Classical MD and water models

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10.637
Lab 3

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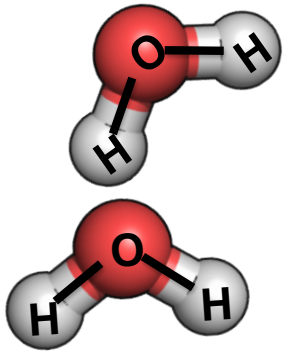
Water: simple models

3-site rigid water models:

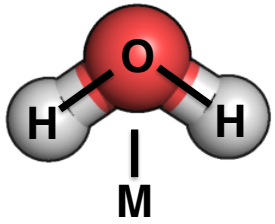
$$E_{ab} = \sum_{i \text{ on } a}^{} \sum_{j \text{ on } b}^{} \frac{k_C q_i q_j}{r_{ij}} + \frac{A}{r_{OO}^{12}} - \frac{B}{r_{OO}^{6}}$$

Parameters	TIP3P	SPC/E
d(O-H) (Å)	0.9572	1.0
H-O-H (º)	104.52	109.47
q(O) = -2q(H)	-0.834	-0.8476
A (kcal Å^{12}/mol)	582000	629400
B (kcal Å^{6}/mol)	595	625.5



Flexible SPC (SPC/Fw): O-H stretch and bend added.
Note: NO such thing as flexible TIP3P, etc!

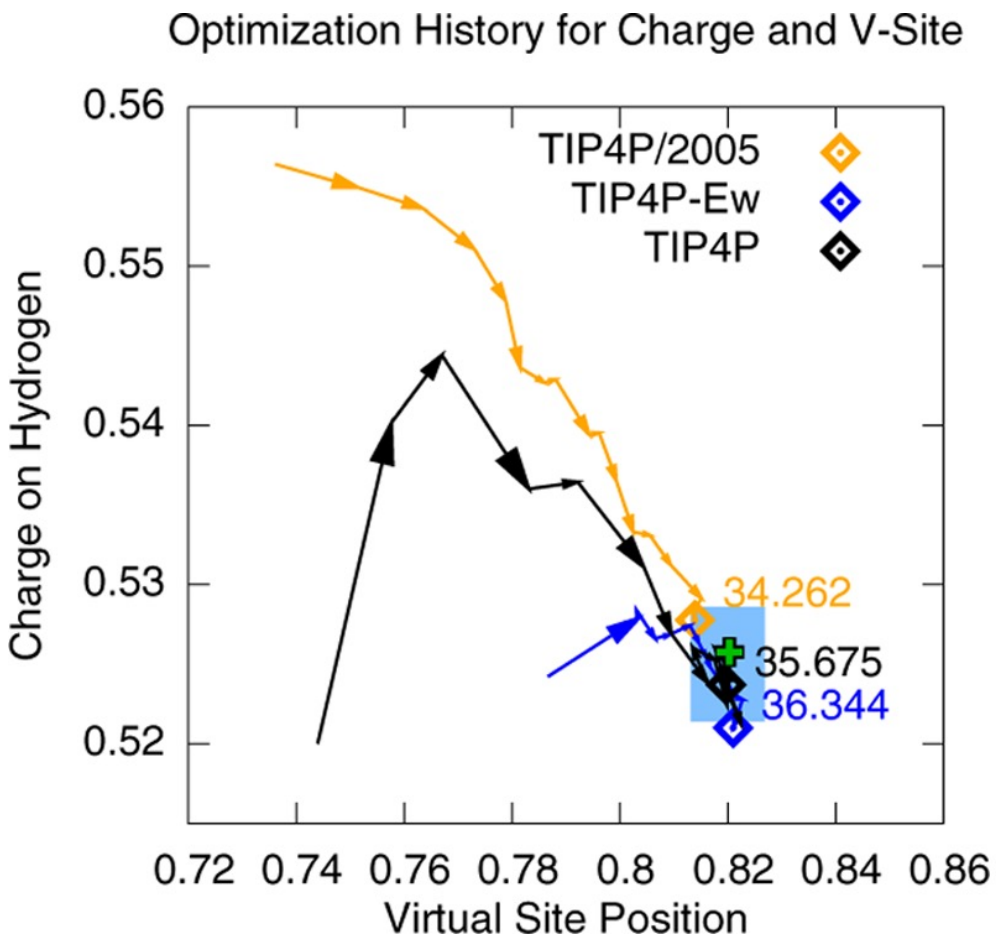
Extension to 4 sites: charge is off-center

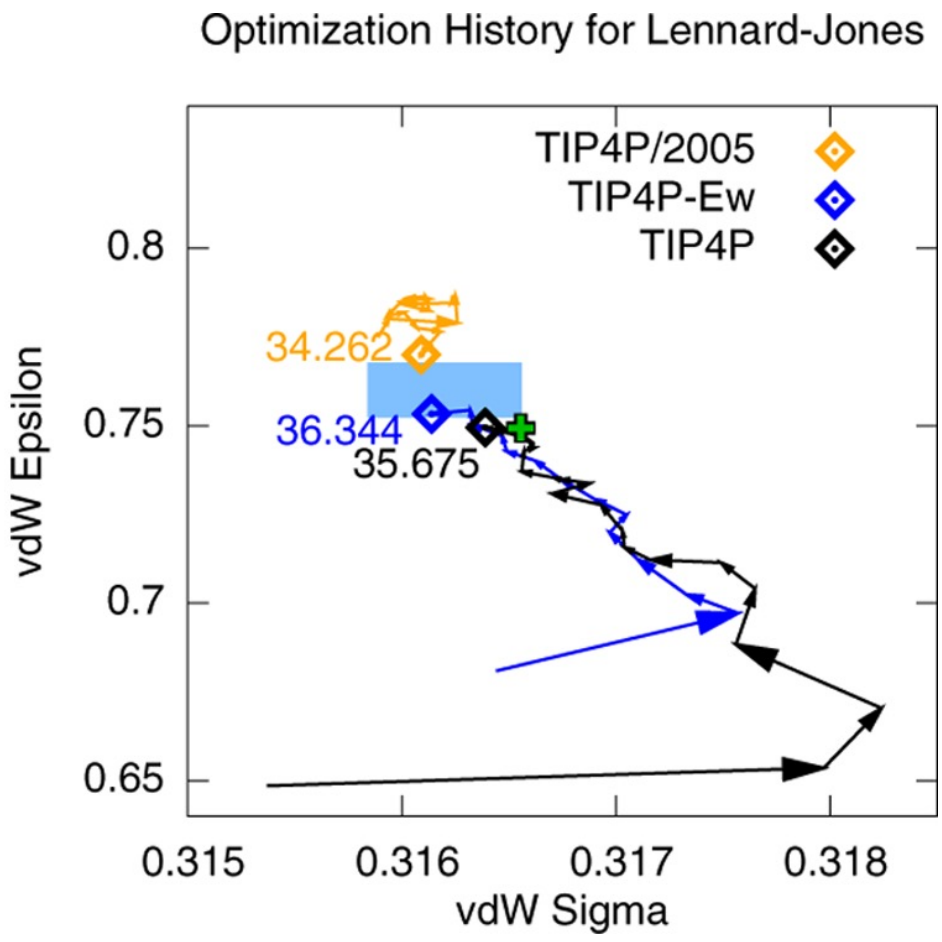


Parameters	TIP4P
d(O-H) (Å)	0.9572
H-O-H (º)	104.52
d(O-M) (Å)	0.15
q(M) = -2q(H)	-1.04
A (kcal Å^{12}/mol)	600000
B (kcal Å^{6}/mol)	610

5- and 6-site water models: charges on lone pair sites + dummy atom.

TIP4PFB: an optimized TIP4P





Wang et al., JPC Lett (2014).

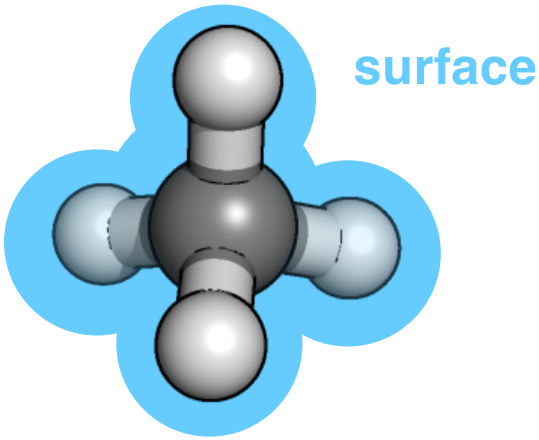
Electrostatic energy

Coulomb interactions between atoms A and B with partial charges:

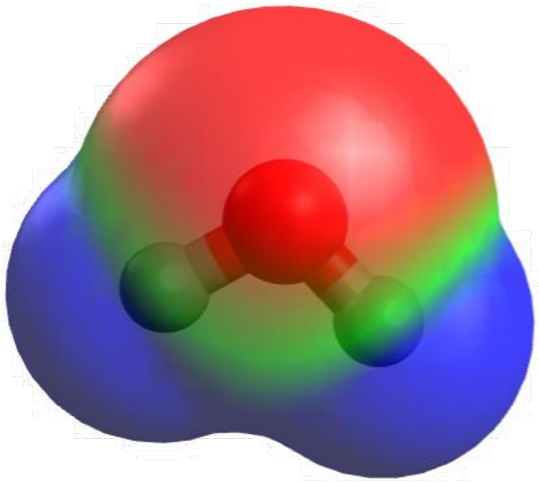
$$E_{\mathrm{el}}(R^{AB}) = \frac{q_{\mathrm{A}} q_{\mathrm{B}}}{\epsilon_{\mathrm{AB}} r_{\mathrm{AB}}}$$

ε is Effective dielectric constant, typically 1 in vacuum.

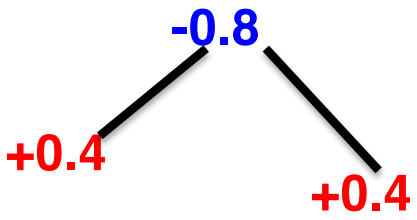
Uncertainty, need for restraint:



Quantum-mechanical electrostatic potential



Reproduce with point charges

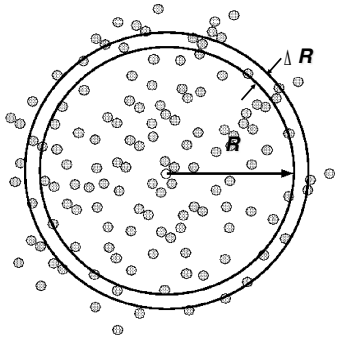


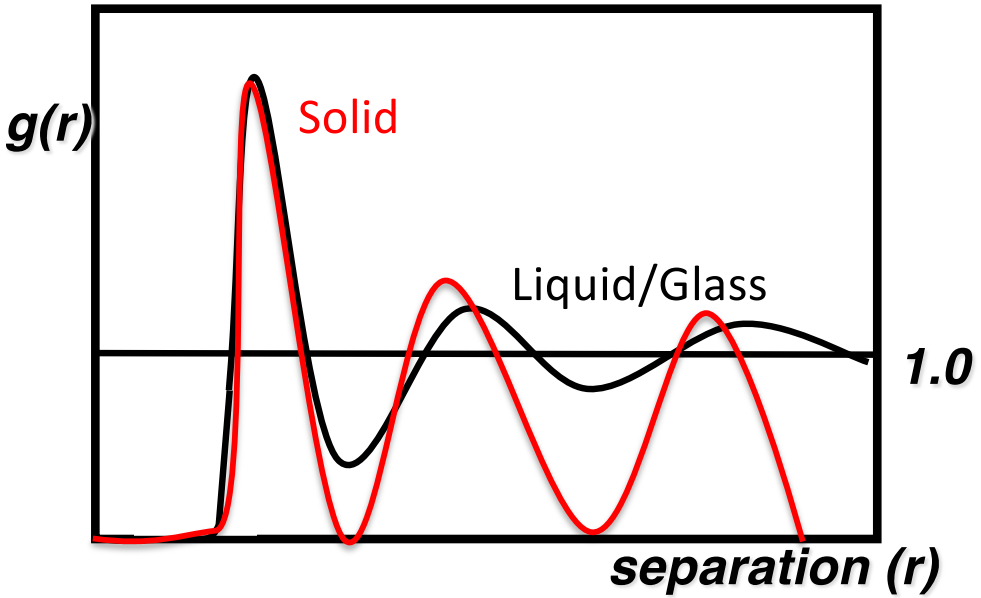
RESP: restrained electrostatic potential charges.

Properties from MD runs

Radial distribution function: $g(r) = \frac{1}{N}\frac{dn(r)}{4\pi r^2 dr\rho}$

Probability of finding two species near each other





What we learn:

- Integrate and get coordination number (e.g., Mg^{2+} is coordinated by 6 water molecules for the life of most MD simulation - microseconds).
- Structure: a solid will have zero probability between coordination shells, glass/liquid has diffusion.
- Can compare to experiment.

Properties from MD runs

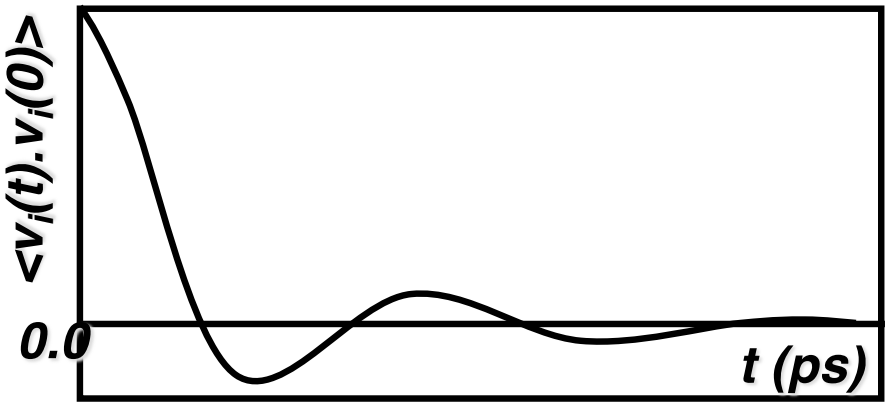
Autocorrelation functions:

$$C_{AA} = \frac{1}{N}\sum_{i=1}^{N}\frac{< A_i(t)A_i(0) > - < A_i(0) >^2}{< A_i(0)A_i(0) > - < A_i(0) >^2}$$

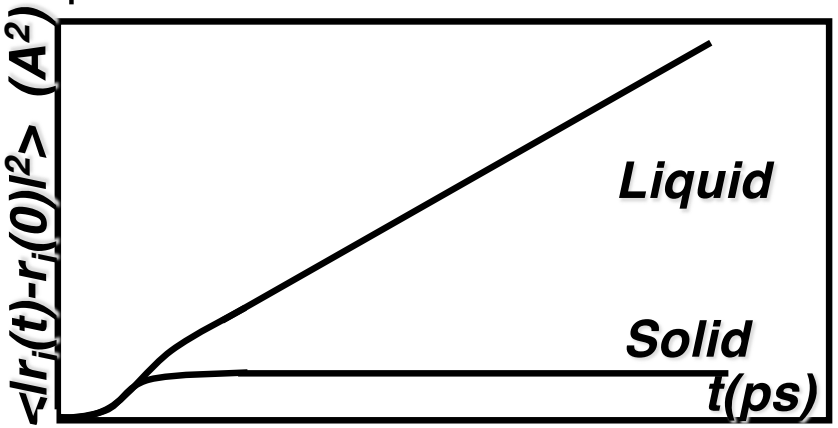
Autocorrelation functions (ACFs) can be defined and calculated for any particle quantity (e.g. v_i) or any system quantity (e.g. U, T, P, r). Starts at 1 and decays usually exponentially with time.

Diffusion coefficient: $$D = \frac{1}{3N}\int_0^\infty \left\langle \sum_{i=0}^{N} \mathbf{v}_i(t)\mathbf{v}_i(0) \right\rangle dt$$

Velocity ACF integrated over time can give diffusion coefficient:



Mean squared displacements for phases of matter:



AMBER nuts and bolts

AMBER dat files + Online repository: force field files, prepin files, to describe proteins, nucleotides, water, and ions.

antechamber/REDS server: generates force field and prepin files for non-standard ligands and residues

We've done these first two steps for you for water, but you will do these for $MgCl_2$ salt solutions (time permitting)…

tleap: organize and load in force field properties, solvate, set box dimensions, neutralize, and generate topology/coordinate files

sander or **pmemd.cuda:** run minimizations and molecular dynamics using topology, coordinates, and input parameters.

cpptraj/ptraj: process and analyze output of trajectories.

Reminder to log on to XSEDE

Make sure you can do the following:

```
ssh <access username>@login.expanse.sdsc.edu
```

If you have never set a password for Expanse, reset your password on the CILogon page on access-ci.org

Note: We are using a special GPU version of the main sander driver called "pmemd.cuda". In job scripts, we have specified this executable and necessary dependent modules.

Expanse SLURM queue

- Comet uses SLURM as a queueing system.
- We write a *job script* and then *submit* it to the *queueing system* to run when resources are available.
- Example job script:

```
#!/bin/bash
#SBATCH -J watermd
#SBATCH -o equil.out
#SBATCH -partition=gpu-shared
#SBATCH -t 1:00:00
#SBATCH -gres=gpu:1
#SBATCH -ntasks-per-node=1
#SBATCH -A itm101

module load slurm
module load gpu/0.15.4 openmpi/4.0.4
module load amber/20

#Example run command
./exec < input > output
```

Expanse SLURM queue

- We issue commands to the SLURM queue to manage our jobs.
- Submit the job script:

```
sbatch <jobscript>
```

- Submit a job that depends on another one:

```
sbatch -d <slurm job #> <jobscript>
```

- Check the status of all of your jobs

```
squeue -u `whoami`
```

- Check the status of everyone's jobs

```
squeue
```

- Check specifics of a running or queued job

```
scontrol show job <slurm job #>
```

- Cancel a job

```
scancel <slurm job #>
```

Parts of today's lab

Sections A and B require a lot of compute resources and should be prioritized:

A. Simulating boxes of water (TIP3P/TIP4PFB)

B. Running $MgCl_2$ salt solutions

C. Typical charges in water and molecular simulations

D. Processing MD results with cpptraj (can be done after class)

Steps for water equilibration (TIP3P & TIP4PFB)

1. Edit "??", in files as discussed in the worksheet, e.g.:

```
nano constV_equil.in
```

2. You will run the minimization, NVT, and NpT equilibration schemes.

3. Submit the queue script

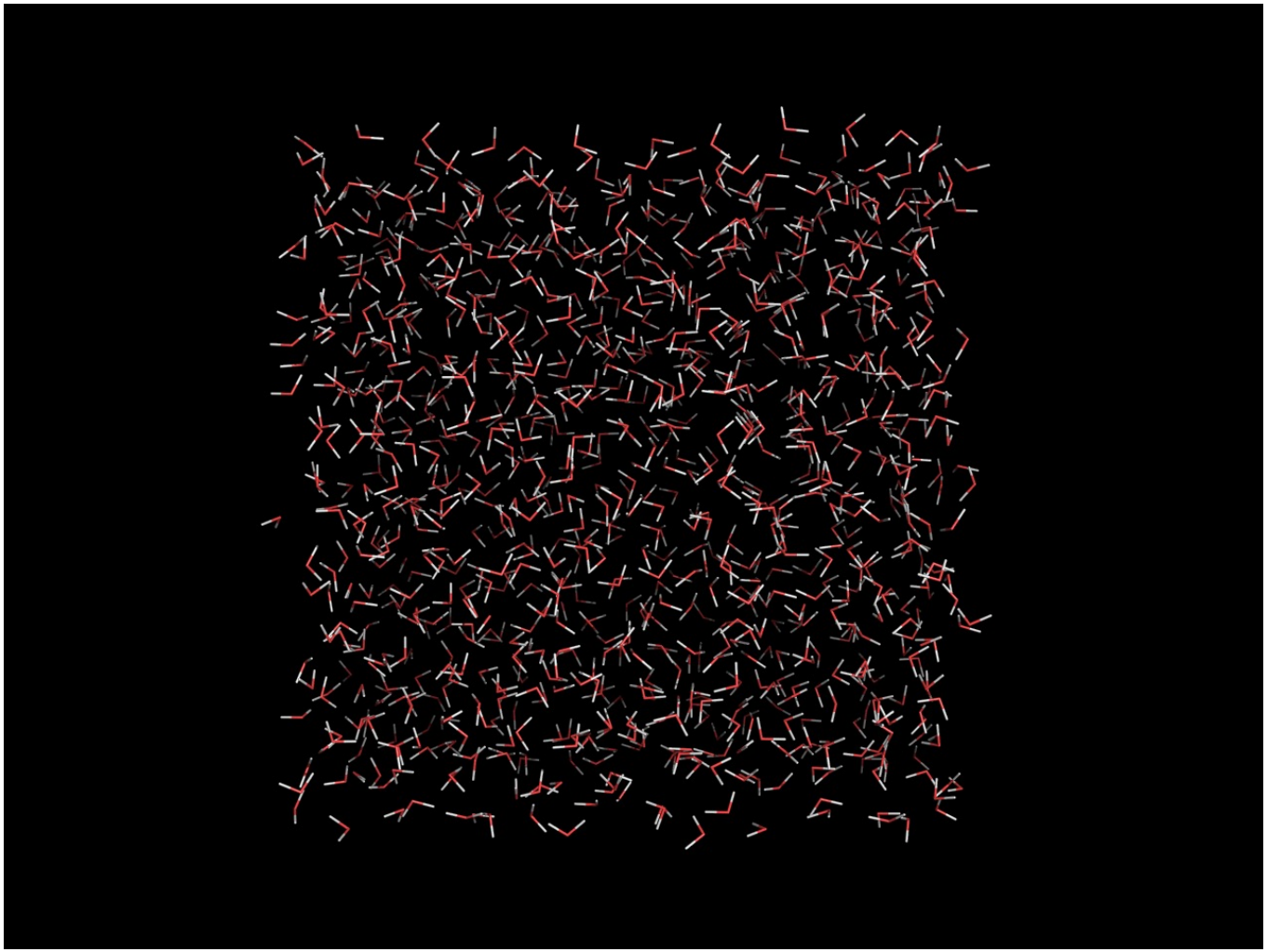
```
sbatch amber_equil.q
```

4. Check on your job

```
squeue -u <username>
```

5. Come back to the script to check that everything worked – once you get a spot in the queue, it should take about **5** minutes.

The initial water box



The density will be too low! An important part of our equilibration scheme

What's needed for a calculation

Topology file (force field parameters/how atoms are connected)
tip3p.prmtop
Coordinate file (initial positions of atoms, could contain velocities)
tip3p.inpcrd
Equilibration queue script
amber_equil.q
Input files for each step of equilibration in AMBER
unrestrained_min.in
constV_equil.in
constP_equil.in
constP_run.in
Input file for production in AMBER
constP_production.in
Production queue script
amber_prod.q