#### <u>A brief introduction to LAMMPS</u>







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#### The basics

- LAMMPS Large-scale Atomic/Molecular Massively Parallel Simulator
  - Developed by Sandia National Laboratories and by its wide user-base
  - Can be downloaded from: https://lammps.sandia.gov/download.html
- Everything we are covering today (and a lot of other info) can be found in the LAMMPS User Manual: https://lammps.sandia.gov/doc/Manual.html



### Overview of this session

- Run first LAMMPS simulation on ARCHER
  - Briefly show how to run simulation locally
- Preparing a simulation:
  - How is simulation box prepared
  - How are particle interactions defined
  - Neighbour lists etc
- Coffee break
- Running a simulation
  - Fixes, computes, and variables
  - What can be output?
- Advanced options
- Questions & quick exercise



#### How molecular dynamics works

Start with all particle positions and velocities at time *t* 

Update particle positions to time  $t+\delta t$ 

From new positions, find new potential energies, forces, and velocities at time  $t+\delta t$ 









#### 1) Simulation box setup

Periodic boundary conditions



Starting simulation setup ( $\rho \sim 0.4$ )





#### 2) Interparticle interactions

• There are 221 different pair styles in LAMMPS



Not discussed here, but LAMMPS also has:

- 17 bond\_style commands
- 22 angle\_style commands
- 17 dihedral commands
- 13 improper\_style commands

• Etc...





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## 3) Neighbour lists







# 4) Fixes and computes

- 264 fixes
  - This sets general parameters
    - Temerature; pressure; gravity; viscosity; background flows; etc. defined by fixes
  - Our simple example has 2:
    - Fix NVT ensemble with temperature T = 1.0
    - Fix background flow to 0 (not needed)
- 138 computes
  - Where LAMMPS shines these commands enable you to output ensemble or per-particle properties of interest





## 5) Simulation run and outputs



#### 6) Advanced inputs Mean-squared dispacement (MSD)



time / δt

# 7) Useful third-party software

#### Visual molecular dynamics (VMD): https://www.ks.uiuc.edu/Research/vmd/



VMD GUI – Wikipedia





OVITO GUI – Wikipedia



DNA binds to single-walled nanotube Xueqing Zou, 2013 Some Python pre- and post-processing packages:

- Pizza.py https://pizza.sandia.gov/
- MDAnalysis https://www.mdanalysis.org/
- PyLAT –

https://github.com/MaginnGroup/PyLAT



# 8) Optional user exercise

- You have access to a LAMMPS input script called 'in.lj\_exercise'
  - This is the same script as before with two changes:
    - The starting density is defined by the variable 'DENSITY'
    - A radial distribution function is output in the main simulation run
- For this exercise, you will look at how varying the system density affects the RDF
  - You should only vary the value of the variable 'Density'
  - In particular, I recommend looking at the RDFs output at densities  $\rho$  = 0.05, 0.8, 1.4



#### Overview for next session

- Questions from this session
- Compiling LAMMPS on Archer (similar to local compilation)
  - Packages, libraries, etc.
- Smarter domain decomposition commands
- Delving deeper into LAMMPS source code

