LAMMPS Basics

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Resources for learning LAMMPS

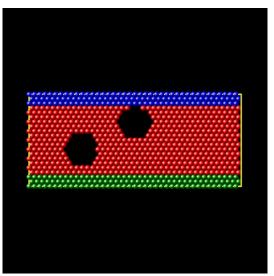
- Examples: about 35 sub-dirs under examples in distro
- Manual: doc/Manual.html
 - Intro, Commands, Packages, Accelerating
 - Howto, Modifying, Errors
- Alphabetized command list: one doc page per command
 - doc/Section_commands.html#cmd_5
- Papers: find a paper similar to what you want to model
- Mail list: topics, search it, post to it
 - http://lammps.sandia.gov/mail.html

Structure of typical input scripts

- Units and atom style
- ② Create simulation box and atoms
 - region, create_box, create_atoms, region commands
 - lattice command vs box units
 - read_data command
 - data file is a text file
 - look at examples/micelle/data.micelle
 - see read_data doc page for full syntax
- Oefine groups
- 4 Attributes of atoms: mass, velocity
- Pair style for atom interactions
- Fixes for time integration and constraints
- Computes for diagnostics
- Output: thermo, dump, restart
- Q Run or minimize
- Rinse and repeat (script executed one command at a time)

Obstacle example

 $input\ script = examples/obstacle/in.obstacle$



1st section = setup box and create atoms

```
# 2d L.I obstacle flow
dimension 2
boundary p s p
atom_style atomic
neighbor 0.3 bin
neigh_modify delay 5
# create geometry
lattice hex 0.7
region box block 0 40 0 10 -0.25 0.25
create_box 3 box
create_atoms 1 box
```

2nd section = define potential and groups of atoms

```
# LJ potentials
pair_style lj/cut 1.12246
pair_coeff * * 1.0 1.0 1.12246
# define groups
region 1 block INF INF INF 1.25 INF INF
group lower region 1
region 2 block INF INF 8.75 INF INF INF
group upper region 2
group boundary union lower upper
group flow subtract all boundary
set group lower type 2
set group upper type 3
```

3rd section = set velocities and fixes

```
# initial velocities
mass * 1.0
compute mobile flow temp
velocity flow create 1.0 482748 temp mobile
fix 1 all nve
fix 2 flow temp/rescale 200 1.0 1.0 0.02 1.0
fix_modify 2 temp mobile
# Poiseuille flow
velocity boundary set 0.0 0.0 0.0
fix 3 lower setforce 0.0 0.0 0.0
fix 4 upper setforce 0.0 NULL 0.0
fix 5 upper aveforce 0.0 -0.5 0.0
fix 6 flow addforce 1.0 0.0 0.0
```

4th section = create 2 obstacles to flow

```
# 2 obstacles
region void1 sphere 10 4 0 3
delete_atoms region void1
region void2 sphere 20 7 0 3
delete_atoms region void2
fix 7 flow indent 100 sphere 10 4 0 4
fix 8 flow indent 100 sphere 20 7 0 4
fix 9 all enforce2d
```

5th section: define output and run simulation

```
# run
timestep 0.003
thermo 1000
thermo_modify temp mobile
#dump 1 all atom 100 dump.obstacle
dump 1 all image 500 image.*.jpg type type &
zoom 1.6 adiam 1.5
dump_modify 1 pad 5
run 25000
```

Obstacle example

Questions on input script?

Exercise: run examples/obstacle/in.obstacle on your box, examine output.

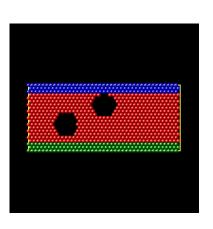
Make a movie

50 JPG files

- image.16500.jpg
- ImageMagick display
- Mac Preview

Make/view a movie

- ImageMagick convert *.jpg image.gif
- open in browser
 open -a Safari image.gif
- Mac QuickTime open image sequence
- Windows Media Player
- VMD, AtomEye, ...



Examine screen output

```
LAMMPS (15 Aug 2013)
Lattice spacing in x,y,z = 1.28436 2.22457 1.28436
Created orthogonal box = (0\ 0\ -0.321089)
            to (51.3743 22.2457 0.321089)
  4 by 1 by 1 MPI processor grid
Created 840 atoms
120 atoms in group lower
120 atoms in group upper
240 atoms in group boundary
600 atoms in group flow
Setting atom values ...
  120 settings made for type
Setting atom values ...
  120 settings made for type
Deleted 36 atoms, new total = 804
Deleted 35 atoms, new total = 769
```

More screen output

```
WARNING: Temperature for thermo pressure is not
        for group all (../thermo.cpp:436)
Setting up run ...
Memory usage per processor = 2.23494 Mbytes
Step Temp E_pair E_mol TotEng Press Volume
0 1 0004177 0 0 0 68689281 0 46210058 1143 0857
1000 1 -0.32494012 0 0.36166587 1.2240503 1282.5239
2000 1 -0.37815616 0 0.30844982 1.0642877 1312.5691
. . .
25000 1 -0.36649381 0 0.32011217 0.98366691 1451.5444
25000 1 -0.38890426 0 0.29770172 0.95284427 1455.9361
Loop time of 1.76555 on 4 procs for
        25000 steps with 769 atoms
```

Timing info

```
Loop time of 1.76555 on 4 procs for 25000 steps with 769 atoms

Pair time (%) = 0.14617 (8.27903)

Neigh time (%) = 0.0467809 (2.64966)

Comm time (%) = 0.307951 (17.4422)

Outpt time (%) = 0.674575 (38.2078)

Other time (%) = 0.590069 (33.4213)
```

Run statistics

Per-processor values at end of run

```
Nlocal: 192.25 ave 242 max 159 min
Histogram: 2 0 0 0 0 1 0 0 0 1
Nghost: 43 ave 45 max 39 min
Histogram: 1 0 0 0 0 0 0 2 1
Neighs: 414 ave 588 max 284 min
Histogram: 2 0 0 0 0 0 1 0 0 1
```

Total # of neighbors = 1656 Ave neighs/atom = 2.15345 Neighbor list builds = 1641 Dangerous builds = 1

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Questions on output?

Defining variables in input scripts

- Styles: index, loop, equal, atom, ...
 - variable x index run1 run2 run3 run4
 - variable x loop 100
 - variable x trap(f_JJ[3])*\${scale}
 - variable x atom $-(c_p[1]+c_p[2]+c_p[3])/(3*vol)$

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 - variable x index run1 run2 run3 run4
 - variable x loop 100
 - variable x trap(f_JJ[3])*\${scale}
 - variable x atom $-(c_p[1]+c_p[2]+c_p[3])/(3*vol)$
- Formulas can be complex
 - see doc/variable.html
 - thermo keywords (temp, press, ...)
 - math operators & functions (sqrt, log, cos, ...)
 - group and region functions (count, xcm, fcm, ...)
 - various special functions (min, ave, trap, stride, stagger, ...)
 - per-atom vectors (x, vx, fx, ...)
 - output from computes, fixes, other variables
- Formulas can be time- and/or spatially-dependent

Using variables in input scripts

- Substitute in any command via \$x or \${myVar}
- Loop using next and jump commands
 - next command increments a variable
 - jump command goes to same or different input script
- Many commands allow them as arguments
 - fix addforce 0.0 v_fy 1.0
 - dump_modify every v_foo
 - region sphere 0.0 0.0 0.0 v_radius

Power tools for input scripts

- Filename options:
 - dump.*.% for per-snapshot or per-processor output
 - read_data data.protein.gz
 - read_restart old.restart.*
- If/then/else via if command
- Insert another script via include command
 - useful for long list of params

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- Filename options:
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- If/then/else via if command
- Insert another script via include command
 - useful for long list of params
- Looping via next and jump commands
- Invoke a shell command or external program
 - shell cd subdir1
 - shell my_analyze out.file \$n \${param}
- Various ways to run multiple simulations from one script
 - see doc/Section_howto 6.4

Example script for multiple runs

```
variable r equal random(1,1000000000,58798)
variable a loop 8
variable t index 0.8 0.85 0.9 0.95 1.0 1.05 1.1 1.15
log log.$a
read data.polymer
velocity all create $t $r
fix 1 all nvt $t $t 1.0
dump 1 all atom 1000 dump.$a.*
run 100000
next t
next a
jump in.polymer
```

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variable a loop 8
variable t index 0.8 0.85 0.9 0.95 1.0 1.05 1.1 1.15
log log.$a
read data.polymer
velocity all create $t $r
fix 1 all nvt $t $t 1.0
dump 1 all atom 1000 dump.$a.*
run 100000
next t
next a
jump in.polymer
```

Run 8 simulations on 3 partitions until finished:

- change a & t to universe-style variables
- mpirun -np 12 lmp_linux -p 3x4 -in in.polymer

Pre-processing tools to build complex systems

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- Data file must include list of bonds, angles, etc
- Data file can include force field assignments
- Tools directory has converters for both steps
 - ch2lmp = CHARMM converter
 - amber2lmp = AMBER converter
 - msi2lmp = Accelrys converter

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 - ch2lmp = CHARMM converter
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 - msi2lmp = Accelrys converter
- Provided builders
 - Moltemplate (Andrew Jewett)
 - Pizza.py = chain and patch tools (Python)
- Builders that can create LAMMPS input
 - see http://lammps.sandia.gov/prepost.html
 - VMD TopoTools (Axel Kohlmeyer)
 - Avogadro
 - Packmol
- attend breakout session B1 on Wed

 $LAMMPS \ lingo \ for \ interaction \ potentials$

LAMMPS lingo for interaction potentials

- A pair style can be true pair-wise or many-body
 - LJ, Coulombic, Buckingham, Morse, Yukawa, ...
 - EAM, Tersoff, REBO, ReaxFF, ...
- Bond/angle/dihedral/improper styles = permanent bonds

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 - EAM, Tersoff, REBO, ReaxFF, ...
- Bond/angle/dihedral/improper styles = permanent bonds
- Variants optimized for GPU and many-core
 - GPU, USER-CUDA, USER-OMP packages
 - lj/cut, lj/cut/gpu, lj/cut/cuda, lj/cut/omp
 - see doc/Section_accelerate.html
 - see Kokkos talk by Christian Trott on Thurs AM
- Coulomb interactions included in pair style
 - lj/cut, lj/cut/coul/cut, lj/cut/coul/wolf, lj/cut/coul/long
 - done to optimize inner loop

Categories of pair styles

- Solids
 - eam, eim, meam, adp
- Bio and polymers
 - charmm, class2, gromacs, dreiding
- Reactive
 - tersoff, bop, airebo, comb, reax, reax/c
- Coarse-grained
 - dpd, granular, sph, peri, colloid, lubricate, brownian, FLD
- Aspherical
 - gayberne, resquared, line, tri

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- Aspherical
 - gayberne, resquared, line, tri
- Pair table for tabulation of any pair-wise interaction
- Pair hybrid style allows for hybrid models
 - polymers on metal
 - CNTs in water
 - solid-solid interface between 2 materials

See doc/Section_commands.html for full list

none	hvbrid	hybrid/overlay	adp	
airebo	beck	body	bop	
born	born/coul/long	born/coul/msm	born/coul/wolf	
brownian	brownian/poly	buck	buck/coul/cut	
buck/coul/long	buck/coul/msm	buck/long/coul/long	colloid	
comb	coul/cut	coul/debye	coul/dsf	
coul/long	coul/msm	coul/wolf	dpd	
dpd/tstat	dsmc	eam	eam/alloy	
eam/fs	<u>eim</u>	gauss	gayberne	
gran/hertz/history	gran/hooke	gran/hooke/history	hbond/dreiding/lj	
hbond/dreiding/morse	kim	lcbop	line/lj	
j/charmm/coul/charmm	lj/charmm/coul/charmm/implicit	lj/charmm/coul/long	lj/charmm/coul/msm	
lj/class2	lj/class2/coul/cut	lj/class2/coul/long	<u>lj/cut</u>	
lj/cut/coul/cut	lj/cut/coul/debye	lj/cut/coul/dsf	lj/cut/coul/long	
lj/cut/coul/msm	lj/cut/dipole/cut	lj/cut/dipole/long	lj/cut/tip4p/cut	
lj/cut/tip4p/long	lj/expand	lj/gromacs	lj/gromacs/coul/gromac	
lj/long/coul/long	lj/long/dipole/long	lj/long/tip4p/long	lj/smooth	
lj/smooth/linear	lj96/cut	lubricate	lubricate/poly	
lubricateU	lubricateU/poly	meam	mie/cut	
morse	peri/lps	peri/pmb	peri/ves	
reax	rebo	resquared	soft	
SW	table	tersoff	tersoff/mod	
tersoff/zbl	tip4p/cut	tip4p/long	tri/lj	
yukawa	yukawa/colloid			

ed by users, which can be used if LAMMPS is built with the appropriate package.

awpmd/cut	coul/diel	eam/cd	edip lj/cut/dipole/sf		
eff/cut	gauss/cut	list			
lj/sdk	lj/sdk/coul/long	lj/sdk/coul/msm	lj/sf		
meam/spline	meam/sw/spline	nb3b/harmonic	reax/c		
sph/heatconduction	sph/idealgas	sph/lj	sph/rhosum		
sph/taitwater	sph/taitwater/morris	tersoff/table			

And they come in accelerated flavors: omp, gpu, cuda

adp/omp	airebo/omp	beck/omp	born/coul/long/cuda	
born/coul/long/gpu	born/coul/long/omp	born/coul/msm/omp	born/coul/wolf/gpu	
born/coul/wolf/omp	born/qpu	born/omp	brownian/omp	
brownian/poly/omp	buck/coul/cut/cuda	buck/coul/cut/gpu	buck/coul/cut/omp	
buck/coul/long/cuda	buck/coul/long/gpu	buck/coul/long/omp	buck/coul/msm/omp	
buck/cuda	buck/long/coul/long/omp	buck/gpu	buck/omp	
colloid/gpu	colloid/omp	comb/omp	coul/cut/omp	
coul/debve/omp	coul/dsf/gpu	coul/long/gpu	coul/long/omp	
coul/msm/omp	coul/wolf	dpd/omp	dpd/tstat/omp	
eam/alloy/cuda	eam/allov/gpu	eam/alloy/omp	eam/alloy/opt	
eam/cd/omp	eam/cuda	eam/fs/cuda	eam/fs/gpu	
eam/fs/omp	eam/fs/opt	eam/gpu	eam/omp	
eam/opt	edip/omp	eim/omp	gauss/gpu	
gauss/omp	gayberne/gpu	gayberne/omp	gran/hertz/history/omp	
gran/hooke/cuda	gran/hooke/history/omp	gran/hooke/omp	hbond/dreiding/lj/omp	
hbond/dreiding/morse/omp	line/li/omp	li/charmm/coul/charmm/cuda	li/charmm/coul/charmm/omp	
li/charmm/coul/charmm/implicit/cuda	li/charmm/coul/charmm/implicit/omp	li/charmm/coul/long/cuda	li/charmm/coul/long/gpu	
li/charmm/coul/long/omp	li/charmm/coul/long/opt	li/class2/coul/cut/cuda	li/class2/coul/cut/omp	
li/class2/coul/long/cuda	li/class2/coul/long/gpu	li/class2/coul/long/omp	li/class2/coul/msm/omp	
li/class2/cuda	li/class2/gpu	li/class2/omp	li/long/coul/long/omp	
li/cut/coul/cut/cuda	li/cut/coul/cut/gpu	li/cut/coul/cut/omp	li/cut/coul/debve/cuda	
li/cut/coul/debve/gpu	li/cut/coul/debye/omp	li/cut/coul/dsf/gpu	li/cut/coul/long/cuda	
li/cut/coul/long/gpu	li/cut/coul/long/omp	li/cut/coul/long/opt	li/cut/coul/msm/opt	
li/cut/cuda	li/cut/dipole/cut/gpu	li/cut/dipole/cut/omp	li/cut/dipole/sf/gpu	
li/cut/dipole/sf/omp	li/cut/experimental/cuda	li/cut/gpu	li/cut/omp	
lj/cut/opt	lj/cut/tip4p/cut/omp	lj/cut/tip4p/long/omp	lj/cut/tip4p/long/opt	
li/expand/cuda	lj/expand/gpu	li/expand/omp	lj/gromacs/coul/gromacs/cuda	
li/gromacs/coul/gromacs/omp	ll/gromacs/cuda	ll/gromacs/omp	li/long/coul/long/opt	
lj/sdk/gpu	li/sdk/omp	lj/sdk/coul/long/gpu	li/sdk/coul/long/omp	
li/sdk/coul/msm/omp	li/sf/omp	lj/smooth/cuda	li/smooth/omp	
lj/smooth/linear/omp	lj96/cut/cuda	lj96/cut/gpu	lj96/cut/omp	
lubricate/omp	lubricate/poly/omp	meam/spline/omp	morse/cuda	
morse/gpu	morse/omp	morse/opt	nb3b/harmonic/omp	
peri/lps/omp	peri/pmb/omp	rebo/omp	resquared/gpu	
resquared/omp	soft/omp	sw/cuda	sw/omp	
table/gpu	table/omp	tersoff/cuda	tersoff/omp	
tersoff/table/omp	tersoff/zbl/omp	tip4p/cut/omp	tip4p/long/omp	
tri/li/omp			yukawa/colloid/gpu	
yukawa/colloid/omp				

See doc/pair.html for one-line descriptions

- · 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 adp angular dependent potential (ADP) of Mishin
- · pair style airebo AIREBO potential of Stuart
- · pair style beck Beck potential
- · pair style body interactions between body particles
- · pair style bop BOP potential of Pettifor · pair style born - Born-Mayer-Huggins potential
- pair style born/coul/long Born-Mayer-Huggins with long-range Coulombics
- pair style born/coul/msm Born-Mayer-Huggins with long-range MSM Coulombics
- pair style born/coul/wolf Born-Mayer-Huggins with Coulombics via Wolf potential
- · pair style brownian Brownian potential for Fast Lubrication Dynamics
- pair style brownian/poly Brownian potential for Fast Lubrication Dynamics with polydispersity
- · pair style buck Buckingham potential pair style buck/coul/cut - Buckingham with cutoff Coulomb
- · pair style buck/coul/long Buckingham with long-range Coulombics
- pair style buck/coul/msm Buckingham long-range MSM Coulombics
- pair style buck/long/coul/long long-range Buckingham with long-range Coulombics
- pair style colloid integrated colloidal potential
- · pair style comb charge-optimized many-body (COMB) potential
- · pair style coul/cut cutoff Coulombic potential
- · pair style coul/debye cutoff Coulombic potential with Debye screening
- · pair style coul/dsf Coulombics via damped shifted forces
- · pair style coul/long long-range Coulombic potential · pair style coul/msm - long-range MSM Coulombics
- · pair style coul/wolf Coulombics via Wolf 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/alloy alloy EAM
- · pair style eam/fs Finnis-Sinclair EAM
- pair style eim embedded ion method (EIM) · pair style gauss - Gaussian potential
- · pair style gayberne 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

Relative CPU cost of potentials

See http://lammps.sandia.gov/bench.html#potentials for details Can estimate how long your simulation will run

Potential	System	Atoms	Timestep	CPU	LJ Ratio
Granular	chute flow	32000	0.0001 tau	5.08e-7	0.34x
FENE bead/spring	polymer melt	32000	0.012 tau	5.32e-7	0.36x
Lennard-Jones	LJ liquid	32000	0.005 tau	1.48e-6	1.0x
DPD	pure solvent	32000	0.04 tau	2.16e-6	1.46x
EAM	bulk Cu	32000	5 fmsec	3.59e-6	2.4x
Tersoff	bulk Si	32000	1 fmsec	6.01e-6	4.1x
Stillinger-Weber	bulk Si	32000	1 fmsec	6.10e-6	4.1x
EIM	crystalline NaCl	32000	0.5 fmsec	9.69e-6	6.5x
SPC/E	liquid water	36000	2 fmsec	1.43e-5	9.7x
CHARMM + PPPM	solvated protein	32000	2 fmsec	2.01e-5	13.6x
MEAM	bulk Ni	32000	5 fmsec	2.31e-5	15.6x
Peridynamics	glass fracture	32000	22.2 nsec	2.42e-5	16.4x
Gay-Berne	ellipsoid mixture	32768	0.002 tau	4.09e-5	28.3x
AIREBO	polyethylene	32640	0.5 fmsec	8.09e-5	54.7x
COMB	crystalline SiO2	32400	0.2 fmsec	4.19e-4	284x
eFF	H plasma	32000	$0.001 \; \mathrm{fmsec}$	4.52e-4	306x
ReaxFF	PETN crystal	16240	0.1 fmsec	4.99e-4	337x
ReaxFF/C	PETN crystal	32480	0.1 fmsec	2.73e-4	185x
VASP/small	water	192/512	0.3 fmsec	26.2	17.7e6
VASP/medium	CO2	192/1024	0.8 fmsec	252	170e6
VASP/large	Xe	432/3456	2.0 fmsec	1344	908e6

Bond styles (also angle, dihedral, improper)

- Used for molecules with fixed bonds
 - Fix bond/break and bond_style quartic can break them
- To learn what bond styles LAMMPS has ... where would you look?

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- doc/Section_commands.html or doc/bond_style.html

none	hybrid	class2	fene
fene/expand	harmonic	morse	nonlinear
quartic	table		

ich can be used if LAMMPS is built with the appropriate package.

harmonic/shift/harmonic/shift/cut

e used if LAMMPS is built with the appropriate accelerated package.

class2/omp	fene/omp	fene/expand/omp	harmonic/omp
harmonic/shift/omp	harmonic/shift /cut/omp	morse/omp	nonlinear/omp
quartic/omp	table/omp		

- · bond style none turn off bonded interactions
- bond_style hybrid define multiple styles of bond interactions
- bond style class2 COMPASS (class 2) bond
- · bond style fene FENE (finite-extensible non-linear elastic) bond
- · bond style fene/expand FENE bonds with variable size particles
- · bond style harmonic harmonic bond
- · bond style morse Morse bond
- bond_style nonlinear nonlinear bond
- bond style quartic breakable quartic bond
- bond style table tabulated by bond length

Long-range Coulombics

KSpace style in LAMMPS lingo, see doc/kspace_style.html

- Options:
 - traditional Ewald, scales as $O(N^{3/2})$
 - PPPM (like PME), scales as $O(N \log(N))$
 - MSM, scales as O(N), lj/cut/coul/msm
- Additional options:
 - non-periodic, PPPM (z) vs MSM (xyz)
 - long-range dispersion (LJ)

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- Additional options:
 - non-periodic, PPPM (z) vs MSM (xyz)
 - long-range dispersion (LJ)
- PPPM is fastest choice for most systems
 - FFTs can scale poorly for large processor counts
- MSM can be faster for low-accuracy or large proc counts

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- Options:
 - traditional Ewald, scales as $O(N^{3/2})$
 - PPPM (like PME), scales as $O(N \log(N))$
 - MSM, scales as O(N), lj/cut/coul/msm
- Additional options:
 - non-periodic, PPPM (z) vs MSM (xyz)
 - long-range dispersion (LJ)
- PPPM is fastest choice for most systems
 - FFTs can scale poorly for large processor counts
- MSM can be faster for low-accuracy or large proc counts
- Ways to speed-up long-range calculations:
 - see doc/Section_accelerate.html
 - cutoff & accuracy settings adjust Real vs KSpace work
 - kspace_style pppm/stagger for PPPM
 - kspace_modify diff ad for smoothed PPPM
 - run_style verlet/split
- See MSM talk by Stan Moore on Wed AM

Most flexible feature in LAMMPS
Allow control of "what" happens "when" within each timestep
Loop over timesteps:

communicate ghost atoms

build neighbor list (once in a while) compute forces communicate ghost forces

output to screen and files

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Loop over timesteps:
  fix initial
                          NVE, NVT, NPT, rigid-body integration
  communicate ghost atoms
  fix neighbor
                                                    insert particles
  build neighbor list (once in a while)
  compute forces
  communicate ghost forces
  fix force
                       SHAKE, langevin drag, wall, spring, gravity
  fix final
                          NVE, NVT, NPT, rigid-body integration
  fix end
                                 volume & T rescaling, diagnostics
  output to screen and files
```

- 100+ fixes in LAMMPS
- You choose what group of atoms to apply fix to
- Already saw some in obstacle example:
 - fix 1 all nve
 - fix 2 flow temp/rescale 200 1.0 1.0 0.02 1.0
 - fix 3 lower setforce 0.0 0.0 0.0
 - fix 5 upper aveforce 0.0 -0.5 0.0
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- To learn what fix styles LAMMPS has ... where would you look?
- doc/Section_commands.html or doc/fix.html
- If you familiarize yourself with fixes, you'll know many things LAMMPS can do
- Many fixes store output accessible by other commands
 - rigid body COM
 - thermostat energy
 - forces before modified

- ∼75 computes in LAMMPS
- Calculate some property of system, in parallel
- Always for the current timestep
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- Calculate some property of system, in parallel
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angle/local	atom/molecule	body/local	bond/local	centro/atom	cluster/atom
cna/atom	com	com/molecule	contact/atom	coord/atom	damage/atom
dihedral/local	displace/atom	erotate/asphere	erotate/sphere	erotate/sphere/atom	event/displace
group/group	gyration	gyration/molecule	<u>heat/flux</u>	improper/local	inertia/molecule
<u>ke</u>	ke/atom	msd	msd/molecule	msd/nongauss	pair
pair/local	<u>pe</u>	pe/atom	pressure	property/atom	property/local
property/molecule	rdf	<u>reduce</u>	reduce/region	slice	stress/atom
temp	temp/asphere	temp/com	temp/deform	temp/partial	temp/profile
temp/ramp	temp/region	temp/sphere	<u>ti</u>	voronoi/atom	

ributed by users, which can be used if LAMMPS is built with the appropriate package.

ackland/atom	basal/atom	ke/eff	ke/atom/eff	meso_e/atom	meso_rho/atom
meso_t/atom	temp/eff	temp/deform/eff	temp/region/eff	temp/rotate	

e styles, which can be used if LAMMPS is built with the appropriate accelerated package.

pe/cuda pressure/cuda temp/cuda temp/partial/cuda

- Key point:
 - computes store their answers
 - other commands invoke them and use the results
 - e.g. thermo output, dumps, fixes
- Output of computes:
 - global vs per-atom vs local
 - scalar vs vector vs array
 - extensive vs intensive values

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Output of computes:

- global vs per-atom vs local
- scalar vs vector vs array
- extensive vs intensive values

• Examples:

- temp & pressure = global scalar or vector
- pe/atom = potential energy per atom (vector)
- displace/atom = displacement per atom (array)
- pair/local & bond/local = per-neighbor or per-bond info
- Many computes are useful with averaging fixes:
 - fix ave/time, ave/spatial, ave/atom
 - fix ave/histo, ave/correlate

Thermo output

One line of output every N timesteps to screen and log file

See doc/thermo_style.html

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- See doc/thermo_style.html
- Any scalar can be output:
 - dozens of keywords: temp, pyy, eangle, lz, cpu
 - any output of a compute or fix: c_ID, f_ID[N], c_ID[N][M]
 - fix ave/time stores time-averaged quantities
 - equal-style variable: v_MyVar
 - one value from atom-style variable: v_xx[N]
 - any property for one atom: q, fx, quat, etc

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- Post-process via:
 - tools/python/logplot.py log.lammps X Y (via GnuPlot)
 - tools/python/log2txt.py log.lammps data.txt X Y ...
 - Pizza.py log tool
 - can read thermo output across multiple runs

Snapshot of per-atom values every N timesteps

• See doc/dump.html

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 - atom, custom (both native LAMMPS)
 - VMD will auto-read if file named *.lammpstraj
 - xyz for coords only
 - cfg for AtomEye
 - DCD, XTC for CHARMM, NAMD, GROMACS
 - good for back-and-forth runs and analysis

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- Two additional styles
 - local: per-neighbor, per-bond, etc info
 - image: instant picture, rendered in parallel
 - see talk by Axel Kohlmeyer on Wed AM

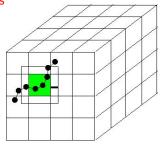
- Any per-atom quantity can be output
 - dozens of keywords: id, type, x, xs, xu, mux, omegax, ...
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- Additional options:
 - control which atoms by group or region
 - control which atoms by threshold
 - dump_modify thresh $c_pe > 3.0$
 - text or binary or gzipped
 - one big file or per snapshot or per proc
 - see dump_modify fileper or nfile

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- Post-run conversion
 - tools/python/dump2cfg.py, dump2pdb.py, dump2xyz.py
 - Pizza.py dump, cfg, ensight, pdb, svg, vtk, xyz

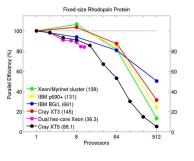
Parallelization in LAMMPS

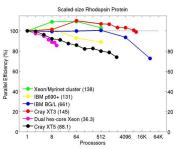
- Physical domain divided into 3d bricks
- One brick per processor
- Atoms carry properties & topology as they migrate
- Comm of ghost atoms within cutoff
 - 6-way local stencil
- Short-range forces ⇒
 CPU cost scales as O(N/P)



Parallel performance

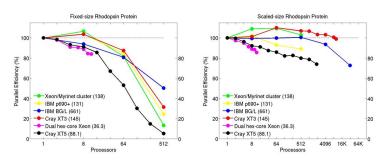
See http://lammps.sandia.gov/bench.html





Parallel performance

See http://lammps.sandia.gov/bench.html



Exercise: run bench/in.lj, change N and P, is it O(N/P)?

- $lmp_linux v \times 2 v y 2 v z 2 < in.lj$
- mpirun -np 2 lmp_linux < in.lj

How to speed-up your simulations

See doc/Section_accelerate.html of manual

- Many ideas for long-range Coulombics
 - PPPM with 2 vs 4 FFTs
 - PPPM with staggered grid
 - run_style verlet/split
 - processor layout

How to speed-up your simulations

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- Many ideas for long-range Coulombics
 - PPPM with 2 vs 4 FFTs
 - PPPM with staggered grid
 - run_style verlet/split
 - processor layout
- We How to for GPU and USER-CUDA and USER-OMP packages
 - GPU:
 - pair style and neighbor list build on GPU
 - can use multiple cores per GPU
 - USER-CUDA:
 - fixes and computes onto GPU (many timesteps)
 - one core per GPU
 - USER-OMP:
 - works via OpenMP, run 1 or 2 MPI tasks/node
 - supports large number of pair styles (+ other styles)
 - GPU benchmark data at http://lammps.sandia.gov/bench.html
 - desktop and Titan (ORNL)

How to speed-up your simulations

- Increase time scale via timestep size
 - fix shake for rigid bonds (2 fs)
 - run_style respa for hierarchical steps (4 fs)
- Increase length scale via coarse graining
 - all-atom vs united-atom vs bead-spring
 - mesoscale models:
 - ASPHERE, BODY, COLLOID, FLD packages
 - GRANULAR, PERI, RIGID, SRD packages
 - see doc/Section_packages.html for details

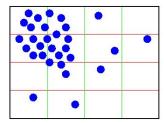
See http://lammps.sandia.gov/features.html

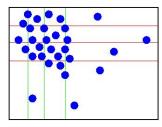
- Units
 - see doc/units.html
 - LJ, real, metal, cgs, si
 - all input/output in one unit system
- Ensembles
 - see doc/Section_howto.html 6.16
 - one or more thermostats (by group)
 - single barostat
 - rigid body dynamics
- Hybrid models
 - pair_style hybrid and hybrid/overlay
 - atom_style hybrid sphere bond ...

- Aspherical particles
 - see doc/Section_howto.html 6.14
 - ellipsoidal, lines, triangles, rigid bodies
 - ASPHERE package
- Mesoscale and continuum models
 - COLLOID, FLD, SRD packages for NPs and colloids
 - PERI package for Peridynamics
 - USER-ATC package for atom-to-continuum (FE)
 - GRANULAR package for granular media
 - add-on LIGGGHTS package for DEM
 - www.liggghts.com/www.cfdem.com
 - see talk by Christoph Kloss on Wed AM
 - breakout session B3 on Wed

- Multi-replica modeling
 - see doc/Section_howto.html 6.14
 - parallel tempering
 - PRD, TAD, NEB

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 - see doc/Section_howto.html 6.14
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- Load balancing
 - balance command for static LB
 - fix balance command for dynamic LB
 - work by adjusting proc dividers in 3d brick grid

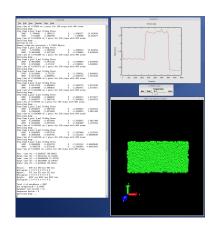




- Energy minimization
 - Via usual dynamics
 - pair_style soft
 - fix nve/limit and fix viscous
 - Via gradient-based minimization
 - min_style cg, htfn, sd
 - Via damped-dynamics minimization
 - min_style quickmin and fire
 - used for nudged-elastic band (NEB)

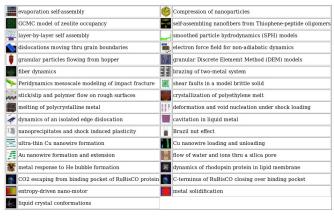
Use LAMMPS as a library

- doc/Section_howto.html
 6.10 and 6.19
- C-style interface (C, C++, Fortran, Python)
- examples/COUPLE dir
- python and python/examples directories



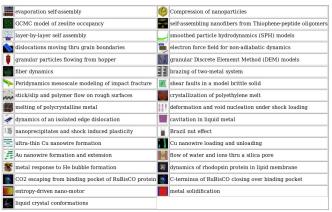
What have people done with LAMMPS?

- Pictures: http://lammps.sandia.gov/pictures.html
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- Papers: http://lammps.sandia.gov/papers.html
 - authors, titles, abstracts for \sim 2500 papers

Customizing and modifying LAMMPS

- 90% of LAMMPS is customized add-on classes, via styles
- Write a new derived class, drop into src, re-compile

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- Write a new derived class, drop into src, re-compile
- Resources:
 - doc/Section_modify.html
 - doc/PDF/Developer.pdf
 - class hierarchy & timestep structure
- Come to breakout session A2 for developers on Wed
 - 30 min overview of this topic
 - look for PDF of Steve Plimpton presentation
- Please contribute your code to add to the LAMMPS distro!

Exercises with the examples

examples/README has one-line descriptions of 30 examples

Quick runs (2d) and visually appealing:

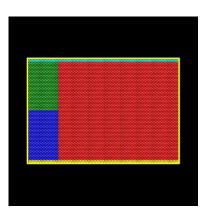
- crack: crack propagation
- flow: Couette and Poiseuille flow in a channel
- friction: frictional contact of spherical asperities
- indent: spherical indenter into solid
- micelle: self-assembly of small lipid-like molecules
- obstacle: flow around two voids in a channel
- shear: sideways shear of solid, with and without a void

Running and visualizing the examples

- Run in serial
 - Imp_linux < in.friction
- Run in parallel
 - mpirun -np 4 lmp_linux < in.friction
- Uncomment dump image and dump_modify lines
 - produce series of JPG (or PPM) files
- Uncomment dump atom line
 - produce snapshot file, can viz with VMD

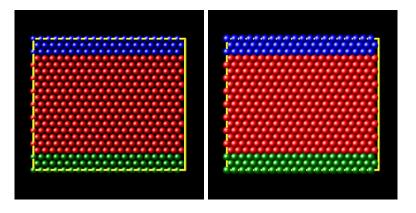
Crack problem

- Tensile pull on 2d LJ solid
- Slit crack between red/green neigh_modify exclude 2 3
- Uniform gradient pull velocity ramp command else shock waves or worse
- Need large system & slow pull else defects besides crack
- Options to play with:
 pull rate
 pair-wise cutoff
 turn off velocity ramp
 change NULL ⇒ 0.0 in fix 2



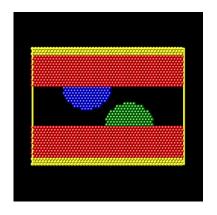
Flow problems

- Couette flow and Poiseuille flow
- Options to play with: wall velocity, force kick, temperature
- Monitor velocity profile via fix ave/spatial



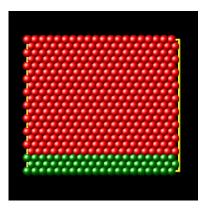
Friction problem

- 2 non-planar surfaces
- Region commands to build geometry
- Options to play with: asperity size, shape asperity separation x-velocity multiple passes



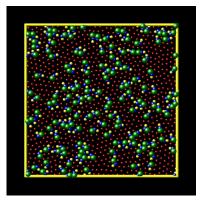
Indent problem

- 2d LJ solid periodic in x free upper y surface
- Spherical indenter downward push, remove
- Defect creation & healing
- Options to play with: speed & depth of indent size of indenter size of system



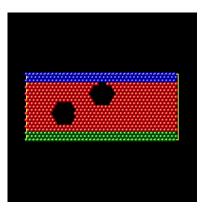
Micelle problem

- Simple lipid model hydrophilic head hydrophobic tail monomer solvent
- 2d self-assembly vesicles, bilayers
- Options to play with: timestep size
 # of timesteps
 pair-wise coeffs



Obstacle problem

- LJ flow around obstacle(s)
- Poiseuille kick added to atoms pressure-gradient flow
- Top surface applies pressure
- Obstacle creation delete_atoms command fix indent command
- Options to play with:
 size of force kick
 size of system
 size & position of obstacles
 shape of obstacles
 add a new obstacle



Shear problems

- Fixed-end shear in fcc Ni
- EAM potential
- Quasi-3d non-periodic XY slab thin in Z, periodic
- Defect formation without and with void
- Options to play with:
 size of system
 shear rate
 turn off velocity ramp
 change void shape, size
 add another void

