# Group Meeting

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> Bogazici University 03/13/2020



# OUTLINE

- > Molecular Dynamics
- LAMMPS
- Reaxff
- Microporous Structures of Carbide-Derived
   Carbon-Based Supercapacitors
- > MD simulations in the constant potential ensemble

# **Molecular dynamics**

- MD is a computer simulation method for analyzing the physical movements of atoms and molecules
- The atoms and molecules interact for a fixed period of time
- The trajectories of atoms and molecules are determined by numerically solving Newton's equations of motion for a system of interacting particles

# **Molecular dynamics**

Goal of the molecular dynamics method?

- Given number of atoms, you want to simulate and predict how atoms will be moving according to time
- Firstly, You need a initial conditions of the molecules such as position, velocity depends on temperature
- Secondly, You need inter atomic energy for each atom, forces and their distances: Coulomb interaction, Van der Waals, standard 12/6 Lennard-Jones potential
- Minimization of energy, energy and geometry optimization



- Acronym for Large-scale Atomic/Molecular Massively Parallel Simulator.
- A molecular dynamics code, but can be used for energy minimization and Monte Carlo Simulations.
- Can model systems from a few particles up to billion of particles slower simulation



- Freely available, open-source code
- Current version is written in C++
- Presently maintained by the Sandia National Lab
- Can run on single-processor laptop/desktop, but optimized for clusters
- Can be installed on MacOS, Linux, Windows



#### •Define the geometry, the simplest a cubic box xlo= 0, xhi = a ylo= 0, yhi = a zlo= 0, zhi = a

p : periodic, infinite replication
f : non-periodic



#### **Thermodynamic ensemble**

Define dynamics

- NVE : micro canonical ensemble
- NVT : canonical ensemble
- NPT : isobaric ensemble

NVE
$$\rightarrow$$
 extensive property $\mu$ PT $\rightarrow$  intensive property

Chemical potential

### **Input Files**

- structure.dat data file: contains the size of the system, the number of atoms, mass of the each type, the position of each atom (potential velocities)
- in.file input file: contains the instructions of the tasks to perform, potential force-field parameters
- pod.mod potential file: if necessary ex: tersoff potential, classic MD



- ReaxFF, a force field for reactive systems
- ReaxFF uses distance-dependent bond-order functions to represent the contributions of chemical bonding to the potential energy.
- Fix NVE, Silicon carbide with O2 → SiO2



### Microporous Structures of Carbide-Derived Carbon-Based Supercapacitors

- Molecular dynamics simulations for modeling microporous amorphous carbon.
- The crystal structure of SiC was used as initial structure and follow a pseudo-mimetic approach using quenched molecular dynamics (QMD).
- The SiC Tersoff potential is used

### Microporous Structures of Carbide-Derived Carbon-Based Supercapacitors

- 1. 50 ps NVT @ RT
- 2. 200 ps NPT @ 2500 K
- 3. Quenching from 2500 K to RT with
- quench rate of 2.2 x 10^12 K/s in NPT ensemble
- 4. Removal of all Si atoms
- 5. 200 ps NVT @ RT

50 ps = ( run x timestep /1000 ) time 2500K/2500ps = 1 K/ps

#### Simulation of Double Layer Capacitors

MD simulations in the constant potential ensemble → to break down the effects of microscopic correlations on electrochemical response

- fixed potential difference  $\Delta \Psi$
- temperature T
- system volume V
- the number of electrolyte molecules N

- Interactions are present in this coarse-grained representation leads to a huge computational savings
- Ionic liquid-solvent mixture is used as electrolyte

1-Butyl-3-methylimidazolium hexafluorophosphate Acetonitrile (ACN)

- T  $\rightarrow$  400 K
- P  $\rightarrow$  1-600 atm
- Porosity  $\rightarrow$  4.5 6.1 6.5 and 6.6 ångstrom
- Electrolyte concentration  $\rightarrow 0.12 0.47 0.63$  and 0.89
- 2 different type of solvent

Total = 32 simulations



Measurements:

- Porosity
- Capacitance
- Electrolyte Molecular Distribution
- Probability Density Distribution
- Mean Square Displacement (MSD)

#### Thank you for your listening!

