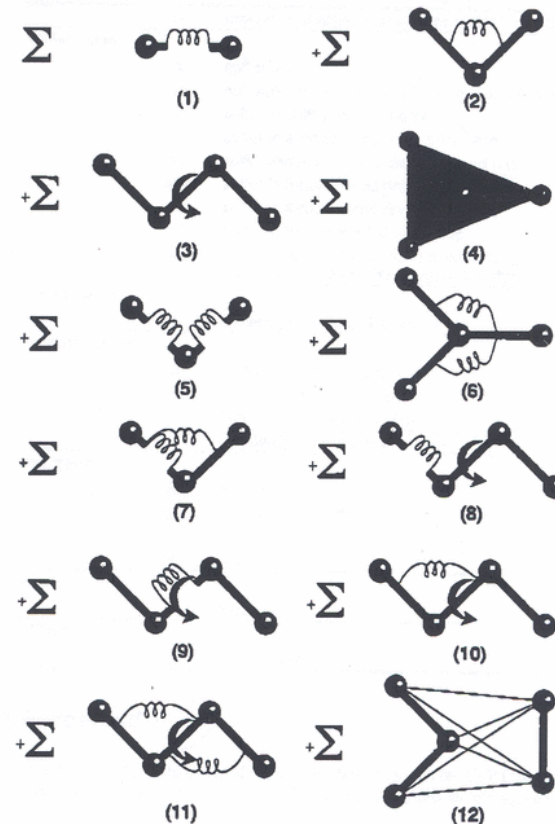
- **MD: molecular dynamics**
- **$F = ma$**
- **Classical dynamics**
- **Rapidly grown in popularity and use in research**
- **Computationally intensive, especially computation of nonbonded interactions**
- **Uses force fields: mathematical models of interatomic interactions**

MD uses empirical force fields

- Particles interact via empirical potentials
 - analytic equations, fast to compute
 - coefficients fit to expt or quantum calcs
- Potential energy = $\Phi = f(\mathbf{x})$
- Force = $-\text{Grad } \Phi$
- Pair-wise forces
 - Van der Waals (dipole-dipole)
 - Coulombic (charge-charge)
- Many-body forces
 - EAM, Tersoff, bond-order, ReaxFF
- Molecular forces
 - springs, torsions, dihedrals, ...
- Long-range Coulombic forces
 - Ewald, particle-mesh methods, FFTs

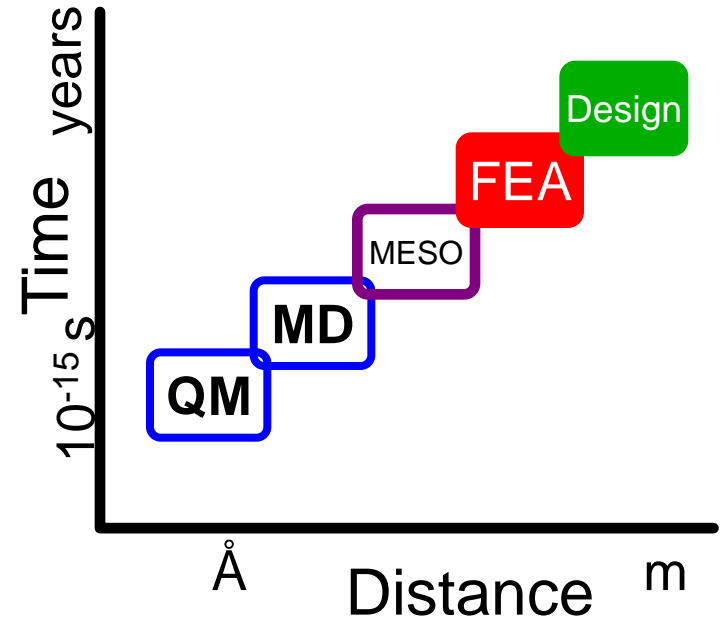
$$E = 4\epsilon \left[\left(\frac{\sigma}{r} \right)^{12} - \left(\frac{\sigma}{r} \right)^6 \right] \quad r < r_c$$

$$E = K(r - r_0)^2$$



MD in the Middle

- Quantum mechanics
 - electronic degrees of freedom, chemical reactions
 - Schrodinger equation, wave functions
 - sub-femtosecond timestep, 1000s of atoms, $O(N^3)$
- Atomistic models
 - molecular dynamics (MD), Monte Carlo (MC)
 - point particles, empirical forces, Newton's equations
 - femtosecond timestep, millions of atoms, $O(N)$
- Mesoscale to Continuum
 - finite elements or finite difference on grids
 - coarse-grain particles: DPD, PeriDynamics, ...
 - PDEs, Navier-Stokes, stress-strain
 - microseconds \rightarrow seconds, microns \rightarrow meters, $O(N^{3/2})$





Algorithmic Issues in MD

- **Speed**
 - parallel implementation
- **Accuracy**
 - long-range Coulombics
- **Time scale**
 - slow versus fast degrees of freedom
- **Length scale**
 - coarse-graining



Classical MD in Parallel

- MD is inherently parallel
 - forces on each atom can be computed simultaneously
 - X and V can be updated simultaneously
- Most MD codes are parallel
 - via distributed-memory message-passing paradigm (MPI)
- Computation scales as N = number of atoms
 - ideally would scale as N/P in parallel
- Can distribute:
 - atoms communication = scales as N
 - forces communication = scales as N/\sqrt{P}
 - space communication = scales as N/P or $(N/P)^{2/3}$



Discussion outline

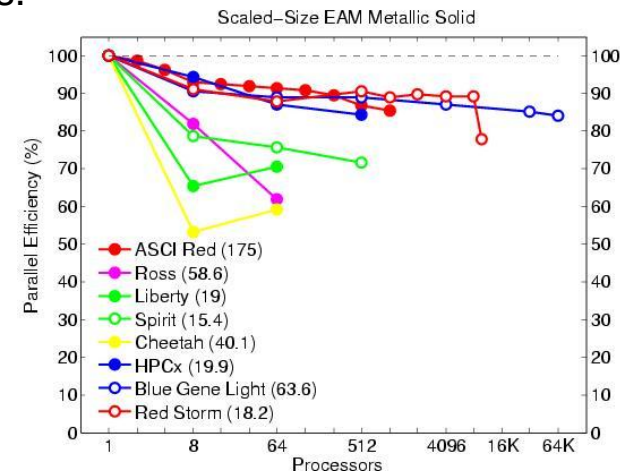
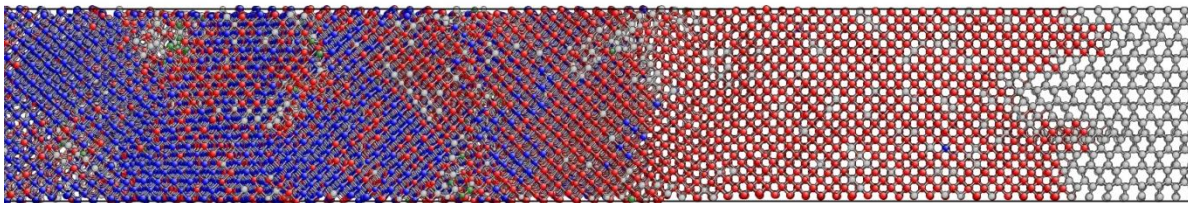
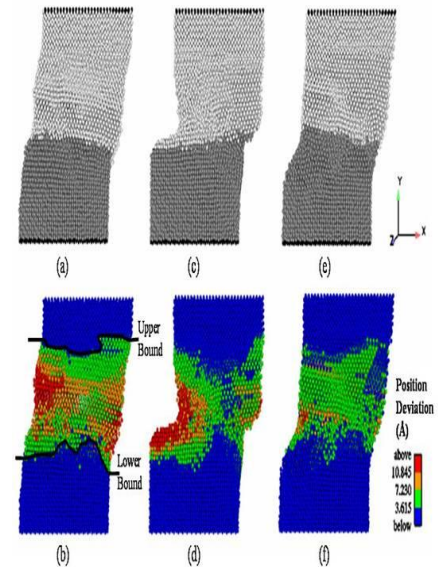
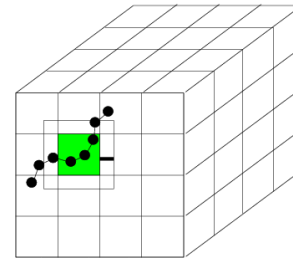
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Why Use LAMMPS?

(Large-scale Atomic/Molecular Massively Parallel Simulator)

<http://lammps.sandia.gov>

- Classical MD code.
- Open source, highly portable C++.
- Freely available for download under GPL.
- Easy to download, install, and run.
- Well documented.
- Easy to modify or extend with new features and functionality.
- Active user's e-mail list with over **650** subscribers.
- Upcoming users' workshop: Aug 9 – 11, 2011.
- Since Sept. 2004: over 50k downloads, grown from 53 to 175 kloc.
- Spatial-decomposition of simulation domain for parallelism.
- Energy minimization via conjugate-gradient relaxation.
- Radiation damage and two temperature model (TTM) simulations.
- Atomistic, mesoscale, and coarse-grain simulations.
- Variety of potentials (including many-body and coarse-grain).
- Variety of boundary conditions, constraints, etc.



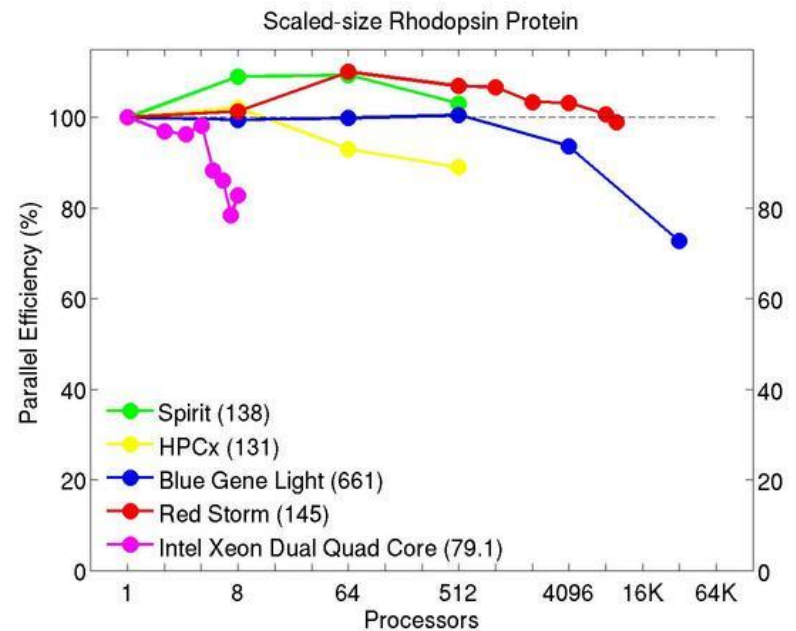
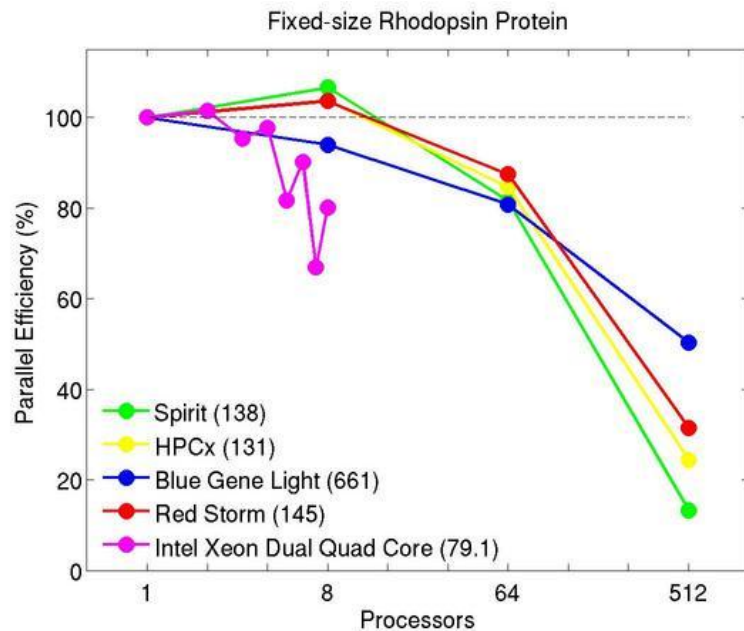
Why Use LAMMPS?

Answer 1: (Parallel) Performance

Protein (rhodopsin) in solvated lipid bilayer

Fixed-size (32K atoms) & scaled-size (32K/proc) parallel efficiencies

Billions of atoms on 64K procs of Blue Gene or Red Storm

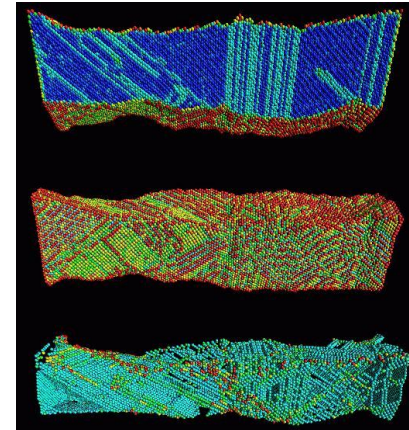
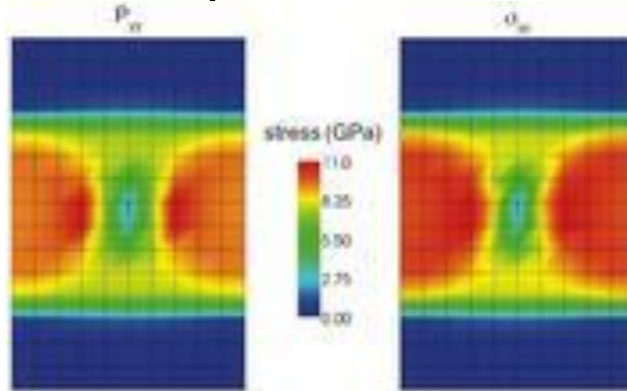


Typical speed: 5E-5 core-sec/atom-step (LJ 1E-6, ReaxFF 1E-3)

Why Use LAMMPS?

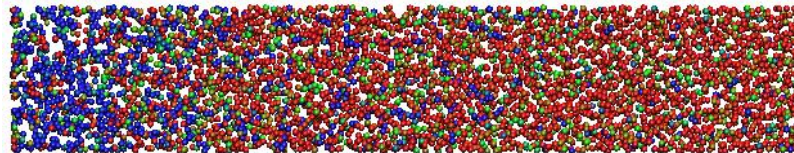
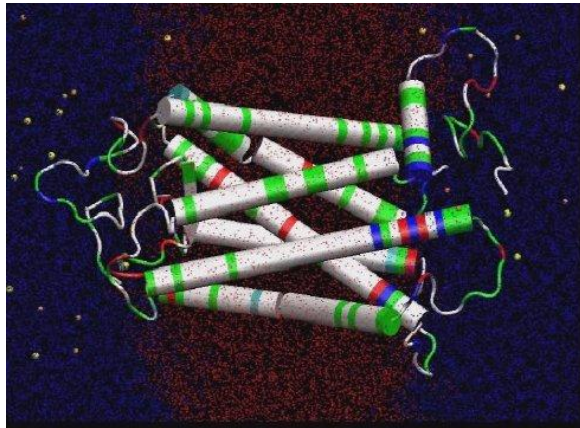
Answer 2: Versatility

**Solid
Mechanics**



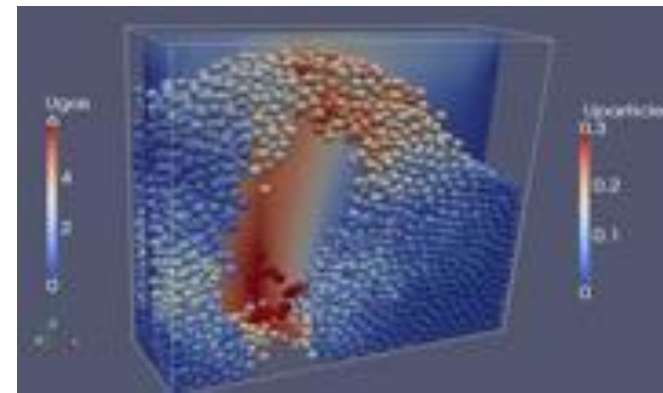
**Materials
Science**

Biophysics



Chemistry

**Granular
Flow**





Why Use LAMMPS?

Answer 3: Modularity

pair_reax.cpp

fix_nve.cpp

pair_reax.h

fix_nve.h

LAMMPS Objects

atom styles: atom, charge, colloid, ellipsoid, point dipole

pair styles: LJ, Coulomb, Tersoff, ReaxFF, AI-REBO, COMB, MEAM, EAM, Stillinger-Weber,

fix_styles: NVE dynamics, Nose-Hoover, Berendsen, Langevin, SLLOD, Indentation,...

compute styles: temperatures, pressures, per-atom energy, pair correlation function, mean square displacements, spatial and time averages

Goal: All computes works with all fixes work with all pair styles work with all atom styles



Why Use LAMMPS?

Answer 4: Potential Coverage

LAMMPS Potentials

pairwise potentials: Lennard-Jones, Buckingham, ...

charged pairwise potentials: Coulombic, point-dipole

manybody potentials: EAM, Finnis/Sinclair, modified EAM

(MEAM), embedded ion method (EIM), Stillinger-Weber, Tersoff, AI-REBO, ReaxFF, COMB

electron force field (eFF)

coarse-grained potentials: DPD, GayBerne, ...

mesoscopic potentials: granular, peridynamics

long-range Coulombics and dispersion: Ewald, PPPM (similar to particle-mesh Ewald)



Why Use LAMMPS?

Answer 4: Potentials

LAMMPS Potentials (contd.)

bond potentials: harmonic, FENE,...

angle potentials: harmonic, CHARMM, ...

dihedral potentials: harmonic, CHARMM,...

improper potentials: harmonic, cvff, class 2 (COMPASS)

polymer potentials: all-atom, united-atom, bead-spring, breakable

water potentials: TIP3P, TIP4P, SPC

implicit solvent potentials: hydrodynamic lubrication, Debye

force-field compatibility with common CHARMM, AMBER, OPLS, GROMACS options



Why Use LAMMPS?

Answer 4: Range of Potentials

LAMMPS Potentials

Biomolecules: CHARMM, AMBER, OPLS, COMPASS (class 2),
long-range Coulombics via PPPM, point dipoles, ...

Polymers: all-atom, united-atom, coarse-grain (bead-spring FENE),
bond-breaking, ...

Materials: EAM and MEAM for metals, Buckingham, Morse, Yukawa,
Stillinger-Weber, Tersoff, AI-REBO, ReaxFF, COMB, eFF...

Mesoscale: granular, DPD, Gay-Berne, colloidal, peri-dynamics, DSMC...

Hybrid: can use combinations of potentials for hybrid systems:
water on metal, polymers/semiconductor interface,
colloids in solution, ...



Why Use LAMMPS?

Answer 5: Easily extensible

- One of the best features of LAMMPS
 - 80% of code is “extensions” via styles
 - only 35K of 175K lines is core of LAMMPS
- Easy to add new features via 14 “styles”
 - new particle types = atom style
 - new long range = kspace style
 - new minimizer = min style
 - new geometric region = region style
 - new output = dump style
 - new integrator = integrate style
 - new computations = compute style (global, per-atom, local)
 - new fix = fix style = BC, constraint, time integration, ...
 - new input command = command style = read_data, velocity, run, ...
- Enabled by C++
 - virtual parent class for all styles, e.g. pair potentials
 - defines interface the feature must provide
 - compute(), init(), coeff(), restart(), etc



How to download, install, and use LAMMPS

- Download page:

lammps.sandia.gov/download.html

- Installation instructions:

lammps.sandia.gov/doc/Section_start.html

go to lammps/src

type “make *your_system_type*”

- To perform a simulation:

Imp < *my_script.in*



Live demo #1

1. Download LAMMPS.

- <http://lammps.sandia.gov/download.html>
- Try the Windows serial executable.

2. Download a simple LAMMPS input script.

- <http://lammps.sandia.gov/inputs/in.lj.txt>

3. Run LAMMPS

- http://lammps.sandia.gov/doc/Section_start.html#2_5



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How to get help with LAMMPS

1. Excellent User's Manual:

<http://lammps.sandia.gov/doc/Manual.html>

http://lammps.sandia.gov/doc/Section_commands.html#3_5

2. Search the web: can include “lammps-users” as a search keyword to search old e-mail archives

3. Send e-mail to the user's e-mail list:

<http://lammps.sandia.gov/mail.html>

4. Contact LAMMPS developers: <http://lammps.sandia.gov/authors.html>

Steve Plimpton, sjplimp@sandia.gov

Aidan Thompson, athomps@sandia.gov

Paul Crozier, pscrozi@sandia.gov

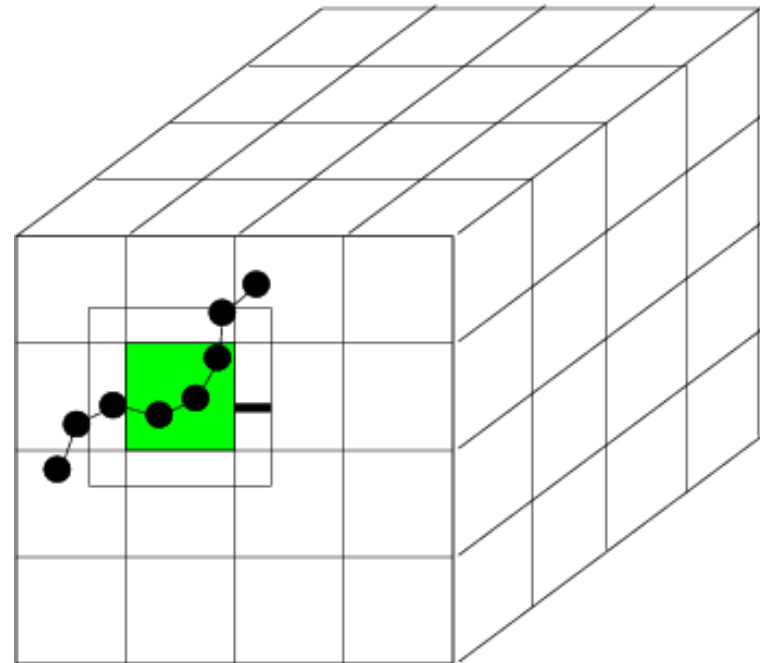


Force fields available in LAMMPS

- **Biomolecules:** CHARMM, AMBER, OPLS, COMPASS (class 2), long-range Coulombics via PPPM, **point dipoles**, ...
- **Polymers:** all-atom, united-atom, coarse-grain (bead-spring FENE), bond-breaking, ...
- **Materials:** EAM and MEAM for metals, Buckingham, Morse, Yukawa, Stillinger-Weber, Tersoff, **AI-REBO**, **Reaxx FF**, ...
- **Mesoscale:** granular, DPD, **Gay-Berne**, **colloidal**, **peri-dynamics**, **DSMC** ...
- **Hybrid:** can use combinations of potentials for hybrid systems: water on metal, polymers/semiconductor interface, colloids in solution, ...

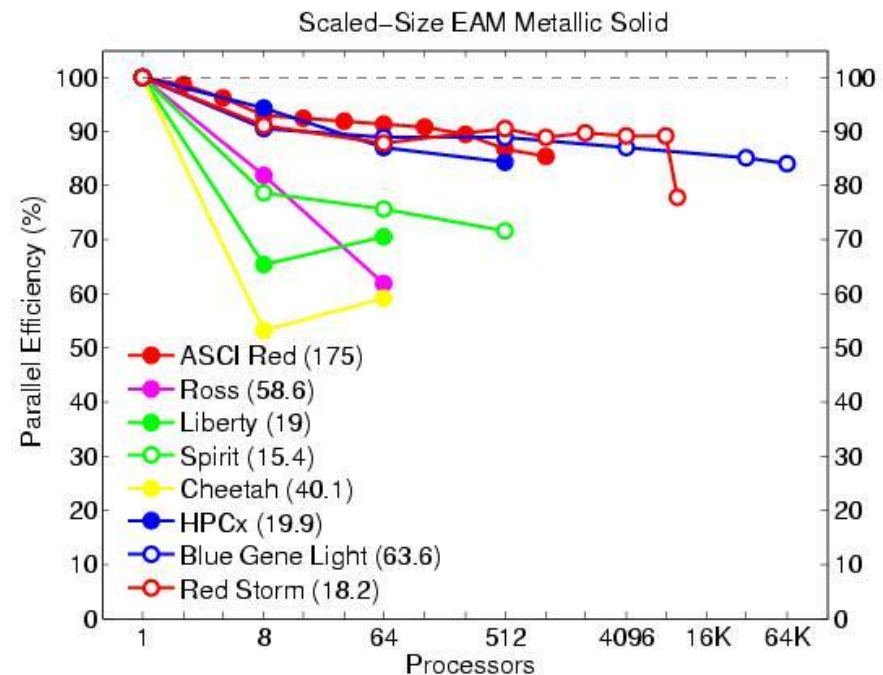
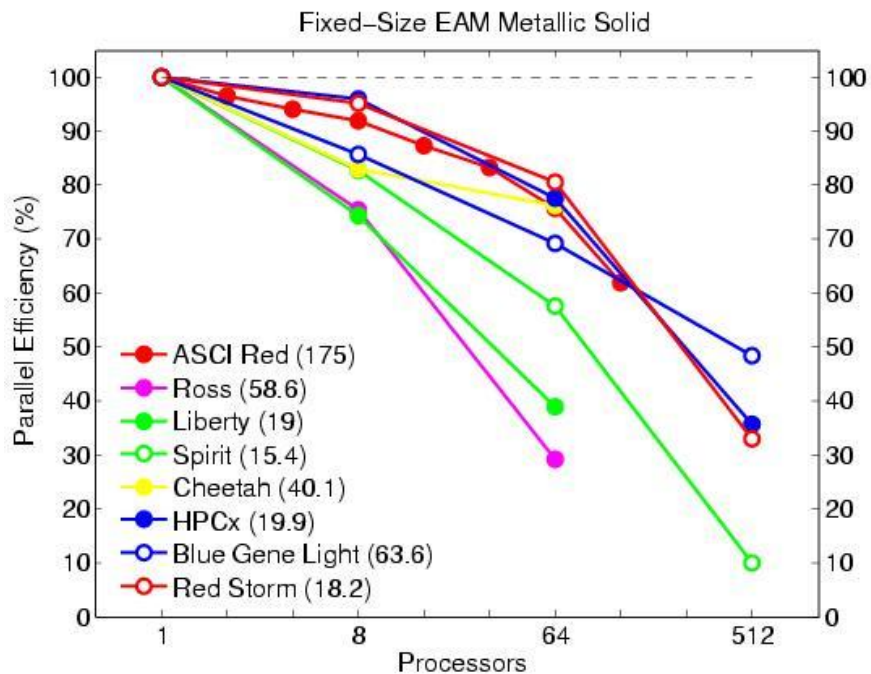
Parallelism via Spatial-Decomposition

- Physical domain divided into 3d boxes, one per processor
- Each proc computes forces on atoms in its box using info from nearby procs
- Atoms "carry along" molecular topology as they migrate to new procs
- Communication via nearest-neighbor 6-way stencil
- Optimal scaling for MD: N/P so long as load-balanced
- Computation scales as N/P
- Communication scales sub-linear as $(N/P)^{2/3}$ (for large problems)
- Memory scales as N/P



LAMMPS's parallel performance

- Fixed-size (32K atoms) and scaled-size (32K atoms/proc) parallel efficiencies
- Metallic solid with EAM potential



- Billions of atoms on 64K procs of Blue Gene or Red Storm
- Opteron processor speed: 5.7E-6 sec/atom/step (0.5x for LJ, 12x for protein)

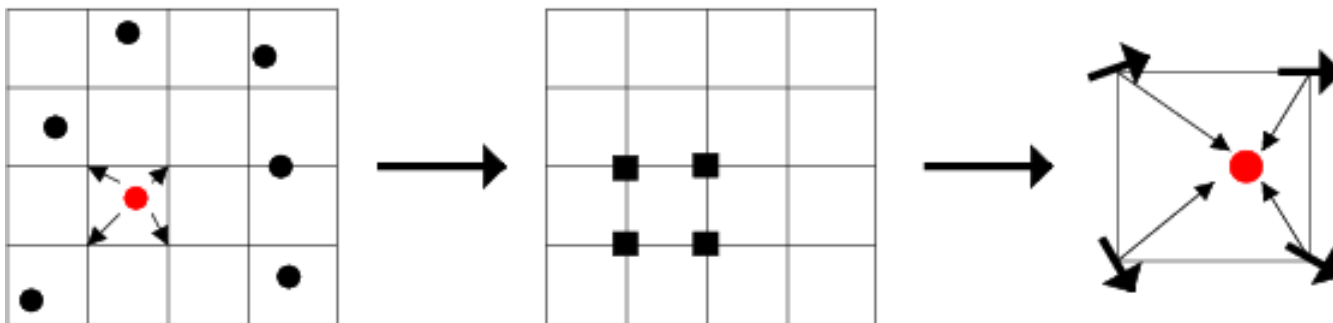


Easily add your own LAMMPS feature

- New user or new simulation → always want new feature not in code
- Goal: make it as easy as possible for us and others to add new features called “styles” in LAMMPS:
 - particle type, pair or bond potential, scalar or per-atom computation
 - “fix”: BC, force constraint, time integration, diagnostic, ...
 - input command: `create_atoms`, `set`, `run`, `temper`, ...
 - over 75% of current 170K+ lines of LAMMPS is add-on styles
- Enabled by C++
 - “virtual” parent class for all pair potentials
 - defines interface: `compute()`, `coeff()`, `restart()`, ...
 - add feature: add 2 lines to header file, add files to src dir, re-compile
 - feature won't exist if not used, won't conflict with rest of code
- Of course, someone has to write the code for the feature!

Particle-mesh Methods for Coulombics

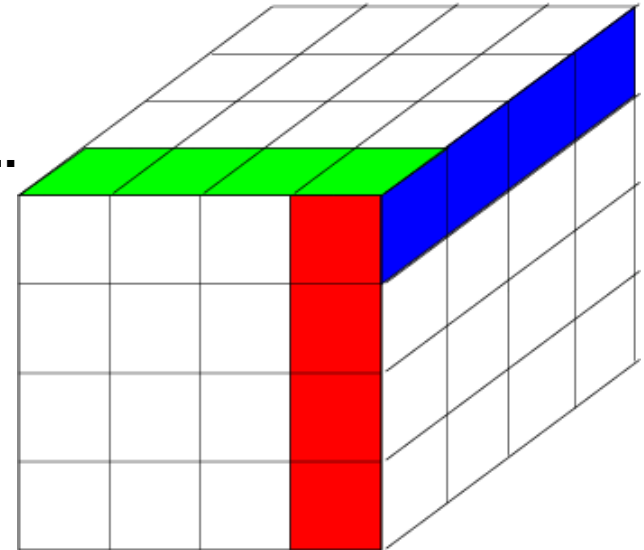
- Coulomb interactions fall off as $1/r$ so require long-range for accuracy
- Particle-mesh methods:
 - partition into short-range and long-range contributions
 - short-range via direct pairwise interactions
 - long-range:
 - interpolate atomic charge to 3d mesh
 - solve Poisson's equation on mesh (4 FFTs)
 - interpolate E-fields back to atoms



- FFTs scale as $N \log N$ if cutoff is held fixed

Parallel FFTs

- 3d FFT is 3 sets of 1d FFTs
in parallel, 3d grid is distributed across procs
perform 1d FFTs on-processor
native library or FFTW (www.fftw.org)
1d FFTs, transpose, 1d FFTs, transpose, ...
"transpose" = data transfer
transfer of entire grid is costly



- FFTs for PPPM can scale poorly
on large # of procs and on clusters
- Good news: Cost of PPPM is only ~2x more than 8-10 Angstrom cutoff



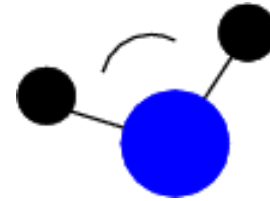
Time Scale of Molecular Dynamics

- Limited timescale is most serious drawback of MD
- Timestep size limited by atomic oscillations:
 - C-H bond = 10 fmsec \rightarrow $\frac{1}{2}$ to 1 fmsec timestep
 - Debye frequency = 10^{13} \rightarrow 2 fmsec timestep
- A state-of-the-art “long” simulation is nanoseconds to a microsecond of real time
- Reality is usually on a much longer timescale:
 - protein folding (msec to seconds)
 - polymer entanglement (msec and up)
 - glass relaxation (seconds to decades)



Extending Timescale

- **SHAKE** = bond-angle constraints, freeze fast DOF
 - up to 2-3 fmsec timestep
 - rigid water, all C-H bonds
 - extra work to enforce constraints
- **rRESPA** = hierarchical time stepping, sub-cycle on fast DOF
 - inner loop on bonds (0.5 fmsec)
 - next loop on angle, torsions (3-4 body forces)
 - next loop on short-range LJ and Coulombic
 - outer loop on long-range Coulombic (4 fmsec)
- **Rigid body time integration via quaternions**
 - treat groups of atom as rigid bodies (portions of polymer or protein)
 - $3N \text{ DOF} \rightarrow 6 \text{ DOF}$
 - save computation of internal forces, longer timestep





Length Scale of Molecular Dynamics

- Limited length scale is 2nd most serious drawback of MD → coarse-graining

- All-atom:

$\Delta t = 0.5\text{-}1.0$ fmsec for C-H

C-C distance = 1.5 Angs

cutoff = 10 Angs

- United-atom:

of interactions is 9x less

$\Delta t = 1.0\text{-}2.0$ fmsec for C-C

cutoff = 10 Angs

20-30x savings over all-atom

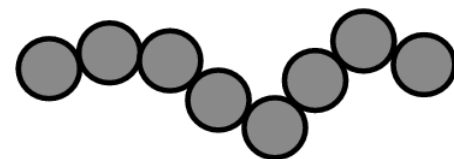
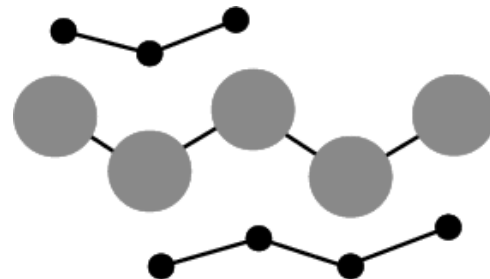
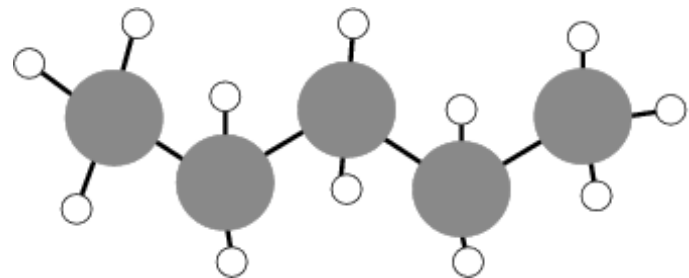
- Bead-Spring:

2-3 C per bead

$\Delta t \leftrightarrow$ fmsec mapping is T-dependent

$2^{1/6} \sigma$ cutoff → 8x in interactions

can be considerable savings over united-atom





Live demo #2

1. **Modify the input script from live demo #1**
 - Add the line “dump 1 all atom 10 atoms.lammpstrj” between the fix and run command lines.
2. **Run LAMMPS with the modified input script.**
3. **Visualize the simulation results using 3rd party software (VMD)**
 - <http://www.ks.uiuc.edu/Research/vmd/>
 - Start up VMD and open the “atoms.lammpstrj” file
 - View the “movie” you’ve made from the LAMMPS trajectory by pressing the play button.



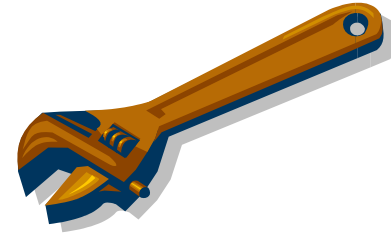
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Six very useful LAMMPS commands

1. **fix**
2. **compute**
3. **pair_style**
4. **variable**
5. **thermo_style**
6. **dump**



fix command

A "fix" is any operation that is applied to the system during time-stepping or minimization.

<http://lammps.sandia.gov/doc/fix.html>

Examples include updating of atom positions and velocities due to time integration, controlling temperature, applying constraint forces to atoms, enforcing boundary conditions, computing diagnostics, etc.

There are dozens of fixes defined in LAMMPS and new ones can be added.

Syntax: fix ID group-ID style args

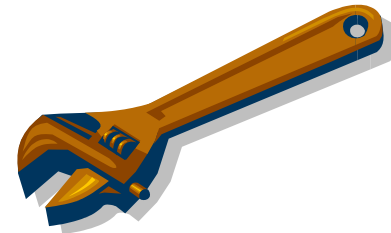
- ID = user-assigned name for the fix
- group-ID = ID of the group of atoms to apply the fix to
- style = one of a long list of possible style names
- args = arguments used by a particular style

Examples:

- fix 1 all nve
- fix 3 all nvt temp 300.0 300.0 0.01
- fix mine top setforce 0.0 NULL 0.0



Available “fixes” in LAMMPS



[adapt](#) - change a simulation parameter over time
[addforce](#) - add a force to each atom
[aveforce](#) - add an averaged force to each atom
[ave/atom](#) - compute per-atom time-averaged quantities
[ave/histo](#) - compute/output time-averaged histograms
[ave/spatial](#) - compute/output time-averaged per-atom quantities by layer
[ave/time](#) - compute/output global time-averaged quantities
[bond/break](#) - break bonds on the fly
[bond/create](#) - create bonds on the fly
[bond/swap](#) - Monte Carlo bond swapping
[box/relax](#) - relax box size during energy minimization
[deform](#) - change the simulation box size/shape
[deposit](#) - add new atoms above a surface
[drag](#) - drag atoms towards a defined coordinate
[dt/reset](#) - reset the timestep based on velocity, forces
[efield](#) - impose electric field on system
[enforce2d](#) - zero out z-dimension velocity and force
[evaporate](#) - remove atoms from simulation periodically
[external](#) - callback to an external driver program
[freeze](#) - freeze atoms in a granular simulation
[gravity](#) - add gravity to atoms in a granular simulation
[heat](#) - add/subtract momentum-conserving heat
[indent](#) - impose force due to an indenter
[langevin](#) - Langevin temperature control
[lineforce](#) - constrain atoms to move in a line
[momentum](#) - zero the linear and/or angular momentum of a group of atoms
[move](#) - move atoms in a prescribed fashion
[msst](#) - multi-scale shock technique (MSST) integration
[neb](#) - nudged elastic band (NEB) spring forces
[nph](#) - constant NPH time integration via Nose/Hoover
[nph/asphere](#) - NPH for aspherical particles
[nph/sphere](#) - NPH for spherical particles
[npt](#) - constant NPT time integration via Nose/Hoover
[npt/asphere](#) - NPT for aspherical particles
[npt/sphere](#) - NPT for spherical particles
[nve](#) - constant NVE time integration
[nve/asphere](#) - NVT for aspherical particles
[nve/limit](#) - NVE with limited step length
[nve/noforce](#) - NVE without forces (v only)
[nve/sphere](#) - NVT for spherical particles
[nvt](#) - constant NVT time integration via Nose/Hoover
[nvt/asphere](#) - NVT for aspherical particles
[nvt/sllod](#) - NVT for NEMD with SLLD equations
[nvt/sphere](#) - NVT for spherical particles
[orient/fcc](#) - add grain boundary migration force
[planeforce](#) - constrain atoms to move in a plane
[poems](#) - constrain clusters of atoms to move as coupled rigid bodies
[pour](#) - pour new atoms into a granular simulation domain
[press/berendsen](#) - pressure control by Berendsen barostat
[print](#) - print text and variables during a simulation
[reax/bonds](#) - write out ReaxFF bond information
[recenter](#) - constrain the center-of-mass position of a group of atoms
[rigid](#) - constrain one or more clusters of atoms to move as a rigid body with NVE integration
[rigid/nve](#) - constrain one or more clusters of atoms to move as a rigid body with alternate NVE integration
[rigid/nvt](#) - constrain one or more clusters of atoms to move as a rigid body with NVT integration
[setforce](#) - set the force on each atom
[shake](#) - SHAKE constraints on bonds and/or angles
[spring](#) - apply harmonic spring force to group of atoms
[spring/rg](#) - spring on radius of gyration of group of atoms
[spring/self](#) - spring from each atom to its origin
[srd](#) - stochastic rotation dynamics (SRD)
[store/force](#) - store force on each atom
[store/state](#) - store attributes for each atom
[temp/berendsen](#) - temperature control by Berendsen thermostat
[temp/rescale](#) - temperature control by velocity rescaling
[thermal/conductivity](#) - Muller-Plathe kinetic energy exchange for thermal conductivity calculation
[tmd](#) - guide a group of atoms to a new configuration
[ttm](#) - two-temperature model for electronic/atomic coupling
[viscosity](#) - Muller-Plathe momentum exchange for viscosity calculation
[viscous](#) - viscous damping for granular simulations
[wall/colloid](#) - Lennard-Jones wall interacting with finite-size particles
[wall/gran](#) - frictional wall(s) for granular simulations
[wall/harmonic](#) - harmonic spring wall
[wall/lj126](#) - Lennard-Jones 12-6 wall
[wall/lj93](#) - Lennard-Jones 9-3 wall
[wall/reflect](#) - reflecting wall(s)
[wall/region](#) - use region surface as wall
[wall/srd](#) - slip/no-slip wall for SRD particles



compute command



A “compute” is a diagnostic performed on a group of atoms, and used to extract quantitative information from a simulation while it is running.

<http://lammps.sandia.gov/doc/compute.html>

Quantities calculated by a compute are instantaneous values, meaning they are calculated from information about atoms on the current timestep or iteration, though a compute may internally store some information about a previous state of the system.

Computes calculate one of three styles of quantities: global, per-atom, or local.

Syntax: compute ID group-ID style args

- ID = user-assigned name for the computation
- group-ID = ID of the group of atoms to perform the computation on
- style = one of a list of possible style names (see below)
- args = arguments used by a particular style

Examples:

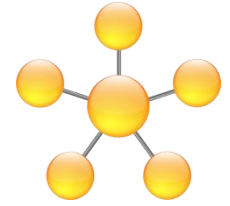
- compute 1 all temp
- compute newtemp flow temp/partial 1 1 0
- compute 3 all ke/atom

Available “computes” in LAMMPS



[angle/local](#) - theta and energy of each angle
[atom/molecule](#) - sum per-atom properties for each molecule
[bond/local](#) - distance and energy of each bond
[centro/atom](#) - centro-symmetry parameter for each atom
[cluster/atom](#) - cluster ID for each atom
[cna/atom](#) - common neighbor analysis (CNA) for each atom
[com](#) - center-of-mass of group of atoms
[com/molecule](#) - center-of-mass for each molecule
[coord/atom](#) - coordination number for each atom
[damage/atom](#) - Peridynamic damage for each atom
[dihedral/local](#) - angle of each dihedral
[displace/atom](#) - displacement of each atom
[erotate/asphere](#) - rotational energy of aspherical particles
[erotate/sphere](#) - rotational energy of spherical particles
[event/displace](#) - detect event on atom displacement
[group/group](#) - energy/force between two groups of atoms
[gyration](#) - radius of gyration of group of atoms
[gyration/molecule](#) - radius of gyration for each molecule
[heat/flux](#) - heat flux through a group of atoms
[improper/local](#) - angle of each improper
[ke](#) - translational kinetic energy
[ke/atom](#) - kinetic energy for each atom

[msd](#) - mean-squared displacement of group of atoms
[msd/molecule](#) - mean-squared displacement for each molecule
[pair](#) - values computed by a pair style
[pair/local](#) - distance/energy/force of each pairwise interaction
[pe](#) - potential energy
[pe/atom](#) - potential energy for each atom
[pressure](#) - total pressure and pressure tensor
[property/atom](#) - convert atom attributes to per-atom vectors/arrays
[property/local](#) - convert local attributes to localvectors/arrays
[property/molecule](#) - convert molecule attributes to localvectors/arrays
[rdf](#) - radial distribution function g(r) histogram of group of atoms
[reduce](#) - combine per-atom quantities into a single global value
[reduce/region](#) - same as compute reduce, within a region
[stress/atom](#) - stress tensor for each atom
[temp](#) - temperature of group of atoms
[temp/asphere](#) - temperature of aspherical particles
[temp/com](#) - temperature after subtracting center-of-mass velocity
[temp/deform](#) - temperature excluding box deformation velocity
[temp/partial](#) - temperature excluding one or more dimensions of velocity
[temp/profile](#) - temperature excluding a binned velocity profile
[temp/ramp](#) - temperature excluding ramped velocity component
[temp/region](#) - temperature of a region of atoms
[temp/sphere](#) - temperature of spherical particles
[ti](#) - thermodynamic integration free energy values



pair_style command

A “pair_style” sets the formula(s) LAMMPS uses to compute pair-wise interactions.

http://lammps.sandia.gov/doc/pair_style.html

Pair potentials are defined between pairs of atoms that are within a cutoff distance and the set of active interactions typically changes over time.

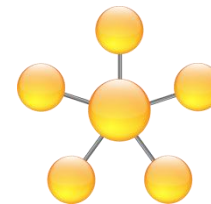
Syntax: pair_style style args

- style = one of the styles from the list below
- args = arguments used by a particular style

Examples:

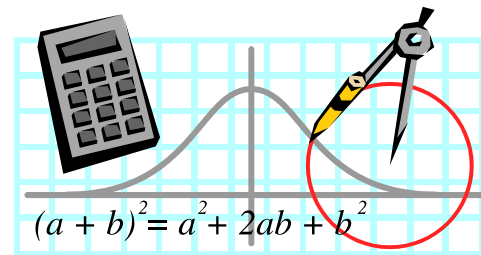
- pair_style lj/cut 2.5
- pair_style eam/alloy
- pair_style hybrid lj/charmm/coul/long 10.0 eam
- pair_style table linear 1000
- pair_style none

Available “pair_styles” in LAMMPS



[pair_style none](#) - turn off pairwise interactions
[pair_style hybrid](#) - multiple styles of pairwise interactions
[pair_style hybrid/overlay](#) - multiple styles of superposed pairwise interactions
[pair_style airebo](#) - AI-REBO potential
[pair_style born](#) - Born-Mayer-Huggins potential
[pair_style born/coul/long](#) - Born-Mayer-Huggins with long-range Coulomb
[pair_style buck](#) - Buckingham potential
[pair_style buck/coul/cut](#) - Buckingham with cutoff Coulomb
[pair_style buck/coul/long](#) - Buckingham with long-range Coulomb
[pair_style colloid](#) - integrated colloidal potential
[pair_style coul/cut](#) - cutoff Coulombic potential
[pair_style coul/debye](#) - cutoff Coulombic potential with Debye screening
[pair_style coul/long](#) - long-range Coulombic potential
[pair_style dipole/cut](#) - point dipoles with cutoff
[pair_style dpd](#) - dissipative particle dynamics (DPD)
[pair_style dpd/tstat](#) - DPD thermostatting
[pair_style dsmc](#) - Direct Simulation Monte Carlo (DSMC)
[pair_style eam](#) - embedded atom method (EAM)
[pair_style eam/opt](#) - optimized version of EAM
[pair_style eam/alloy](#) - alloy EAM
[pair_style eam/alloy/opt](#) - optimized version of alloy EAM
[pair_style eam/fs](#) - Finnis-Sinclair EAM
[pair_style eam/fs/opt](#) - optimized version of Finnis-Sinclair EAM
[pair_style eim](#) - embedded ion method (EIM)
[pair_style gauss](#) - Gaussian potential
[pair_style gayberne](#) - Gay-Berne ellipsoidal potential
[pair_style gayberne/gpu](#) - GPU-enabled Gay-Berne ellipsoidal potential
[pair_style gran/hertz/history](#) - granular potential with Hertzian interactions
[pair_style gran/hooke](#) - granular potential with history effects
[pair_style gran/hooke/history](#) - granular potential without history effects
[pair_style hbond/dreiding/lj](#) - DREIDING hydrogen bonding LJ potential
[pair_style hbond/dreiding/morse](#) - DREIDING hydrogen bonding Morse potential

[pair_style lj/charmm/coul/charmm](#) - CHARMM potential with cutoff Coulomb
[pair_style lj/charmm/coul/charmm/implicit](#) - CHARMM for implicit solvent
[pair_style lj/charmm/coul/long](#) - CHARMM with long-range Coulomb
[pair_style lj/charmm/coul/long/gpu](#) - GPU-enabled version of CHARMM with long-range Coulomb
[pair_style lj/charmm/coul/long/opt](#) - optimized version of CHARMM with long-range Coulomb
[pair_style lj/class2](#) - COMPASS (class 2) force field with no Coulomb
[pair_style lj/class2/coul/cut](#) - COMPASS with cutoff Coulomb
[pair_style lj/class2/coul/long](#) - COMPASS with long-range Coulomb
[pair_style lj/cut](#) - cutoff Lennard-Jones potential with no Coulomb
[pair_style lj/cut/gpu](#) - GPU-enabled version of cutoff LJ
[pair_style lj/cut/opt](#) - optimized version of cutoff LJ
[pair_style lj/cut/coul/cut](#) - LJ with cutoff Coulomb
[pair_style lj/cut/coul/cut/gpu](#) - GPU-enabled version of LJ with cutoff Coulomb
[pair_style lj/cut/coul/debye](#) - LJ with Debye screening added to Coulomb
[pair_style lj/cut/coul/long](#) - LJ with long-range Coulomb
[pair_style lj/cut/coul/long/gpu](#) - GPU-enabled version of LJ with long-range Coulomb
[pair_style lj/cut/coul/long/tip4p](#) - LJ with long-range Coulomb for TIP4P water
[pair_style lj/expand](#) - Lennard-Jones for variable size particles
[pair_style lj/gromacs](#) - GROMACS-style Lennard-Jones potential
[pair_style lj/gromacs/coul/gromacs](#) - GROMACS-style LJ and Coulombic potential
[pair_style lj/smooth](#) - smoothed Lennard-Jones potential
[pair_style lj96/cut](#) - Lennard-Jones 9/6 potential
[pair_style lj96/cut/gpu](#) - GPU-enabled version of Lennard-Jones 9/6
[pair_style lubricate](#) - hydrodynamic lubrication forces
[pair_style meam](#) - modified embedded atom method (MEAM)
[pair_style morse](#) - Morse potential
[pair_style morse/opt](#) - optimized version of Morse potential
[pair_style peri/lps](#) - peridynamic LPS potential
[pair_style peri/pmb](#) - peridynamic PMB potential
[pair_style reax](#) - ReaxFF potential
[pair_style resquared](#) - Everaers RE-Squared ellipsoidal potential
[pair_style soft](#) - Soft (cosine) potential
[pair_style sw](#) - Stillinger-Weber 3-body potential
[pair_style table](#) - tabulated pair potential
[pair_style tersoff](#) - Tersoff 3-body potential
[pair_style tersoff/zbl](#) - Tersoff/ZBL 3-body potential
[pair_style yukawa](#) - Yukawa potential
[pair_style yukawa/colloid](#) - screened Yukawa potential for finite-size particles



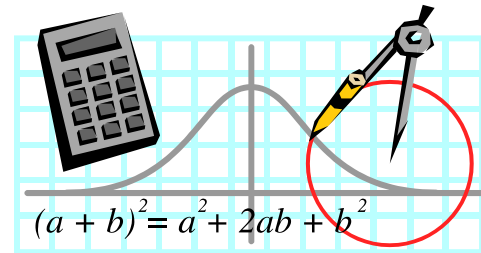
variable command

This command assigns one or more strings to a variable name for evaluation later in the input script or during a simulation.

<http://lammps.sandia.gov/doc/variable.html>

- A variable can be referenced elsewhere in an input script to become part of a new input command.
- For variable styles that store multiple strings, the [next](#) command can be used to increment which string is assigned to the variable.
- Variables of style *equal* store a formula which when evaluated produces a single numeric value which can be output either directly (see the [print](#), [fix print](#), and [run every](#) commands) or as part of thermodynamic output (see the [thermo_style](#) command), or used as input to an averaging fix (see the [fix ave/time](#) command).
- Variables of style *atom* store a formula which when evaluated produces one numeric value per atom which can be output to a dump file (see the [dump custom](#) command) or used as input to an averaging fix (see the [fix ave/spatial](#) and [fix ave/atom](#) commands).

variable command (cont.)



Syntax: variable name style args ...

- name = name of variable to define
- style = *delete* or *index* or *loop* or *world* or *universe* or *uloop* or *string* or *equal* or *atom*

Examples:

- variable x index run1 run2 run3 run4 run5 run6 run7 run8
- variable LoopVar loop \$n
- variable beta equal temp/3.0
- variable b1 equal x[234]+0.5*vol
- variable b1 equal "x[234] + 0.5*vol"
- variable b equal xcm(mol1,x)/2.0
- variable b equal c_myTemp
- variable b atom x*y/vol variable foo myfile
- variable temp world 300.0 310.0 320.0 \${Tfinal}
- variable x universe 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
- variable x uloop 15 pad
- variable x delete



thermo_style command

Set the style and content for printing data to the screen and log file.

http://lammps.sandia.gov/doc/thermo_style.html

Syntax: thermo_style style args

- **style = *one* or *multi* or *custom***
- **args = list of arguments for a particular style**

Examples:

- **thermo_style multi**
- **thermo_style custom step temp pe etotal press vol**
- **thermo_style custom step temp etotal c_myTemp v_abc**



Available “thermo_style” attributes

step = timestep

elapsed = timesteps since start of this run

elaplong = timesteps since start of initial run in a series of runs

dt = timestep size

cpu = elapsed CPU time in seconds

tpcpu = time per CPU second

spcpu = timesteps per CPU second

atoms = # of atoms

temp = temperature

press = pressure

pe = total potential energy

ke = kinetic energy

etotal = total energy (pe + ke)

enthalpy = enthalpy (etotal + press*vol)

evdwl = VanderWaal pairwise energy

ecoul = Coulombic pairwise energy

epair = pairwise energy (evdwl + ecoul + elong + etail)

ebond = bond energy

eangle = angle energy

edihed = dihedral energy

eimp = improper energy

emol = molecular energy (ebond + eangle + edihed + eimp)

elong = long-range kspace energy

etail = VanderWaal energy long-range tail correction

vol = volume

lx,ly,lz = box lengths in x,y,z

xlo,xhi,ylo,yhi,zlo,zhi = box boundaries

xy,xz,yz = box tilt for triclinic (non-orthogonal) simulation boxes

xlat,ylat,zlat = lattice spacings as calculated by "lattice"_lattice.html command

pxx,pyy,pzz,pxy,pxz,pyz = 6 components of pressure tensor

fmax = max component of force on any atom in any dimension

fnorm = length of force vector for all atoms

c_ID = global scalar value calculated by a compute with ID

c_ID[I] = Ith component of global vector calculated by a compute with ID

c_ID[I]\[J] = I,J component of global array calculated by a compute with ID

f_ID = global scalar value calculated by a fix with ID

f_ID[I] = Ith component of global vector calculated by a fix with ID

f_ID[I]\[J] = I,J component of global array calculated by a fix with ID

v_name = scalar value calculated by an equal-style variable with name



dump command



Dump a snapshot of atom quantities to one or more files every N timesteps in one of several styles.

<http://lammps.sandia.gov/doc/dump.html>

Syntax:

- **dump ID group-ID style N file args** ID = user-assigned name for the dump
- **group-ID** = ID of the group of atoms to be dumped
- **style** = *atom* or *cfg* or *dcd* or *xtc* or *xyz* or *local* or *custom*
- **N** = dump every this many timesteps
- **file** = name of file to write dump info to
- **args** = list of arguments for a particular style *atom*

Examples:

- **dump myDump all atom 100 dump.atom**
- **dump 2 subgroup atom 50 dump.run.bin**
- **dump 4a all custom 100 dump.myforce.* id type x y vx fx**
- **dump 4b flow custom 100 dump.%.myforce id type c_myF[3] v_ke**
- **dump 2 inner cfg 10 dump.snap.*.cfg id type xs ys zs vx vy vz**
- **dump snap all cfg 100 dump.config.*.cfg id type xs ys zs id type c_Stress2**
- **dump 1 all xtc 1000 file.xtc**
- **dump e_data all custom 100 dump.eff id type x y z spin eradius fx fy fz eforce**

Available “dump” atom attributes



id = atom ID
mol = molecule ID
type = atom type
mass = atom mass
x,y,z = unscaled atom coordinates
xs,ys,zs = scaled atom coordinates
xu,yu,zu = unwrapped atom coordinates
ix,iy,iz = box image that the atom is in
vx,vy,vz = atom velocities
fx,fy,fz = forces on atoms
q = atom charge
mux,muy,muz = orientation of dipolar atom
radius = radius of extended spherical particle
omegax,omegay,omegaz = angular velocity of extended particle
angmomx,angmomy,angmomz = angular momentum of extended particle
quatw,quati,quatj,quatk = quaternion components for aspherical particles
tqx,tqy,tqz = torque on extended particles
spin = electron spin
eradius = electron radius
ervel = electron radial velocity
erforce = electron radial force
c_ID = per-atom vector calculated by a compute with ID
c_ID[N] = Nth column of per-atom array calculated by a compute with ID
f_ID = per-atom vector calculated by a fix with ID
f_ID[N] = Nth column of per-atom array calculated by a fix with ID
v_name = per-atom vector calculated by an atom-style variable with name



Live demo #3

1. **Modify the LAMMPS input script from demo #2 so that it includes at least one example of each of the following six commands:**
 1. **fix**
 2. **compute**
 3. **pair_style**
 4. **variable**
 5. **thermo_style**
 6. **dump**
2. **Run LAMMPS with the modified input script.**



Discussion outline

1. MD basics
2. Why use LAMMPS?
3. Live demo #1
4. Basic information about LAMMPS
5. Live demo #2
6. Six very useful LAMMPS commands
7. Live demo #3
8. Vignettes of some LAMMPS research
9. Future areas of LAMMPS development
10. How to add a new feature to LAMMPS
11. Homework assignment

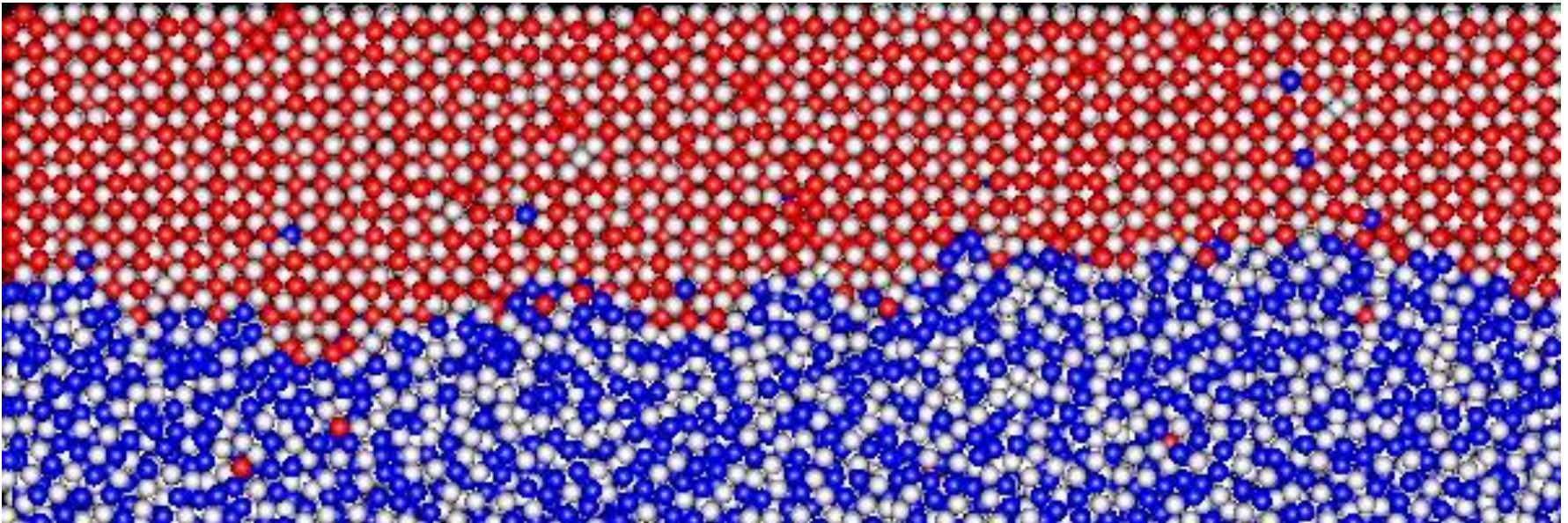


Vignettes of some LAMMPS research

- Interfaces in melting solids
- Adhesion properties of polymers
- Shear response in metals
- Tensile pull on nanowires
- Surface growth on mismatched lattice
- Shock-induced phase transformations
- Silica nanopores for water desalination
- Coated nanoparticles in solution and at interfaces
- Self-assembly (2d micelles and 3d lipid bilayers)
- Rhodopsin protein isomerization
- Whole vesicle simulation
- Radiation damage

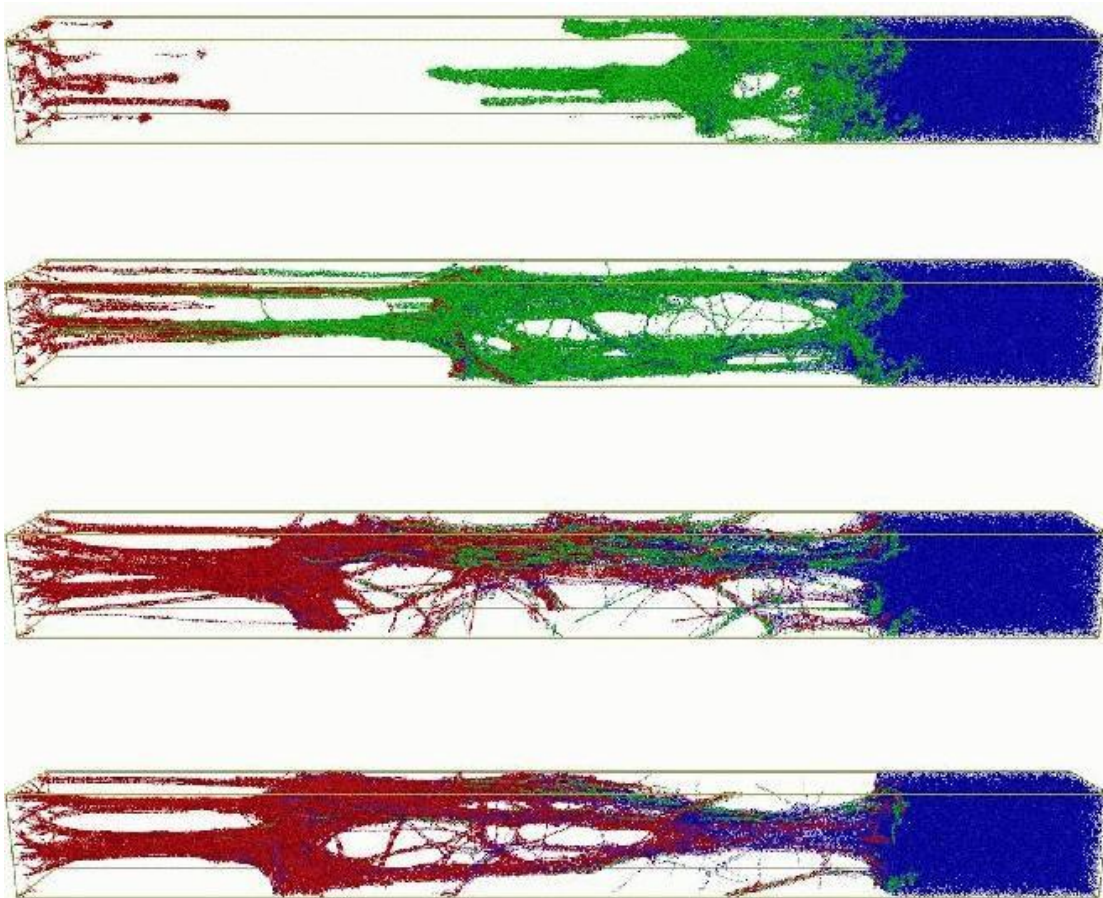
Melt Interface in NiAl

- Mark Asta (UC Davis) and Jeff Hoyt (Sandia)
- Careful thermostatting and equilibration of alloy system
- Track motion and structure of melt interface



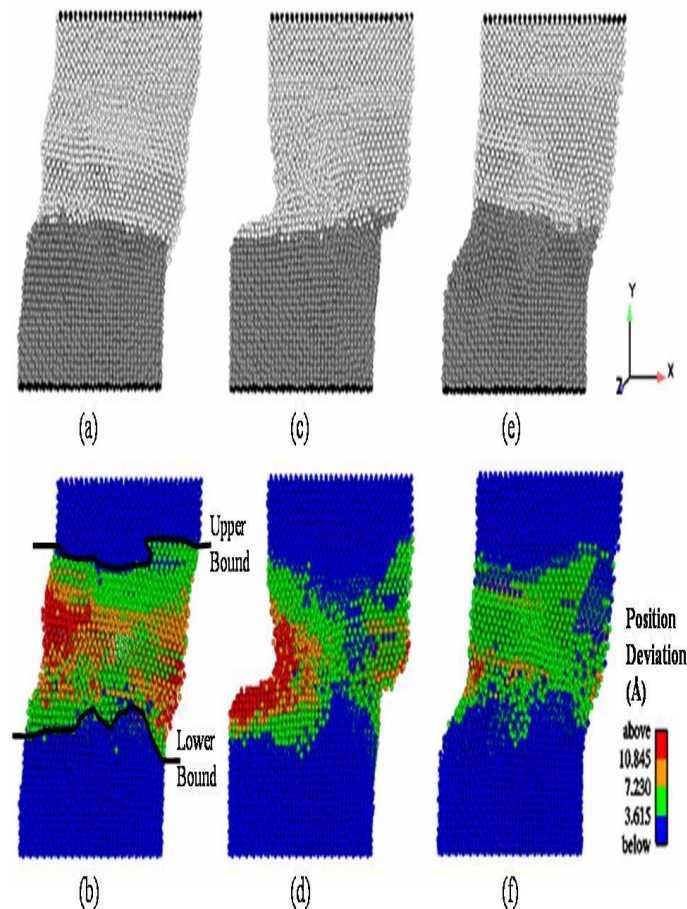
Polymer Adhesive Properties

- Mark Stevens and Gary Grest (Sandia)
- Bead/spring polymer model, allow for bond breaking



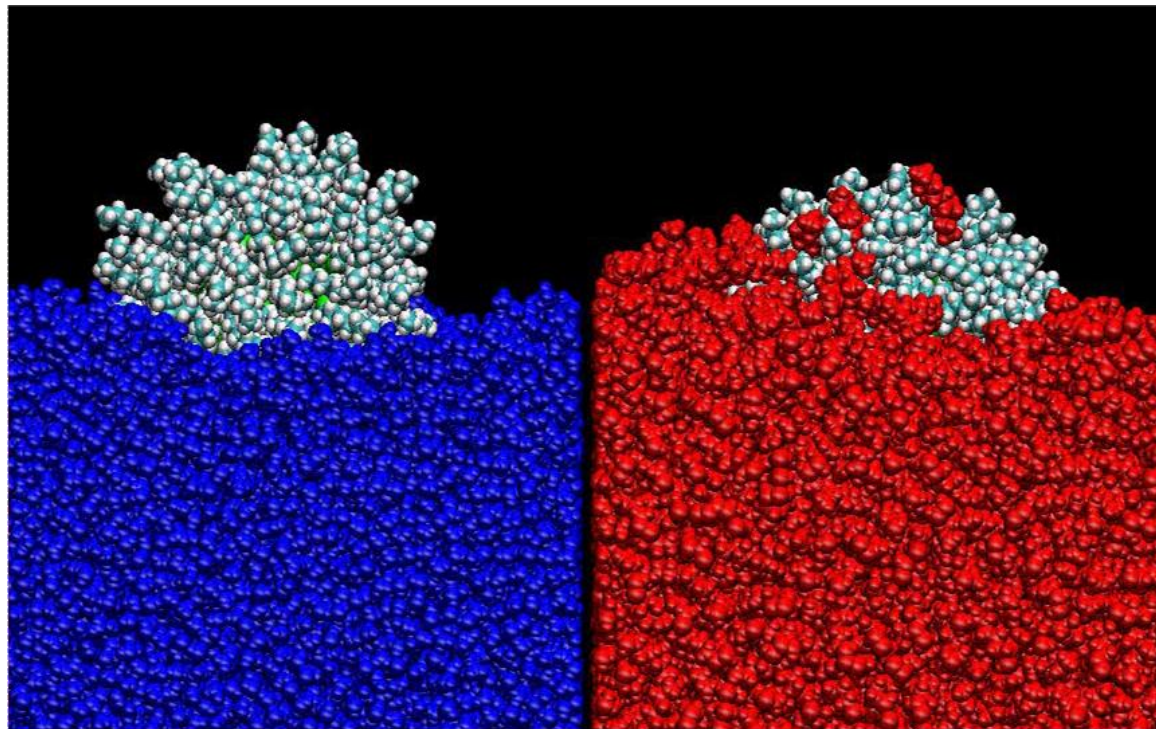
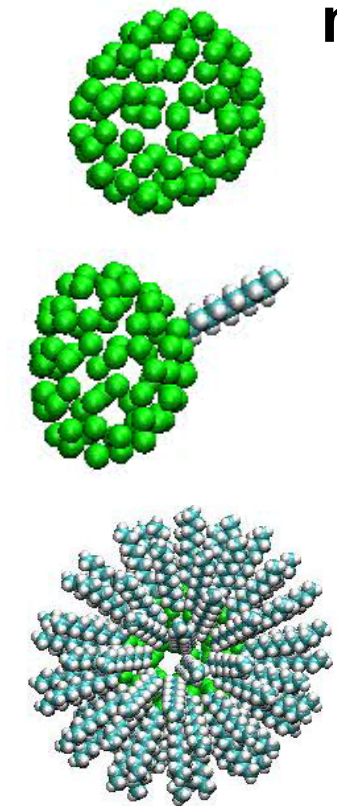
Shear Response of Cu Bicrystal

- David McDowell group (GA Tech)
- Defect formation, stress relaxation, energetics of boundary region



Coated Nanoparticles at Interfaces

- Matt Lane, Gary Grest (Sandia)
- S sites on Au nanoparticle, alkane-thiol chains, methyl-terminated, 3 ns sim

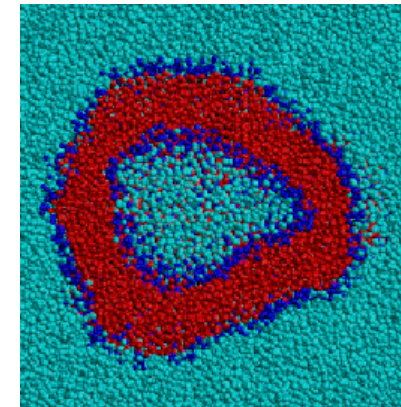
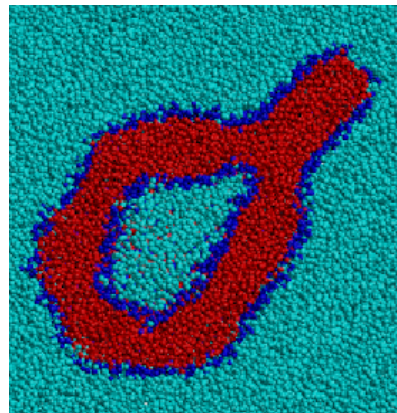
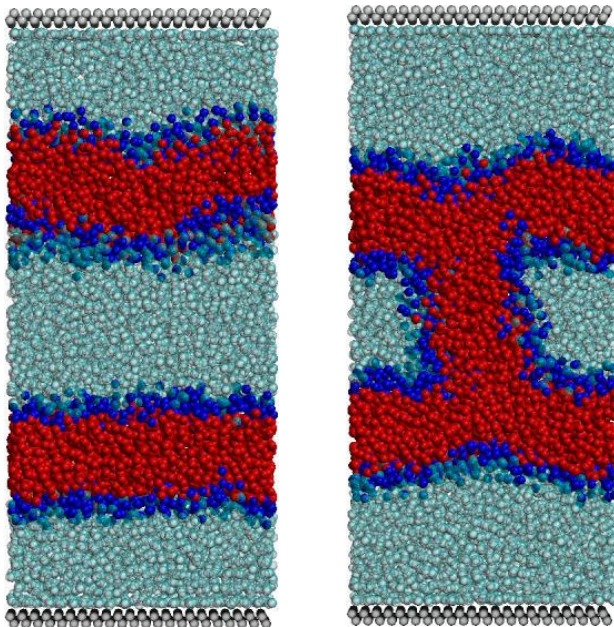
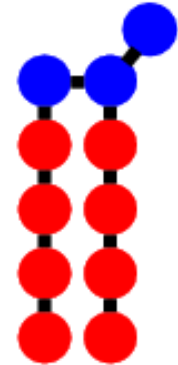


water

decane

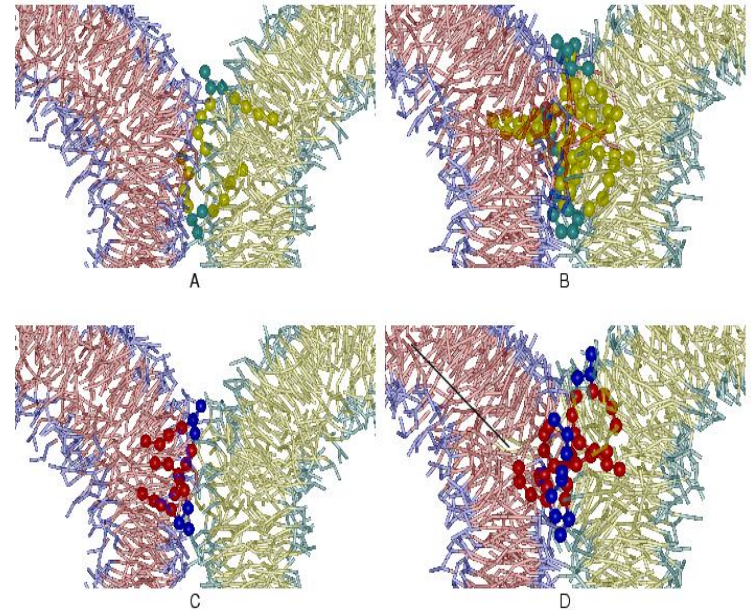
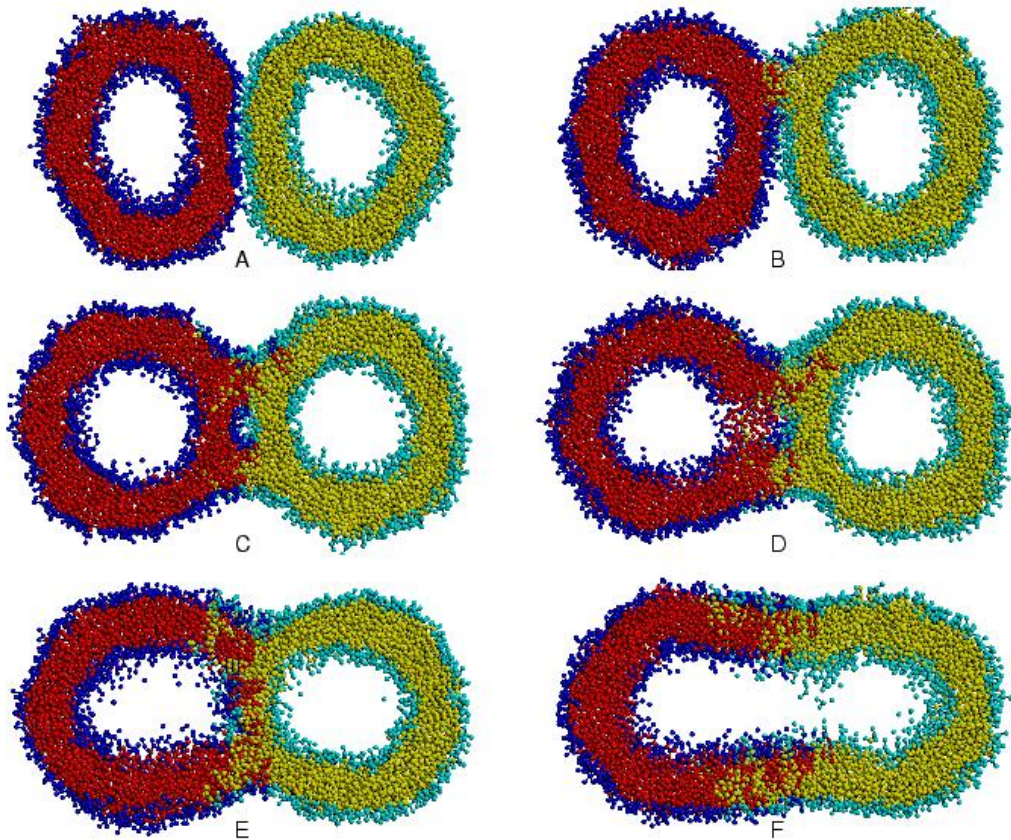
3d Membrane Self-Assembly

- Mark Stevens (Sandia)
- Coarse-grain lipid model in monomeric solvent
- Angle terms for rigidity
- Hydrophilic head-group & solvent, hydrophobic tail
- 100Ks of particles for millions of timesteps
- Bilayer & vesicle formation



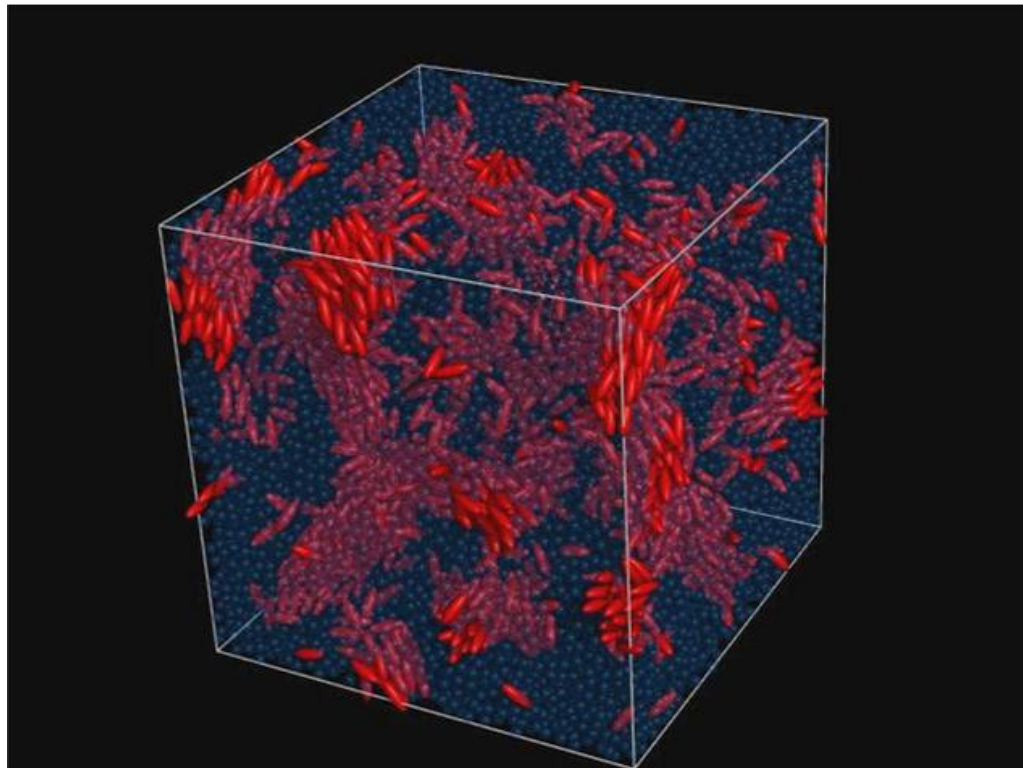
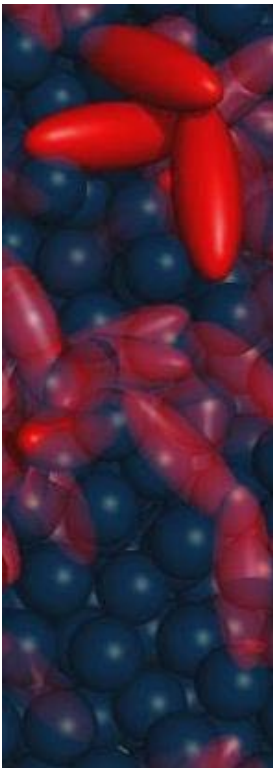
15K monomers for 1M steps

Membrane Fusion



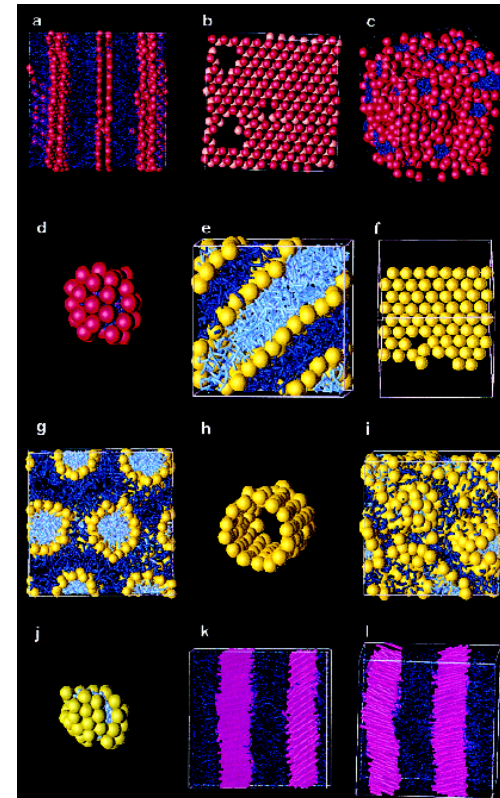
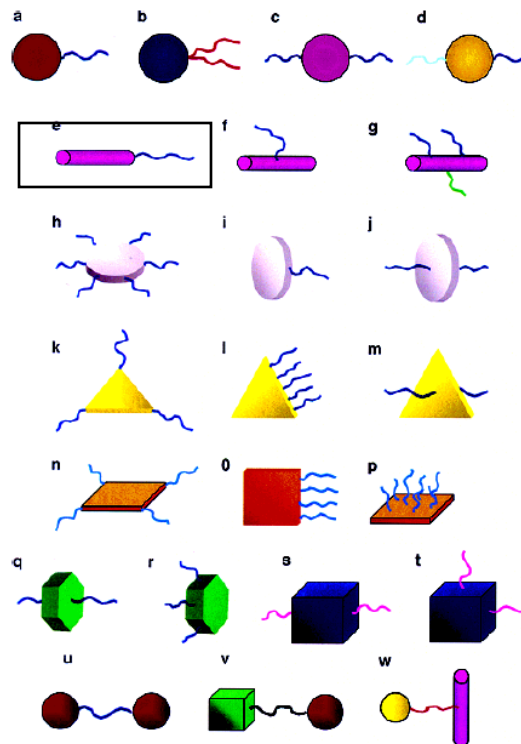
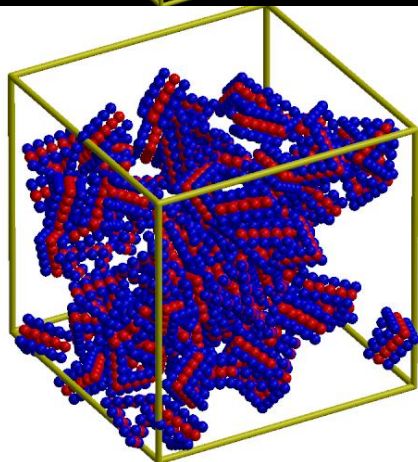
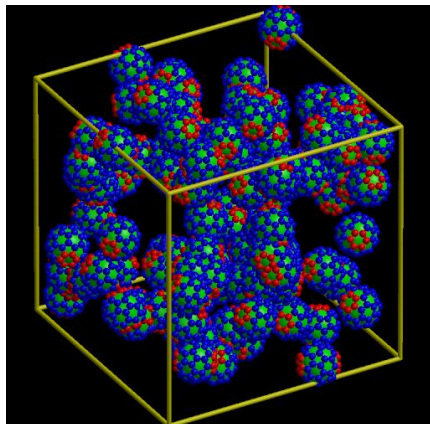
Aspherical Nanoparticles

- Mike Brown (Sandia)
- Ellipsoidal particles interacting via Gay-Berne potentials (LC), LJ solvent
- Nanodroplet formation in certain regimes of phase space



Rigid Nanoparticle Self-Assembly

- Multiple rigid bodies
- Quaternion integration
- Brownian dynamics
- Self-assembly → phases



(Sharon Glotzer *et al.*, *Nano Letters*, **3**, 1341 (2003).)



LAMMPS's Reactive Force Fields Capability

Why Reactive Force Fields?

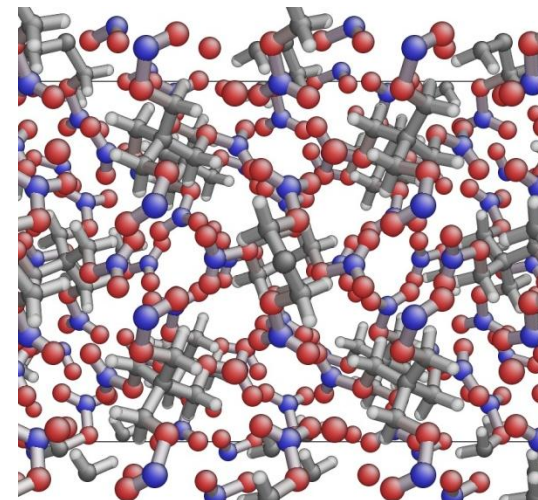
- Material behavior often dominated by chemical processes
- HE, Complex Solids, Polymer Aging
- Quantum methods limited to hundreds of atoms
- Ordinary classical force fields limited accuracy
- We need to have the best of both worlds \Rightarrow Reactive force fields

Why build Reactive Force Fields into LAMMPS?

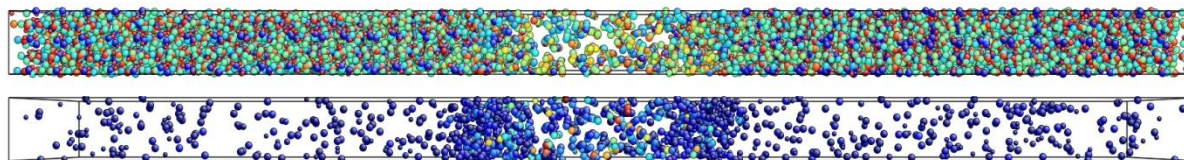
- Reactive force fields typically exist as custom serial MD codes
- LAMMPS is a general parallel MD code

LAMMPS+ReaxFF enables direct simulation of detailed initial energy propagation in HE

- Improved understanding of sensitivity will aid development of more reliable microenergetic components
- Goal: Identify the specific atomistic processes that cause orientation-dependent detonation sensitivity in PETN
- Thermal excitation simulations used as proof-of-concept
- Collaborating with parallel DoD-funded effort at Caltech (Bill Goddard, Sergey Zybin)
- Now running multi-million atom shock-initiated simulations with different orientations
- Contracted Grant Smith to extend his HMX/RDX non-reactive force field to PETN



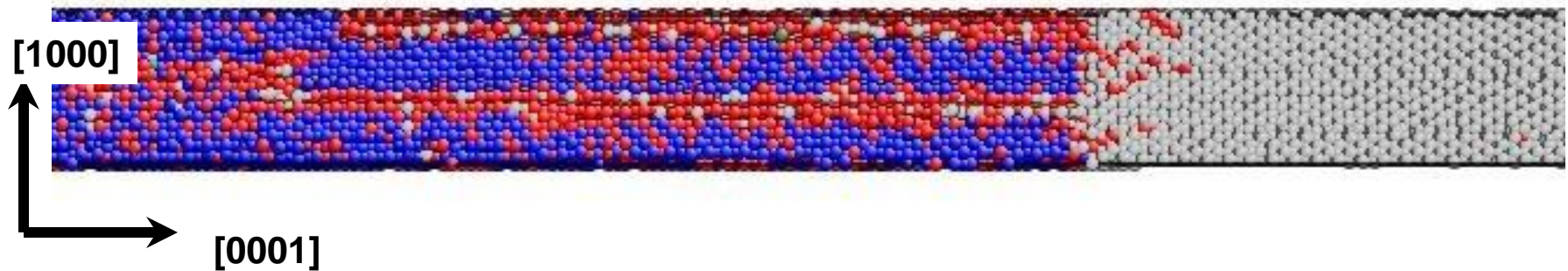
Complex molecular structure of unreacted tetragonal PETN crystal, C (gray), N (blue), O (red), and H (white).



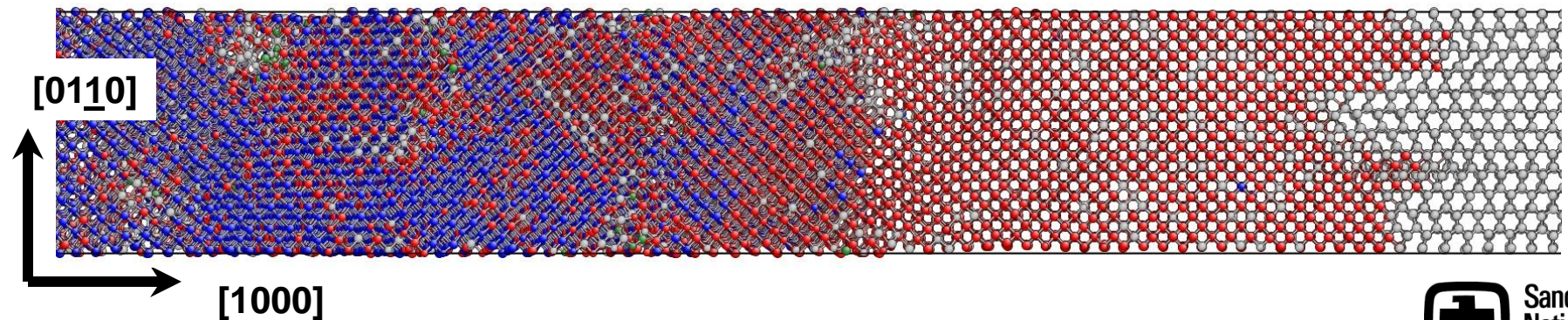
Propagation of reaction front due to thermal excitation of a thin layer at the center of the sample for 10 picoseconds. Top: atoms colored by potential energy. Bottom: atoms colored by temperature (atoms below 1000K are not shown).

MD Simulation of Shock-induced Structural Phase Transformation in Cadmium Selenide

c-direction: 2-Wave Structure: rocksalt emerges directly from elastically compressed material

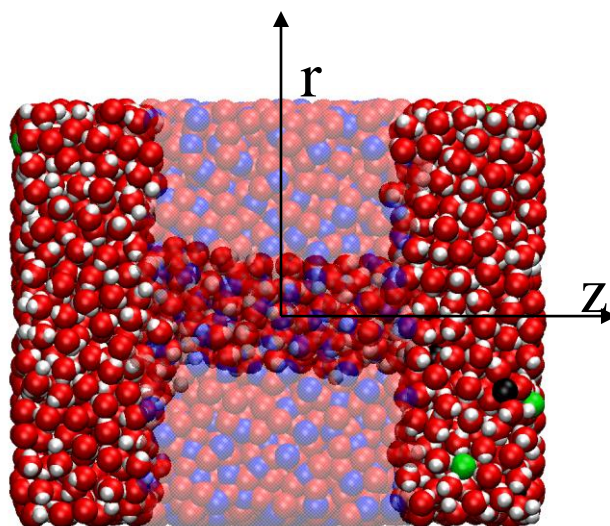
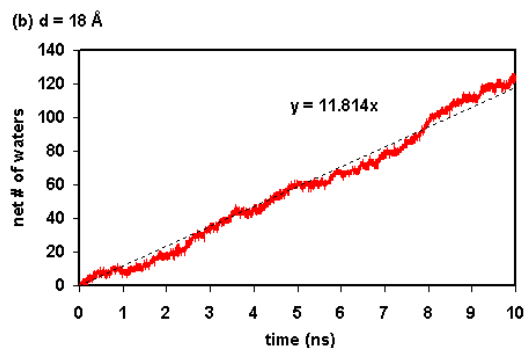
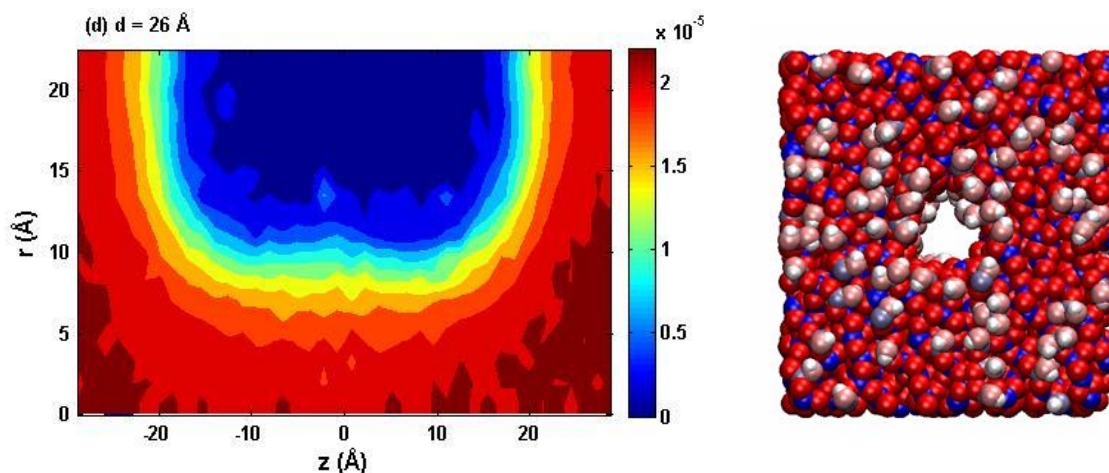


a-direction: 3-Wave Structure: tetragonal region forms between elastic wave and rocksalt phase



Non-equilibrium MD simulations of brackish water flow through silica and titania nanopores

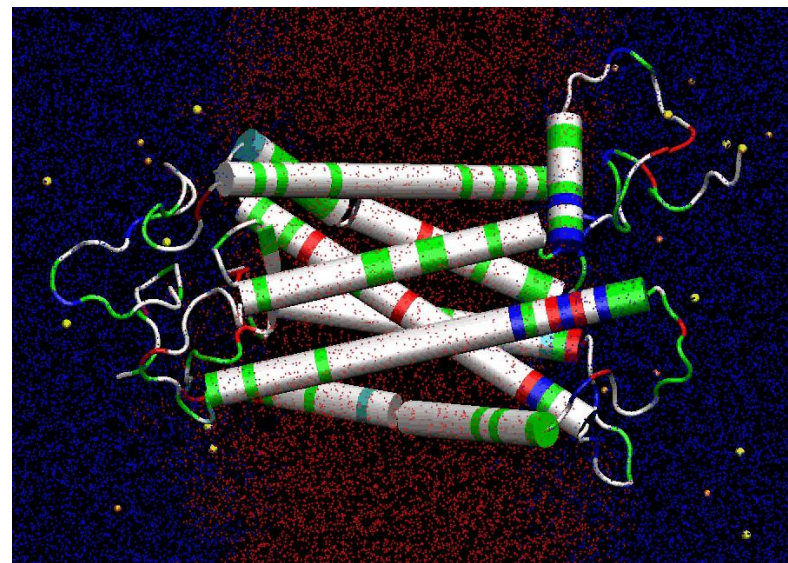
- Small flow field successfully induces steady state solvent flow through amorphous SiO_2 and TiO_2 nanopores in NEMD simulations.
- Complex model systems built through a detailed process involving melting, quenching, annealing, pore drilling, defect capping, and equilibration.
- 10-ns simulations carried out for a variety of pore diameters for both SiO_2 and TiO_2 nanopores.
- Densities, diffusivities, and flows of the various species computed spatially, temporally, and as a function of pore diameter.



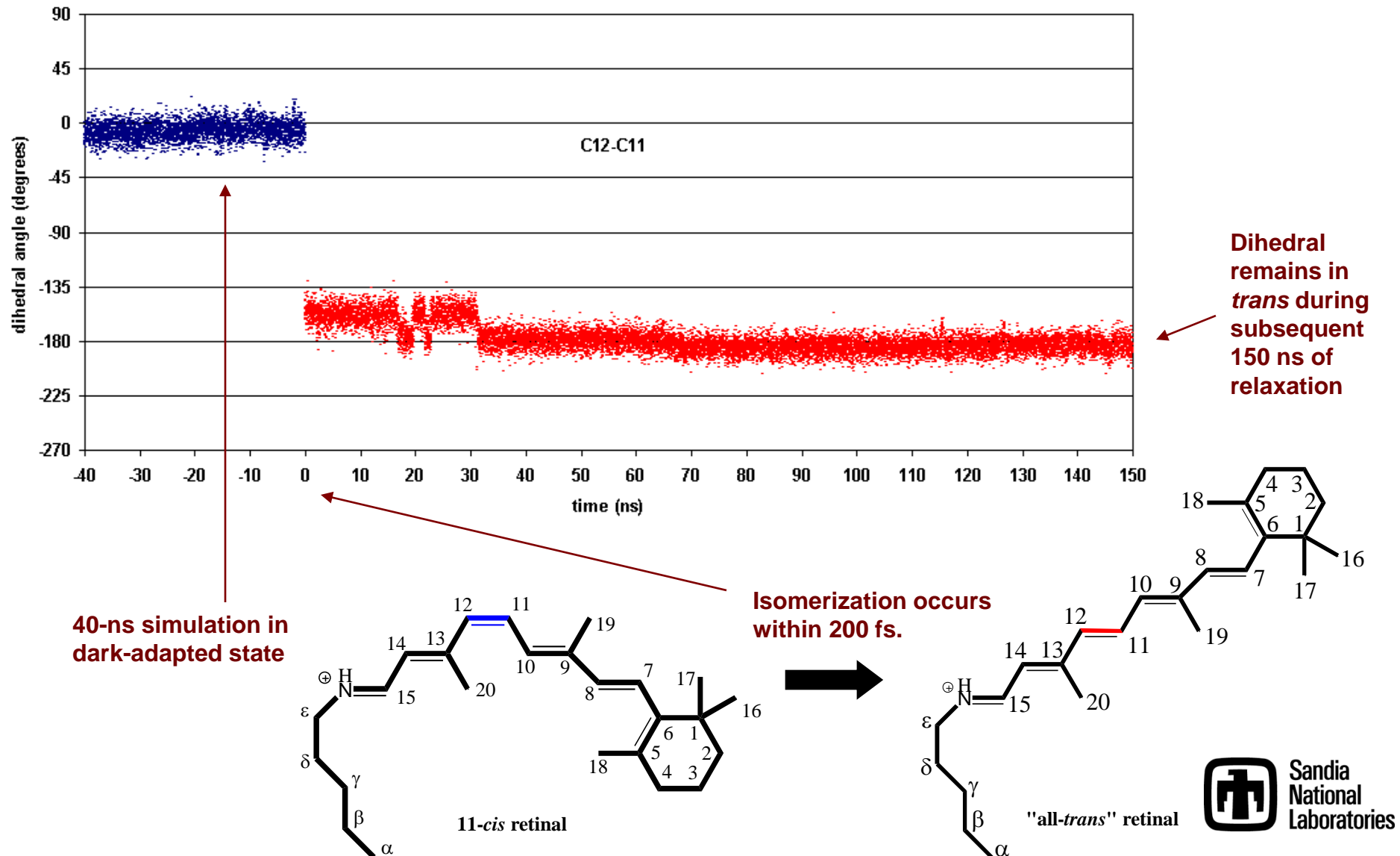
- Water is tightly bound to hydrophilic TiO_2 surface, greatly hampering mobility within 5 \AA of the surface.
- Simulations show that amorphous nanopores of diameter at least 14 \AA can conduct water as well as Na^+ and Cl^- ions.
- No evidence of selectivity that allows water passage and precludes ion passage --- functional groups on pore interior may be able to achieve this.

Rhodopsin photoisomerization simulation

- 190 ns simulation
 - 40 ns in dark-adapted state (*J. Mol. Biol.*, **333**, 493, (2003))
 - 150 ns after photoisomerization
- CHARMM force field
- P³M full electrostatics
- Parallel on ~40 processors; more than 1 ns simulation / day of real time
- Shake, 2 fs time step, velocity Verlet integrator
- Constant membrane surface area
- System description
 - All atom representation
 - 99 DOPC lipids
 - 7441 TIP3P waters
 - 348 rhodopsin residues
 - 41,623 total atoms
 - $L_x=55$ Å, $L_y=77$ Å, $L_z=94-98$ Å

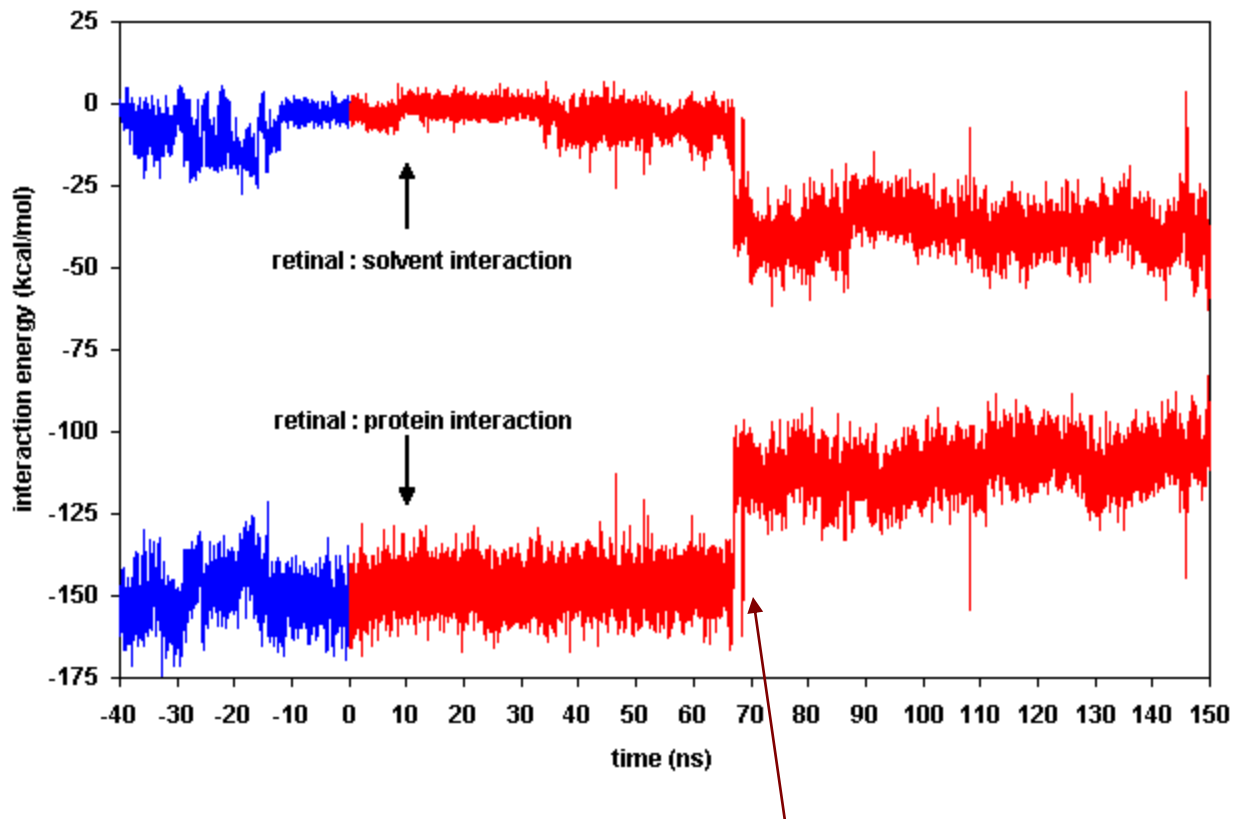
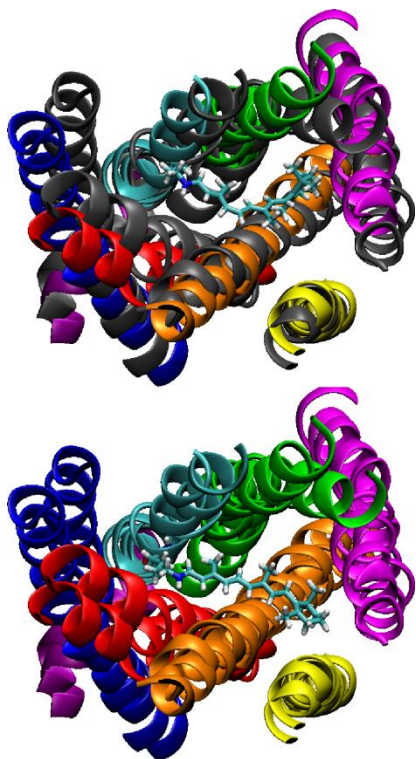


Photoisomerization of retinal



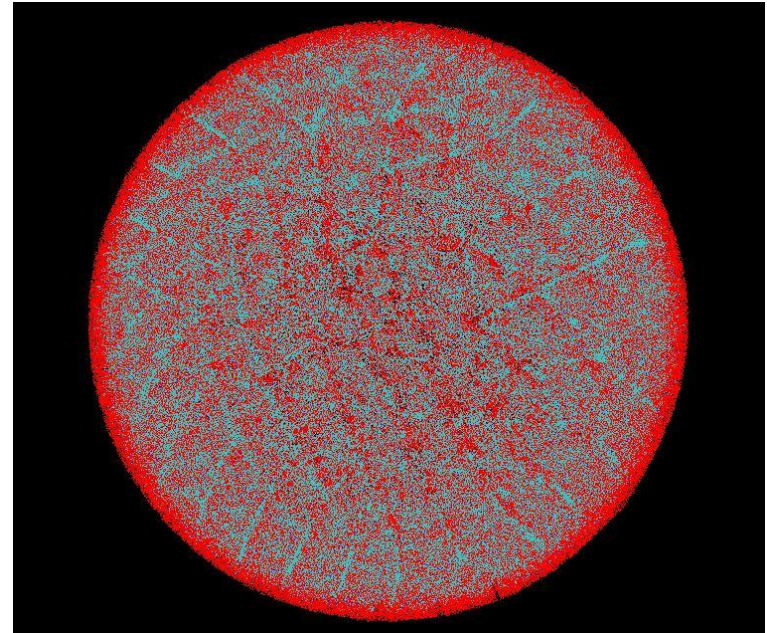
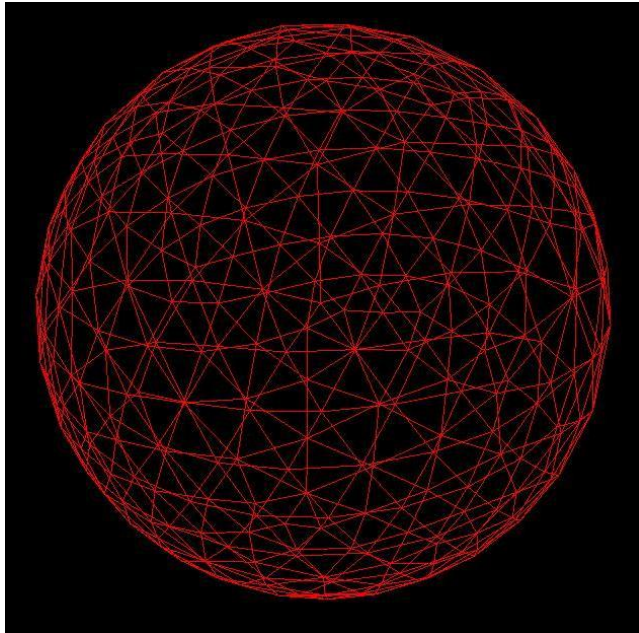
Transition in retinal's interaction environment

Retinal's interaction with the rest of the rhodopsin molecule weakens and is partially compensated by a stronger solvent interaction



Most of the shift is caused by breaking of the salt bridge between Glu 113 and the PSB

Whole vesicle simulation



- Enormous challenge due to sheer size of the system
 - 5 million atoms prior to filling box with water
 - Estimate > 100 million atoms total
- Sphere of tris built using Cubit software, then triangular patches of DOPC lipid bilayers were cut and placed on sphere surface.

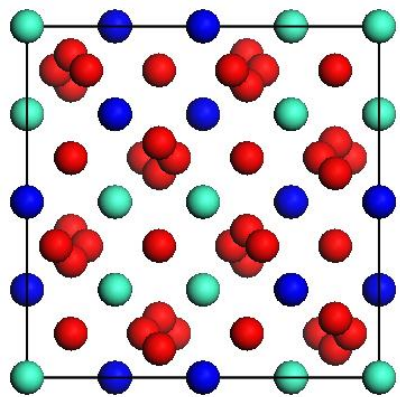


Radiation damage simulations

- ▶ Radiation damage is directly relevant to several nuclear energy applications
 - Reactor core materials
 - Fuels and cladding
 - Waste forms
- ▶ Experiments are not able to elucidate the mechanism involved in structural disorder following irradiation
- ▶ Classical simulations can help provide atomistic detail for relaxation processes involved
- ▶ Electronic effects have been successfully used in cascade simulations of metallic systems

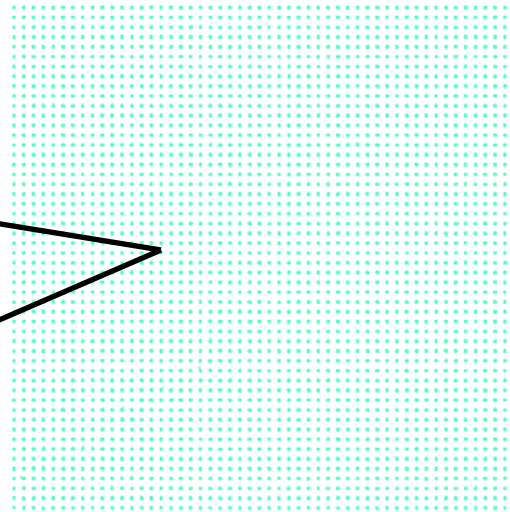
MD model for radiation damage simulations

- ▶ Gadolinium pyrochlore waste form ($\text{Gd}_2\text{Zr}_2\text{O}_7$)
- ▶ Natural pyrochlores are stable over geologic times and shown to be resistant to irradiation (Lumpkin, *Elements* **2006**).
- ▶ Recent simulations (without electronic effects) exist for comparison (Todorov et al, *J. Phys. Condens. Matter* **2006**).



10.8 Å

1 unit cell, 88 atoms

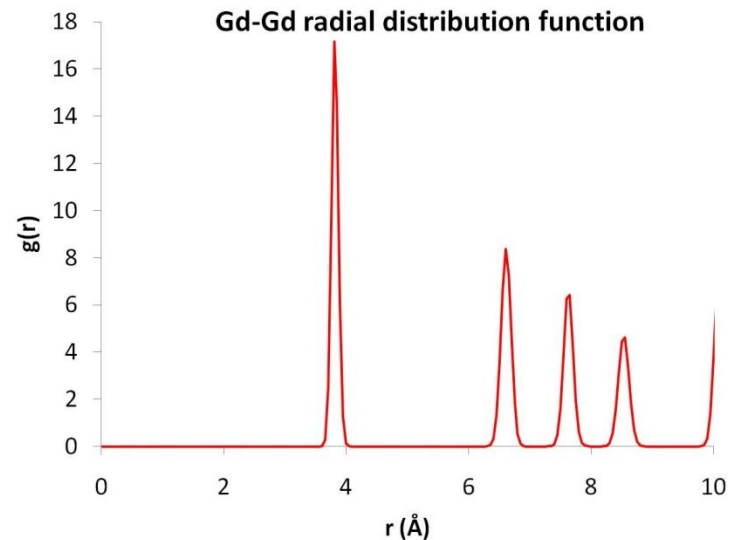


162 Å

15 x 15 x 15 supercell, 297k atoms
(only Gd atoms shown)

Defect analysis

- ▶ How the defect analysis works:
 1. Shape matching algorithm was used.*
 2. Nearest neighbors defined as those atoms in the first RDF peak.
 3. Clusters formed by each Gd atom and its nearest Gd neighbors are compared with clusters formed by those neighbors and their nearest Gd neighbors.
 4. If the cluster shapes match, the atom is considered “crystalline”; otherwise, it is considered “amorphous.”
- ▶ Why only Gd atoms were used:
 1. RDF analysis produces clear picture of crystal structure.
 2. Clearly shows the cascade damage.



* Auer and Frenkel, *J. Chem. Phys.* **2004**
Ten et al, *J. Chem. Phys.* **1996**



Discussion outline

1. MD basics
2. Why use LAMMPS?
3. Live demo #1
4. Basic information about LAMMPS
5. Live demo #2
6. Six very useful LAMMPS commands
7. Live demo #3
8. Vignettes of some LAMMPS research
9. Future areas of LAMMPS development
10. How to add a new feature to LAMMPS
11. Homework assignment



Future areas of LAMMPS development

- **Alleviations of time-scale and spatial-scale limitations**
- **Improved force fields for better molecular physics**
- **New features for the convenience of users**

LAMMPS development areas

Timescale & spatial scale

Faster MD

On a single processor

In parallel, or with load balancing

novel architectures, or N/P < 1

Accelerated MD

Temperature accelerated dynamics

Parallel replica dynamics

Forward flux sampling

Multiscale simulation

Couple to quantum

Couple to fluid solvers

Couple to KMC

Coarse graining

Aggregation

Rigidification

Peridynamics

Force fields

Auto generation

FF parameter data base

Biological & organics

Solid materials

Electrons & plasmas

Chemical reactions

ReaxFF

Bond making/swapping/breaking

Functional forms

Charge equilibration

Long-range dipole-dipole interactions

Allow user-defined FF formulas

Aspherical particles

Features

Informatics traj analysis

NPT for non-orthogonal boxes

User-requested features



How to add a new feature to LAMMPS

Case study: simulation of gas uptake into microporous materials.



What are microporous materials and what are their uses?

“A microporous material is a material containing pores with diameters less than 2 nm. Porous materials are classified into several kinds by their size.”

“Microporous materials have pore diameters of less than 2 nm, mesoporous materials have pore diameters between 2 nm and 50 nm and macroporous materials have pore diameters of greater than 50 nm.”

- **Facilitate contaminant-free exchange of gases.** Mold spores, bacteria, and other airborne contaminants will become trapped, while allowing gases to pass through the material.
- **Microporous materials are also used in first aid.**

http://en.wikipedia.org/wiki/Microporous_material

- **Radioactive materials separation or storage.**



What are ZIFs?

ZIF = zeolitic imidazolate framework

“ZIFs are one kind of metal-organic frameworks' subsidiaries which could be used to keep industrial emissions of carbon dioxide out of the atmosphere. One litre of the crystals could store about 83 litres of CO₂. **The crystals are non-toxic and require little energy to create**, making them an attractive possibility for carbon capture and storage. **The porous structures can be heated to high temperatures without decomposing** and can be boiled in water or solvents for a week and remain stable, making them suitable for use in hot, energy-producing environments like power plants.”

“Like zeolites and other porous materials, zeolitic imidazolate framework membranes can be used for the **separation of gases** because of its highly porous structure, large accessible pore volume with fully exposed edges and faces of the organic links, pore apertures in the range of the kinetic diameter of several gas molecules, and high CO₂ adsorption capacity.”

http://en.wikipedia.org/wiki/Zeolitic_imidazolate_frameworks



ZIF-8

Synonym:

2-Methylimidazole zinc salt, ZIF 8

CAS Number:

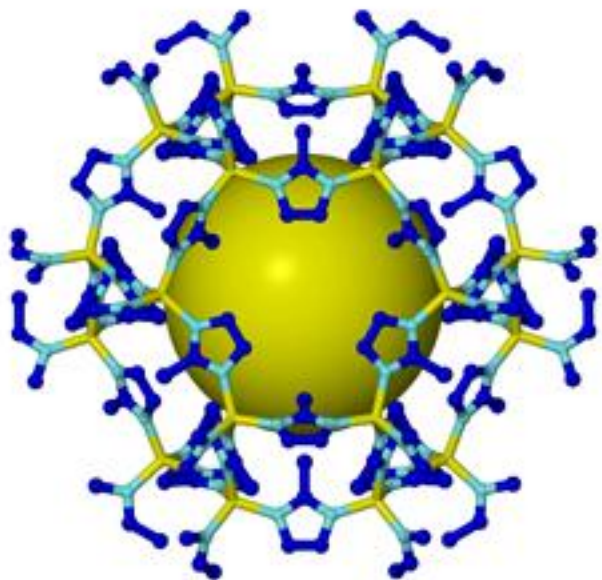
59061-53-9

Empirical Formula (Hill Notation):

$\text{C}_8\text{H}_{12}\text{N}_4\text{Zn}$

Molecular Weight:

229.60



Crystal structure of ZIF-8 with void space shown in yellow.

Figure credit: Praveen K. Thallapally



What questions about iodine uptake in ZIF-8 might we hope to address with molecular simulation?

1. How much I_2 can ZIF-8 hold? (What is the loading vs pressure relationship? Can we compute a loading isotherm?)
2. How mobile is I_2 once it is adsorbed within the ZIF-8 framework?
3. What is the structure of I_2 -loaded ZIF-8 and where are the main binding locations?
4. How well do simulation results compare with available experimental measurements?



What simulation tools might we use to address our questions?

Molecular dynamics (MD): is computer simulation of physical movements by atoms and molecules.

http://en.wikipedia.org/wiki/Molecular_dynamics

Monte Carlo (MC): This approach relies on statistical mechanics rather than molecular dynamics. Instead of trying to reproduce the dynamics of a system, it generates states according to appropriate Boltzmann probabilities.

(http://en.wikipedia.org/wiki/Monte_Carlo_molecular_modeling)

Grand canonical Monte Carlo (GCMC): a very versatile and powerful Monte Carlo technique that explicitly accounts for **density fluctuations at fixed volume and temperature**. This is achieved by means of **trial insertion and deletion of molecules**. Although this feature has made it the preferred choice for the study of interfacial phenomena, in the last decade grand-canonical ensemble simulations have also found widespread applications in the study of bulk properties. Such applications had been hitherto limited by the very low particle insertion and deletion probabilities, but the development of the configurational bias grand canonical technique has very much improved the situation. (<http://www.sklogwiki.org>)

Gibbs ensemble Monte Carlo (GEMC): The Gibbs ensemble Monte Carlo method has been specifically designed to **characterize phase transitions**. It was mainly developed by Panagiotopoulos (Refs. 1 and 2) to avoid the problem of finite size interfacial effects. **In this method, an NVT (or NpT) ensemble containing two (or more) species is divided into two (or more) boxes**. In addition to the usual particle moves in each one of the boxes, the algorithm includes moves steps to change the volume and composition of the boxes at mechanical and chemical equilibrium. Transferring a chain molecule from a box to the other requires the use of an efficient method to insert chains. The configurational bias method is specially recommended for this purpose.

(<http://www.sklogwiki.org>)



Which molecular simulation tool is best suited for each task?

Molecular dynamics (MD)

How much I_2 can ZIF-8 hold?

Monte Carlo (micro-canonical) (MC)

How mobile is I_2 once it is adsorbed within the ZIF-8 framework?

Grand canonical Monte Carlo (GCMC)

What is the structure of I_2 -loaded ZIF-8 and where are the main binding locations?

Gibbs ensemble Monte Carlo (GEMC)



Which molecular simulation tool is best suited for each task?

How much I_2 can ZIF-8 hold?

How mobile is I_2 once it is adsorbed within the ZIF-8 framework?

What is the structure of I_2 -loaded ZIF-8 and where are the main binding locations?

Molecular dynamics (MD)

Monte Carlo (micro-canonical) (MC)

Grand canonical Monte Carlo (GCMC)

Gibbs ensemble Monte Carlo (GEMC)



Why would we want to use LAMMPS to perform molecular simulation of gas uptake into a ZIF?

Can already do the following for free:

- Molecular dynamics
- Model ZIF-8 force fields we'd like to use
- I/O: we already know how to work with LAMMPS input, output, versatile scripting options, etc.
- Many useful computes, fixes, available.
- Combine features in new useful combinations.
- Runs efficiently on available HPC resources.
- Great user support.
- New features can be donated to the community.

Can't do (yet): GCMC



What would we have to add to LAMMPS to be able to do GCMC simulations?

- A new “fix” (i.e. BC, constraint, mid-step instruction).
- Let’s call it “fix GCMC.”
- Need to find a textbook GCMC algorithm to implement.
- Should include the following features:
 - Support particle creation/destruction.
 - Compute pre- and post-creation/deletion potential energies.
 - Work efficiently, and in parallel on multiple processors.
 - Written in LAMMPS coding style and include documentation so that it can be shared.
 - Be compatible with other LAMMPS features (MD, ensembles, force fields, computes, etc.)
 - Allow creation/deletion of molecules.
 - Report relevant statistics to users.

GCMC algorithm by Frenkel and Smit *

```
SUBROUTINE mcexc  
  
if (ranf().lt.0.5) then  
  if (npart.eq.0) return  
  o=int(npart*ranf())+1  
  call ener(x(o),eno)  
  arg=npart*exp(beta*eno)  
+  /(zz*vol)  
  if (ranf().lt.arg) then  
    x(o)=x(npart)  
    npart=npart-1  
  endif  
else  
  xn=ranf()*box  
  call ener(xn,enn)  
  arg=zz*vol*exp(-beta*enn)  
+  /(npart+1)  
  if (ranf().lt.arg) then  
    x(npart+1)=xn  
    npart=npart+1  
  endif  
endif  
return  
end
```

attempt to exchange a particle
with a reservoir
decide to remove or add a particle
test whether there is a particle
select a particle to be removed
energy particle o
acceptance rule (5.6.9)

accepted: remove particle o

new particle at a random position
energy new particle
acceptance rule (5.6.8)

accepted: add new particle

* Frenkel and Smit, “*Understanding Molecular Simulation*,” Academic Press, London, 2002.



Excerpts from LAMMPS's new fix GCMC

(GCMC algorithm: select move, deletion, or insertion)

```
// perform ncycles MC cycles
.
for (int i = 0; i < ncycles; i++) {
    int random_int_fraction = static_cast<int>(random->uniform() * ncycles) + 1;
    if (random_int_fraction <= nmcmoves) {
        attempt_move();
    } else {
        if (random->uniform() < 0.5) {
            attempt_deletion();
        } else {
            attempt_insertion();
        }
    }
}
```



Excerpts from LAMMPS's new fix GCMC

(move algorithm)

```
int success = 0;
iwhichglobal = static_cast<int>(ngas*random->uniform());
if ((iwhichglobal >= ngas_before) && (iwhichglobal < ngas_before + ngas_local)) {
    iwhichlocal = iwhichglobal - ngas_before;
    i = local_gas_list[iwhichlocal];
    double energy_before = energy(i, x[i]);
    coord[0] = x[i][0] + displace*(random->uniform() - 0.5);
    coord[1] = x[i][1] + displace*(random->uniform() - 0.5);
    coord[2] = x[i][2] + displace*(random->uniform() - 0.5);
    double energy_after = energy(i, coord);
    if (random->uniform() < exp(-beta*(energy_after - energy_before))) {
        x[i][0] = coord[0];
        x[i][1] = coord[1];
        x[i][2] = coord[2];
        success = 1;
    }
}
```



Excerpts from LAMMPS's new fix GCMC

(deletion algorithm)

```
// choose particle randomly across all procs and delete it
// keep ngas, ngas_local, ngas_before, and local_gas_list current after each deletion
.
int success = 0;
iwhichglobal = static_cast<int> (ngas*random->uniform());
if ((iwhichglobal >= ngas_before) && (iwhichglobal < ngas_before + ngas_local)) {
    iwhichlocal = iwhichglobal - ngas_before;
    i = local_gas_list[iwhichlocal];
    double deletion_energy = energy(i, atom->x[i]);
    if (random->uniform() < ngas*exp(beta*deletion_energy)/(zz*volume)) {
        avec->copy(atom->nlocal-1, i);
        atom->nlocal--;
        local_gas_list[iwhichlocal] = local_gas_list[ngas_local-1];
        ngas_local--;
        success = 1;
    }
}
```



Excerpts from LAMMPS's new fix GCMC

(insertion algorithm)

```
.success = 0;
if (flag) {
  int nall = atom->nlocal + atom->nghost;
  double insertion_energy = energy(nall, coord);
  if (random->uniform() < zz*volume*exp(-beta*insertion_energy)/(ngas+1)) {
    atom->avec->create_atom(ntype, coord);
    int m = atom->nlocal - 1;
    atom->type[m] = ntype;
    atom->mask[m] = 1 | groupbit;
    atom->v[m][0] = random->gaussian()*sigma;
    atom->v[m][1] = random->gaussian()*sigma;
    atom->v[m][2] = random->gaussian()*sigma;
    int nfix = modify->nfix;
    Fix **fix = modify->fix;
    for (int j = 0; j < nfix; j++)
      if (fix[j]->create_attribute) fix[j]->set_arrays(m);
    if (atom->nlocal > nmax) {
      nmax = atom->nmax;
      local_gas_list = (int *) memory->srealloc(local_gas_list, nmax*sizeof(int), "GCMC:local_gas_list");
    }
    local_gas_list[ngas_local] = atom->nlocal;
    ngas_local++;
    success = 1;
  }
}
```



How do we know that we've implemented the algorithm correctly?

Verification exercise: code-to-code comparison versus an established Monte Carlo code (Towhee).

Gas = Kr (with LJ parameters from Pellenq and Levitz)

T = 300 K

μ = -10.284 kcal/mol

P = ?

If ideal gas:
$$\mu = -k_B T \ln \left[\left(\frac{2\pi m k_B T}{h_0^2} \right)^{3/2} \frac{V}{N} \right]$$

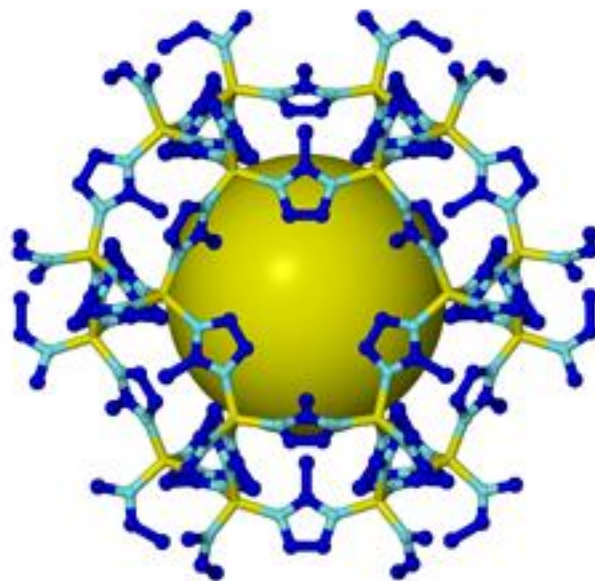
✓ **$P_{(\text{ideal gas})} = 1 \text{ bar}$**

✓ **Also, from Towhee calculation: $P_{(\text{Towhee})} = 1 \text{ bar}$**

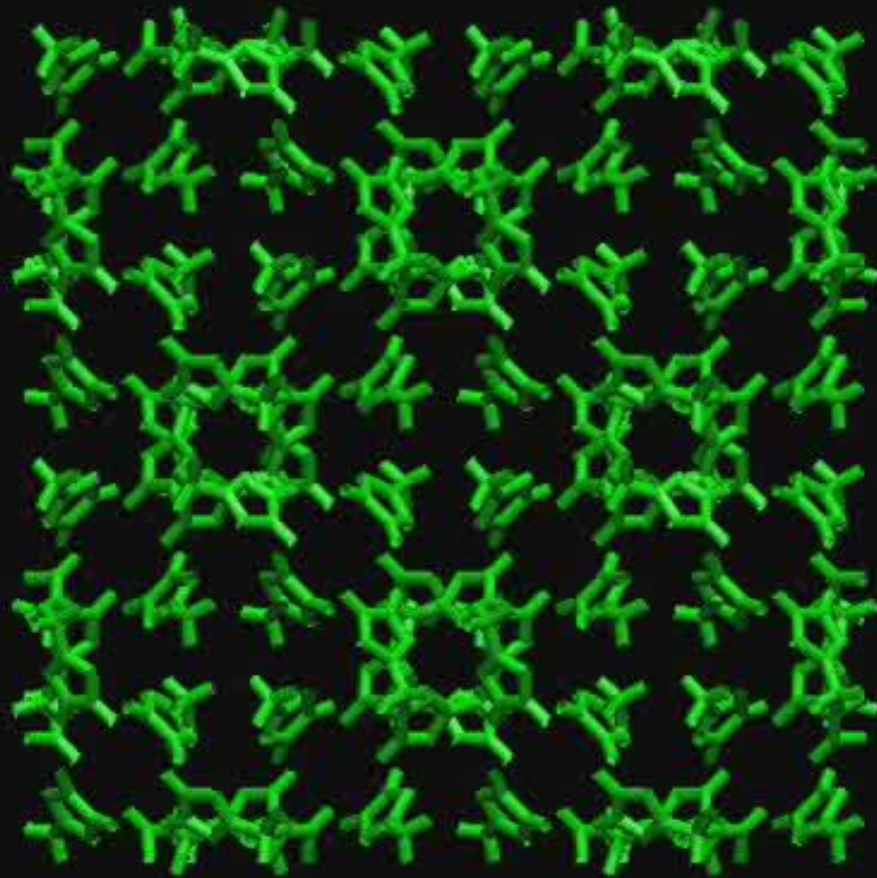
✓ **Corrected a sign error in the new code that caused a slight discrepancy**

✓ **Now, with our new fix GCMC for LAMMPS, we have: $P_{(\text{LAMMPS})} = 1 \text{ bar}$**

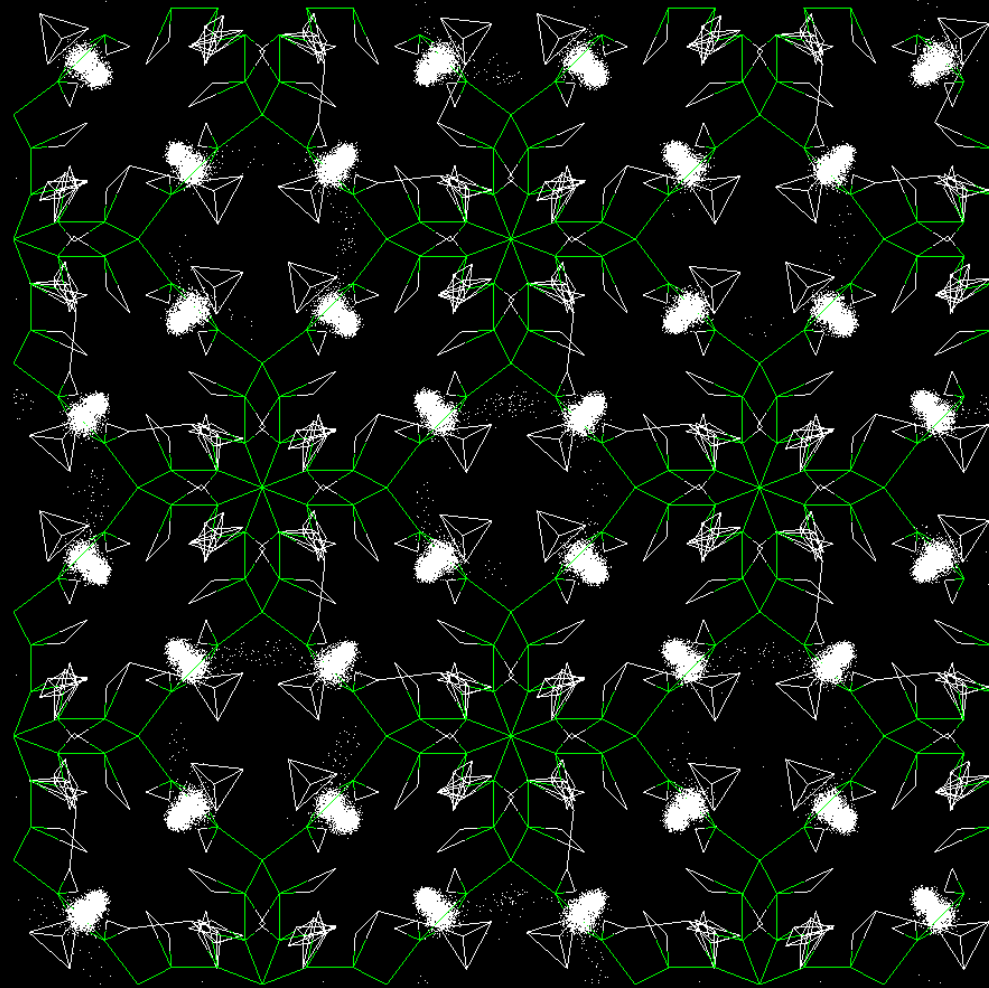
Results of GCMC simulations of I₂ loading of ZIF-8 structure



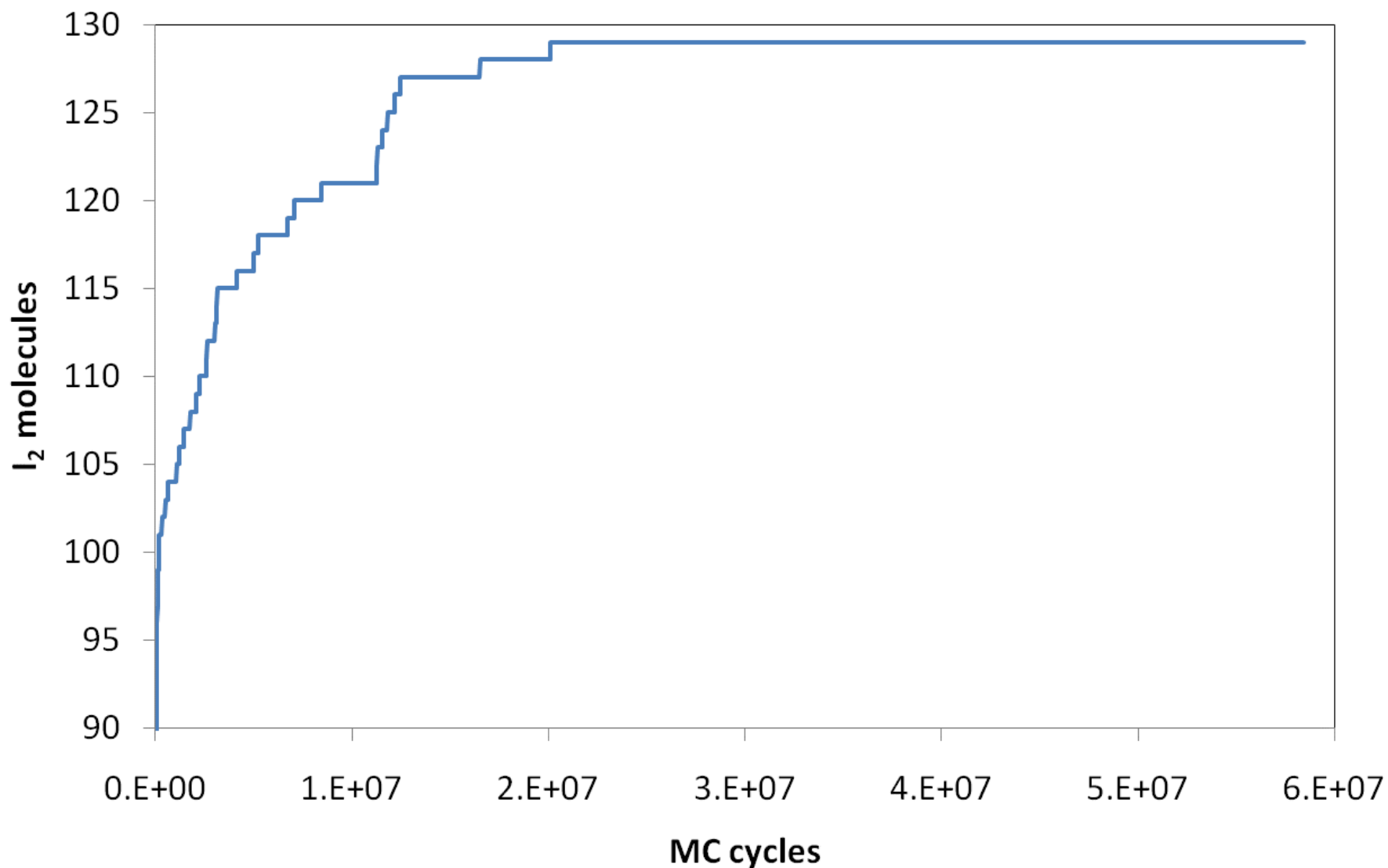
GCMC loading movie



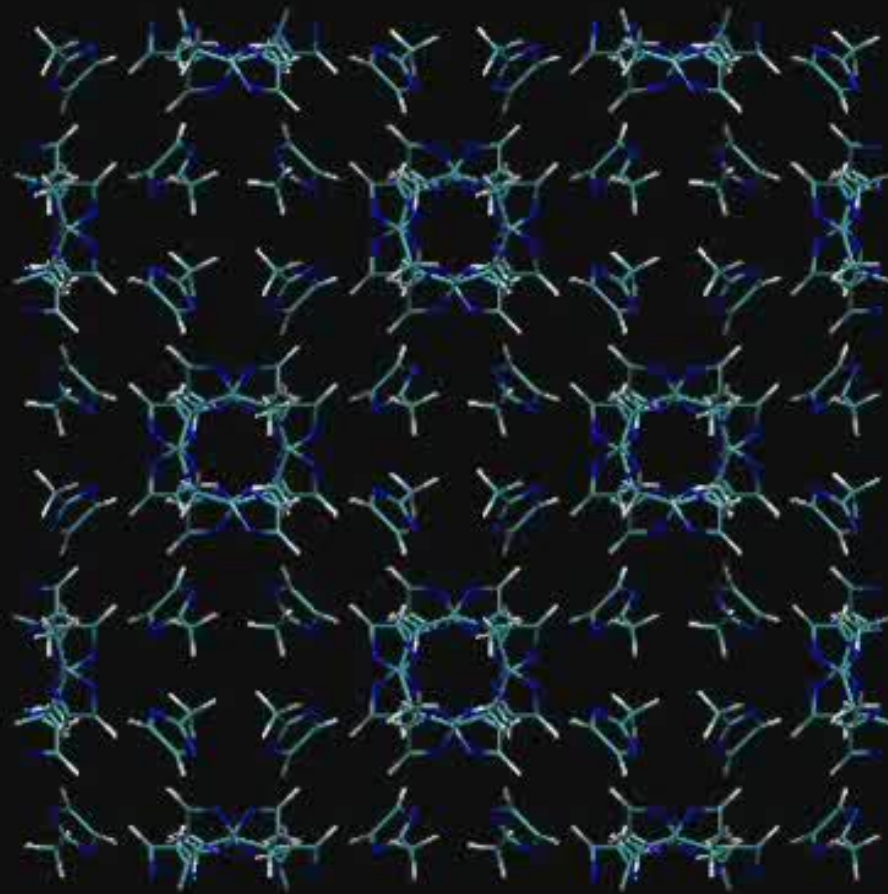
Time-lapse image of MC loading simulation



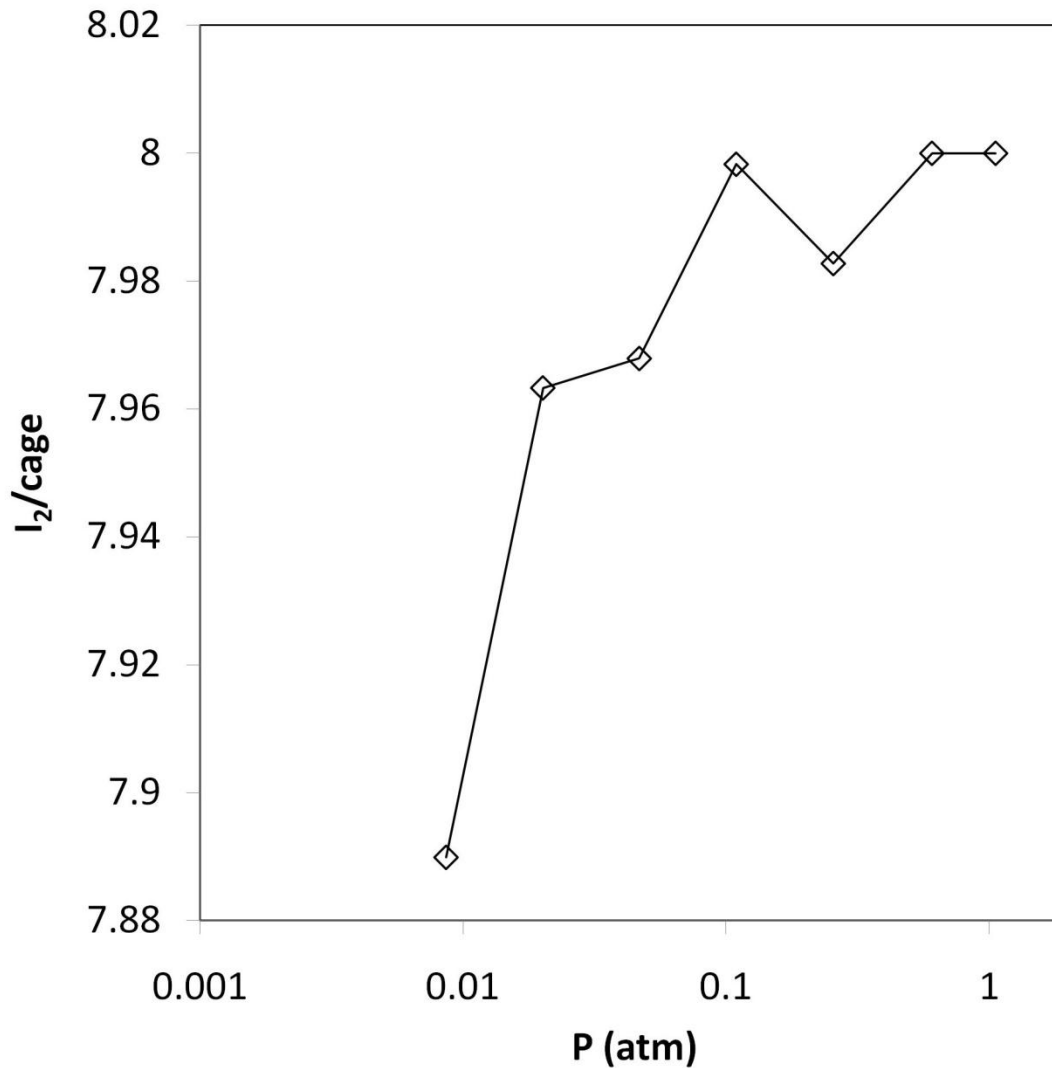
I₂ loading of 16 ZIF-8 cages vs MC cycles



GCMC saturation movie



Loading isotherm





Homework assignment

Repeat the live demo exercises yourself, with your own personal modifications.



HW #1

1. Download LAMMPS.

- <http://lammps.sandia.gov/download.html>
- Try the Windows serial executable.

2. Download a simple LAMMPS input script.

- <http://lammps.sandia.gov/inputs/in.lj.txt>

3. Run LAMMPS

- http://lammps.sandia.gov/doc/Section_start.html#2_5



HW #2

1. **Modify the input script from live demo #1**
 - Add the line “dump 1 all atom 10 atoms.lammpstrj” between the fix and run command lines.
2. **Run LAMMPS with the modified input script.**
3. **Visualize the simulation results using 3rd party software (VMD)**
 - <http://www.ks.uiuc.edu/Research/vmd/>
 - Start up VMD and open the “atoms.lammpstrj” file
 - View the “movie” you’ve made from the LAMMPS trajectory by pressing the play button.



HW #3

1. **Modify the LAMMPS input script from demo #2 so that it includes at least one example of each of the following six commands:**
 1. **fix**
 2. **compute**
 3. **pair_style**
 4. **variable**
 5. **thermo_style**
 6. **dump**
2. **Run LAMMPS with the modified input script.**