Molecular Dynamics

CHEM8711/7711

Molecular Dynamics (MD)

- Molecular dynamics uses Newton's laws (classical mechanics) to study the behavior of molecules over time
- Newton's Laws
  - 1st: motion continues in a straight line at constant velocity in the absence of force
  - 2nd: force equals mass times acceleration
  - 3rd: action generates equal and opposite reaction

Newton's Second Law

$$\mathbf{F_i (t) = m_i a_i (t)}$$

$$\frac{\partial^2 x_i}{\partial t^2} = \frac{F_{x_i}}{m_i}$$

Forces

- Collisions between particles
- Forces between collisions
  - None ($\Delta x_i = v_i \delta t$)
  - Constant (example: uniform electric field)
  - Variable (forces due to other particles in motion)

Practical Issues

- Starting geometry
- Equilibration
- Trajectory – time steps
- Timescales
- Ensembles
- Periodic boundary conditions
- Solvent

Starting Geometry

- Need to start from a fully optimized geometry
  - Improves equilibration
  - Reduces likelihood of explosions

Class Exercise I

- Generate four different starting geometries for the same molecule
  - Fully minimized
  - Stretched (bonds that are too long)
  - Compressed (bonds that are too short)
  - Overlapped (atoms on top of each other)
- Perform MD simulations using the default parameters for each structure – save to different databases

Equilibration

- Equilibration of the added kinetic energy across the system should be monitored
- Will be reflected in the temperature, pressure, and energy values
  - NVT simulations should reach constant desired temperature with reasonable standard deviations
  - NPT simulations should reach constant desired pressure with reasonable standard deviations
  - Energies (U, E, H) should not oscillate wildly

Energetics Reminder

$$U = \frac{k_B T^2}{Q}\left(\frac{\partial Q}{\partial T}\right)_V = k_B T^2\left(\frac{\partial \ln Q}{\partial T}\right)_V$$

$$U = \langle E \rangle = \frac{1}{M}\sum_{i=1}^{M} E_i$$

- Practically
  - Internal energy is the ensemble average for states examined during a simulation (usually either molecular dynamics or monte carlo)
- ΔHf can be calculated through the addition of parameterized bond energies to the steric energy

Class Exercise II

- Open each of the databases you created in the first exercise
- Look at the temperature values as a function of time (Use plot function)
- Use the database calculator (Compute-> Calculator) to determine means and standard deviations for temperature, pressure and energy values
- Which (if any) of your simulations was equilibrated?

Trajectory

- Force and position are used to calculate new positions after short time intervals
- Why <u>short</u> time intervals?

Consider ethane (CH_3-CH_3) with a C-C equilibrium bond distance of 1.54 Å

Original Distance	New distance after				
	1fs	2fs	3fs	4fs	10fs
1.52 Å	1.58 Å	1.64 Å	1.70 Å	1.76 Å	2.12 Å

Time Intervals (steps)

- Time intervals approaching the fastest vibration will result in breakage of bonds – essentially a simulated explosion
- Workaround
  - Fastest vibrations are typically bonds to H
  - Fastest vibrations can be constrained to their equilibrium values (algorithms: SHAKE, RATTLE...)
  - Longer time steps (~double) can be used
- Common time intervals: 1 fs (10^{-15} sec)

Class Exercise III

- Perform MD simulations on the same, minimized geometry with time steps of:
  - 1 fs
  - 5 fs
  - 10 fs
  - 50 fs
  - 100 fs
- Evaluate means and standard deviations for temperature, pressure and energies
- Which simulation(s) are best equilibrated?

Timescales

Log Time (sec)	Chemical Process	Spectroscopic Method
-14	Bond vibrations	IR
-12		
-10	Trans/gauche isomerism Small molecule rotation	Microwave
-8		
-6		Radiowaves (NMR)
-4	Protein rotation	
-2		
0		
2		
4	Amphiphilic solute bilayer crossings	
6		

Class Exercise IV

- Perform MD simulations on an alkane (5-6 carbons) with the following simulation times (equilibrium phase):

1 ps	10 ps	100 ps	1000 ps

- You might coordinate with a neighbor to start from different conformations of the same molecule
- Did you observe any isomerism between trans and gauche conformations?

Simulating Longer Timescales

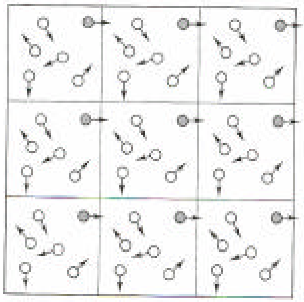
- Langevin (Brownian) Dynamics
- Not atomic resolution – larger bodies are usually simulated with intramolecular attraction terms
- Simulates solvation through use of friction and thermal fluctuation terms

Ensembles

- Microcanonical: NVE (constant number of particles, volume, and internal energy
- Gibbs: NPT (constant number of particles, pressure, and temperature)
- Helmholtz: NVT (constant number of particles, volume, and temperature

- Only in the limit of infinite sampling are these the ‘true’ thermodynamic values

Periodic Boundary Conditions



Solvent

- Can be explicitly included
- Periodic boundary conditions allow determination of solvent effects with simulation of fewer solvent molecules

Reading

- First Edition
  - Chapter 6, sections 1-7, 9
  - Chapter 5, section 5
- Second Edition
  - Chapter 7, sections 1-7, 9
  - Chapter 6, section 5