Whirlwind tour of more advanced topics

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8th LAMMPS Workshop Tutorial Virtual meeting – August 2023







Tell you about ...

- Additional features and options in LAMMPS
- Where to go for more information about them
- Whirlwind fashion, one slide (or bullet!) per feature
- Not enough time to cover all the details
- But you can look into topics that interest you later

Each of these is a command with its own doc page

General:

- info = print info about this LAMMPS executable
- include = insert commands from another script
- if = conditional, including elif and else options
- print = print message to the screen, can contain variables
- quit = force LAMMPS to exit

Used for looping:

- label = flag a position in the input script
- next = increment one or more variables
- jump = jump to a label

See variable command doc page

Lots of uses:

- One-time definition of values used in many places
 - also settable from command-line that invokes LAMMPS
- Many variable styles:
 - store strings or numbers or formulas
 - produce scalar or vector or per-atom values
- Formulas are C-like
 - use math functions, boolean logic, groups, regions, etc
 - use scalar or per-atom inputs
 - use output from computes, fixes, other variables
 - can be time-dependent or spatially-dependent
- Many LAMMPS commands allow variables as inputs
 - command invokes variable internally
 - example: define a time- or spatially-dependent E-field

Each of these is a command with its own doc page

- Action = perform a simulation
 - run = dynamics simulation (molecular dynamics)
 - minimize = energy minimization (molecular statics)
 - rerun = zero-step runs on snapshots from a dump file

Multi-replica simulations:

- temper = parallel tempering
- neb = nudged-elastic band for barrier heights
- prd = parallel replica dynamics
- tad = temperature-accelerated dynamics
- hyper = global or local hyperdynamics

Three more input script features

- Run multiple simulations from one script
 - run N simulations on P procs split into M partitions
 - see Section 8.1.3 of User Guide
- Shell command to invoke an external program with args
 - example: shell cd subdir1
 - example: shell my_analyze.exe out.file \$n \${param}
 - see shell command doc page
- Invoke Python functions from your script:
 - pass arguments to the function
 - return value(s) in variables
 - the Python function can access internal LAMMPS data
 - Python code can be embedded in script or in another file
 - see Section 2 in Programmer Guide

LAMMPS packages

- Package = one or more style files with common theme
- Currently \sim 90 package folders within src dir
- At compile time, optionally include individual packages or not
- See Section 6.1 of User Guide for one-liners, click for more

Package	Description	Doc page
ADIOS	dump output via ADIOS	dump adios
ASPHERE	aspherical particle models	Howto spherical
ATC	Atom-to-Continuum coupling	fix atc
AWPMD	wave packet MD	pair_style awpmd/cut
BOCS	BOCS bottom up coarse graining	fix bocs
BODY	body-style particles	Howto body
BROWNIAN	Brownian dynamics, self-propelled particles	fix brownian, fix propel/self
CG-DNA	coarse-grained DNA force fields	src/CG-DNA/README
CG-SDK	SDK coarse-graining model	pair_style lj/sdk
CLASS2	class 2 force fields	pair_style lj/class2

Coarse grained and meso/continuum scale models

Motivation: increase accessible length and time scales Some packages overlap these 3 categories

- Packages for coarse-grained (CG) models:
 - Bio systems: CG-DNA, CG-SDK
 - DPD variants: DPD-BASIC, DPD-MESO, DPD-REACT, DPD-SMOOTH
 - Surfaces: MANIFOLD
 - Multi-scaling CG: MSCG
- Packages for mesoscale models:
 - Aspherical particles: ASPHERE, BODY
 - Large particles: COLLOID
 - Rigid bodies: POEMS, RIGID
 - Solvent models: FLD, LATBOLTZ, SRD
 - Nanotubes: MESONT
- Packages for continum-scale models
 - ATC = couple to finite elements
 - GRANULAR = granular systems
 - PERI = meshless continuum model for fracture
 - SPH, MACHDYN = smoothed particle hydro for liquids & solids



May not normally think of these in the context of MD

- ATC Atom to continuum coupling via finite elements
- DIFFRACTION x-ray and electron diffraction intensities
- LATBOLTZ Lattice-Boltzman model
- MC Monte Carlo methods
- MDI
 Code coupling, e.g. for AIMD or QM/MM
- ML-* Variety of machine-learned potentials
- PERI Meshless continuum Peridynamics model
- REACTION Heuristic chemical reactions
- RIGID Rigid-body constraints
- SPH Smoothed particle hydrodynamics model
- SPIN Magnetic atomic spin dynamics
- VORONOI Voronoi tesselations around atoms/particles

LAMMPS does not build molecular systems or auto-magically assign force field parameters for you

- Data file must list bonds/angles/etc and FF params
- Converter programs:
 - ch2Imp = CHARMM converter
 - amber2Imp = AMBER converter
 - msi2lmp = Accelrys converter
 - see Section 10 of User Guide and lammps/tools dir
- 3rd-party builders which can create LAMMPS input
 - See website Pre/Post processing for free & commercial
 - VMD TopoTools, Moltemplate
 - Avogadro, Packmol, ATB (Auto Topology Builder)
 - Enhanced Monte Carlo see breakout: Fri

Example systems created by builder tools



Load balancing

- Can be especially useful for coarse-grained systems
- Use balance command for static balancing
- Use fix balance command for dynamic balancing

(A) Imbalanced (B) Adjust proc dividers (C) Recursive bisectioning



• Can balance by particle count, weighted particles, or CPU time

See minimize and min_style doc pages

- Via gradient-based minimization
 - min_style cg, hftn, sd
 - can include bond-length constraints, e.g. SHAKE
- Via damped-dynamics minimization
 - min_style quickmin and fire
 - also used for nudged-elastic band (NEB) calculations
- Possible to just un-overlap via usual dynamics
 - pair_style soft command
 - fix nve/limit and fix viscous commands

45 entries in Howto section 8 of User Guide

8.1. General howto

- 8.1.1. Restart a simulation
- 8.1.2. Visualize LAMMPS snapshots
- 8.1.3. Run multiple simulations from one input script
- 8.1.4. Multi-replica simulations
- 8.1.5. Library interface to LAMMPS
- 8.1.6. Coupling LAMMPS to other codes
- 8.1.7. Using LAMMPS with the MDI library for code coupling
- 8.1.8. Broken Bonds

8.2. Settings howto

- 8.2.1. 2d simulations
- 8.2.2. Type labels
- · 8.2.3. Triclinic (non-orthogonal) simulation boxes
- 8.2.4. Thermostats
- 8.2.5. Barostats
- 8.2.6. Walls
- 8.2.7. NEMD simulations
- 8.2.8. Long-range dispersion settings

8.3. Analysis howto

- 8.3.1. Output from LAMMPS (thermo, dumps, computes, fixes, variables)
- 8.3.2. Use chunks to calculate system properties
- 8.3.3. Using distributed grids
- 8.3.4. Calculate temperature
- 8.3.5. Calculate elastic constants
- 8.3.6. Calculate thermal conductivity
- 8.3.7. Calculate viscosity
- 8.3.8. Calculate diffusion coefficients
- 8.3.9. Output structured data from LAMMPS

8.4. Force fields howto

- 8.4.1. CHARMM, AMBER, COMPASS, and DREIDING force fields
- 8.4.2. AMOEBA and HIPPO force fields
- 8.4.3. TIP3P water model
- 8.4.4. TIP4P water model
- 8.4.5. TIP5P water model
- 8.4.6. SPC water model

8.5. Packages howto

- 8.5.1. Finite-size spherical and aspherical particles
- 8.5.2. Granular models
- 8.5.3. Body particles
- 8.5.4. Bonded particle models
- 8.5.5. Polarizable models
- 8.5.6. Adiabatic core/shell model
- 8.5.7. Drude induced dipoles
- 8.5.8. Tutorial for Thermalized Drude oscillators in LAMMPS
- 8.5.9. Peridynamics with LAMMPS
- 8.5.10. Manifolds (surfaces)
- 8.5.11. Magnetic spins

8.6. Tutorials howto

- 8.6.1. Using CMake with LAMMPS tutorial
- 8.6.2. LAMMPS GitHub tutorial
- 8.6.3. PyLammps Tutorial
- 8.6.4. Using LAMMPS on Windows 10 with WSL