

Program

I. OVERVIEW

1. Modern methods of computational chemistry (MM, ab initio, DFT and Hybrid methods).
2. Introduction to the Emerson Center's facilities
3. Intro (cont.)

II. Molecular mechanics and Molecular Dynamics

4. Molecular Mechanics and Molecular Dynamics methods
5. Applications and Practical sessions on Problem solving

III. Transition Metal Chemistry and Catalysis

6. Computational approaches to the Transition Metal Chemistry
7. Computational Catalysis (including Organic, Inorganic and Enzymatic)
8. Practical sessions on Problem solving.

IV. PhotoChemistry and Excited State Studies

9. Introduction, Overview of Methodology, and some Typical Examples
10. A problem solving session on Spectroscopy, Radicals and PhotoChemistry

Lecture 5

Part I:

- **A Practical Session on water dimer with AMBER**
- **Visualization of trajectories with VMD**
- **Numerical Analysis with VMD**

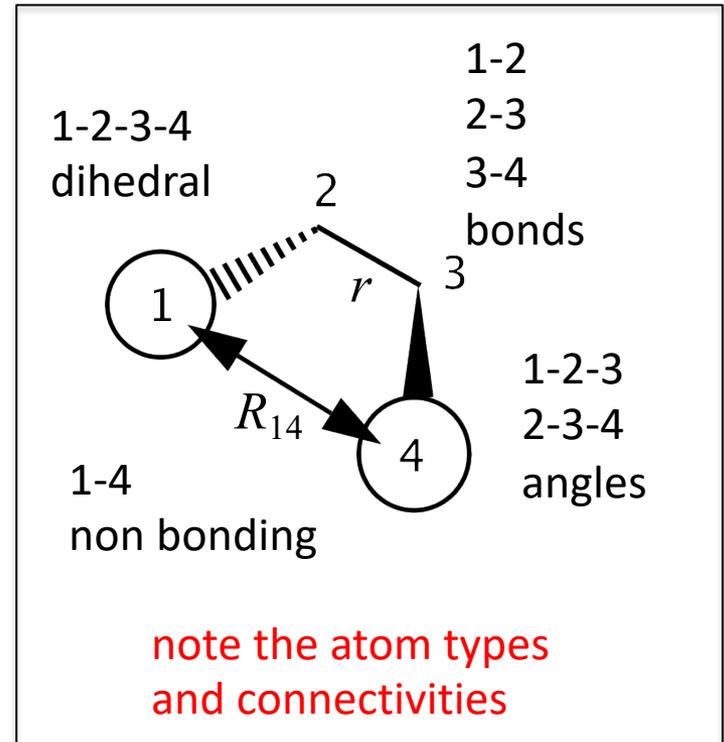
Part II:

- **Monte Carlo Search Techniques in AMBER**

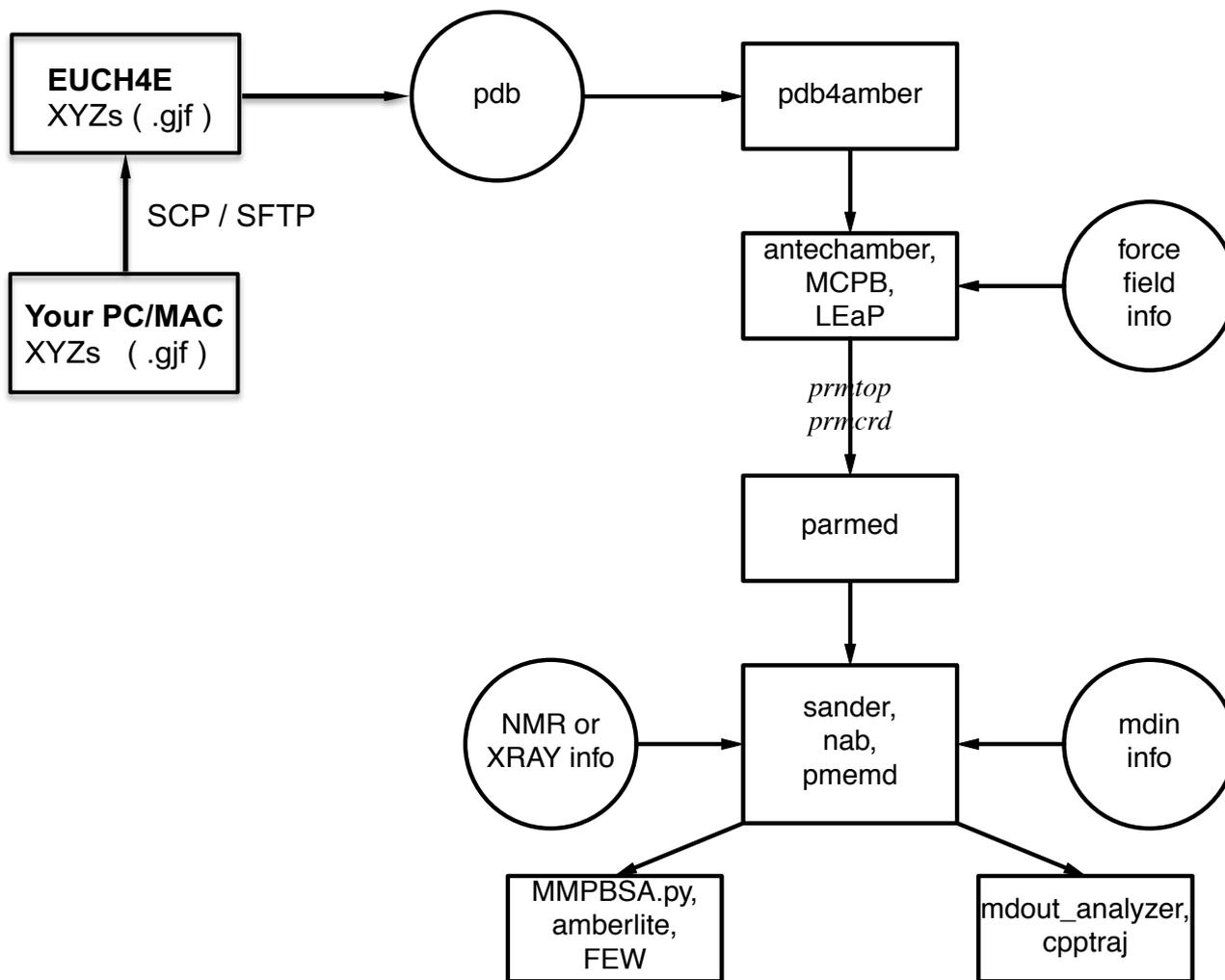
A Generic Force Field: Parameters, Atom types, and Connectivities

$$\begin{aligned}
 E_{total} = & \sum_{bonds} k_b (r - r_0)^2 \\
 & + \sum_{angles} k_\theta (\theta - \theta_0)^2 \\
 & + \sum_{dihedrals} V_n [1 + \cos(n\phi - \gamma)] \\
 & + \sum_{i=1}^{N-1} \sum_{j=i+1}^N \left[\frac{A_{ij}}{R_{ij}^{12}} - \frac{B_{ij}}{R_{ij}^6} + \frac{q_i q_j}{\epsilon R_{ij}} \right]
 \end{aligned}$$

k_b	r_0	bonds
k_θ	θ_0	angles
V_n	γ	dihedrals
A_{ij}, B_{ij}		van der Waals
q_i		partial charges



standard information flow in AMBER



GaussView: making a water dimer

double click

choose *sp*³ O

AMBER: start GV + make water dimer

1) start **GaussView**; make water dimer using the “Fragment” Tool

Calculate -> Gaussian Calculation Setup -> General
deselect connectivity -> Retain

2) save file as Gaussian Input: File->Save **water_dimer.gjf**

3) MAC/PC USERS (command line method):

```
scp water_dimer.gjf eclab@euch4e.chem.emory.edu:./star/YOUR_ID/
```

PC USERS (alternative method):

Download and use WinSCP, an open source scp client

<https://winscp.net/eng/index.php>

AMBER: setup procedure on EC servers

4) `ssh -Y eclab@euch4e.chem.emory.edu`

```
/home/chemistry/ch_res/eclab/: ssh -Y star  
eclab@star:~> cd YOUR_ID  
eclab@star:~> ls  
water_dimer.gjf  
eclab@star:~> cat water_dimer.gjf
```

5) process GAUSSIAN INPUT into PDB using AMBER

```
> antechamber -i water_dimer.gjf -fi gcrt \  
-o water_dimer.pdb -fo pdb
```

AMBER: setup procedure on EC servers

6) generate atomic charges

```
> antechamber -i water_dimer.pdb -fi pdb \  
              -o water_dimer.mol2 -fo mol2 -c bcc
```

7) check all parameters (any missing ones will be reported)

```
> parmchk -i water_dimer.mol2 -f mol2 -p \  
$AMBERHOME/dat/leap/parm/gaff.dat -o water_dimer.frcmod
```

AMBER: setup procedure on EC servers

8) start TLEAP interface to make parameter and XYZ files:

```
water_dimer.prmtop -- parameter topology file  
water_dimer.prmcrd -- initial XYZ file
```

> tleap

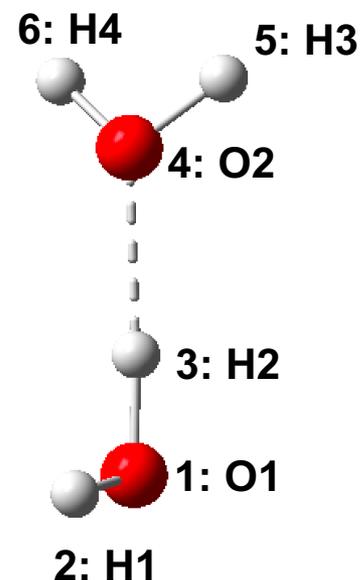
```
> source /libs/amber11/dat/leap/cmd/leaprc.gaff  
> file = loadMol2 water_dimer.mol2  
> loadAmberParams water_dimer.frcmod  
> saveAmberParm file water_dimer.prmtop water_dimer.prmcrd  
> Quit
```

AMBER atom type assignment: contents of **ATOMTYPE.INF** file

```
-ring property (III)-
atom[ 1] (O1 ) is not in any ring (nr[1]=1)
atom[ 2] (H1 ) is not in any ring (nr[2]=1)
atom[ 3] (H2 ) is not in any ring (nr[3]=1)
atom[ 4] (O2 ) is not in any ring (nr[4]=1)
atom[ 5] (H3 ) is not in any ring (nr[5]=1)
atom[ 6] (H4 ) is not in any ring (nr[6]=1)
```

```
-electronic property-
atom [ 1] (O1 ) is an electron-withdrew atom
atom [ 2] (H1 ) is not an electron-withdrew atom
atom [ 3] (H2 ) is not an electron-withdrew atom
atom [ 4] (O2 ) is an electron-withdrew atom
atom [ 5] (H3 ) is not an electron-withdrew atom
atom [ 6] (H4 ) is not an electron-withdrew atom
```

```
-connectivity property-
atom[ 1] (O1 )      2      H1
atom[ 1] (O1 )      3      H2
atom[ 2] (H1 )      1      O1
atom[ 3] (H2 )      1      O1
atom[ 4] (O2 )      5      H3
atom[ 4] (O2 )      6      H4
atom[ 5] (H3 )      4      O2
atom[ 6] (H4 )      4      O2
```



AMBER: internal structure of .prmtop file

```

%FLAG ATOM_NAME
%FORMAT(20a4)
O1 H1 H2 O2 H3 H4
%FLAG CHARGE * 18.222
%FORMAT(5E16.8)
-1.46507292E+01 7.32536460E+00 7.32536460E+00 -1.46507292E+01 7.32536460E+00
7.32536460E+00
%FLAG MASS
%FORMAT(5E16.8)
1.60000000E+01 1.00800000E+00 1.00800000E+00 1.60000000E+01 1.00800000E+00
1.00800000E+00
%FLAG BOND_FORCE_CONSTANT (kcal/mol)/Å2
%FORMAT(5E16.8)
3.69600000E+02
%FLAG BOND_EQUIL_VALUE Å
%FORMAT(5E16.8)
9.74000000E-01
%FLAG ANGLE_FORCE_CONSTANT (kcal/mol)/rad2
%FORMAT(5E16.8)
4.19300000E+01
%FLAG ANGLE_EQUIL_VALUE rad
%FORMAT(5E16.8)
1.82910584E+00
%FLAG LENNARD_JONES_ACOEF
%FORMAT(5E16.8)
5.81803229E+05 0.00000000E+00 0.00000000E+00
%FLAG LENNARD_JONES_BCOEF
%FORMAT(5E16.8)
6.99746810E+02 0.00000000E+00 0.00000000E+00
%FLAG AMBER_ATOM_TYPE
%FORMAT(20a4)
oh ho ho oh ho ho

```

GEOMETRY OPTIMIZATION

9) create/copy input, "min.in", for structure optimization

```
cp ~/min.in ~/YOUR_ID
```

```
#title: optimization  
&cntrl  
maxcyc=1000, imin=1, cut=12.0, ntb=0, ntp=1
```

10) perform a geometry optimization (command line interactive)

```
> sander -O -i min.in -o min.out -p water_dimer.prmtop \  
-c water_dimer.prmcrd -r water_dimer.xyz
```

MOLECULAR DYNAMICS

9b) create/copy input, "md.in", for a molecular dynamics run

```
cp ~/md.in ~/YOUR_ID
```

```
#title: md run
```

```
&cntrl
```

```
imin=0, irest=0, cut=12.0, ntb=0,
```

```
nstlim=100000, dt=0.001,
```

```
ntt=2, tempi=300.0, temp0=300.0,
```

```
ntpr=10, ntwx=10
```

femtosecond

Kelvin

MOLECULAR DYNAMICS

10b) perform an MD simulation (command line interactive)

```
> sander -O -i md.in -o md.out -p water_dimer.prmtop \  
-c water_dimer.prmcrd -r water_dimer.xyz -x water_dimer.crd
```

Using the queue for larger MD jobs

```
#!/bin/ksh
# @ initialdir = /star/chemistry/ch_res/eclab/YOU
# @ requirements = (Arch == "R6000") && (OpSys == "AIX53")
# @ class = stars
# @ notify_user = YOUR_ID@emory.edu
# @ group = ch_res
# @ error = error
# @ queue
#
sander -O -i md.in -o md.out -p water_dimer.prmtop -c
water_dimer.prmcrd -r water_dimer.xyz -x water_dimer.crd
```

Visualization & Analysis

- Visual Molecular Dynamics **VMD**
(UIUC by K. Schulten & group)
- Spectral densities
- Radial Distribution Functions
- X11 graphics session...

Starting Graphics Session on STAR

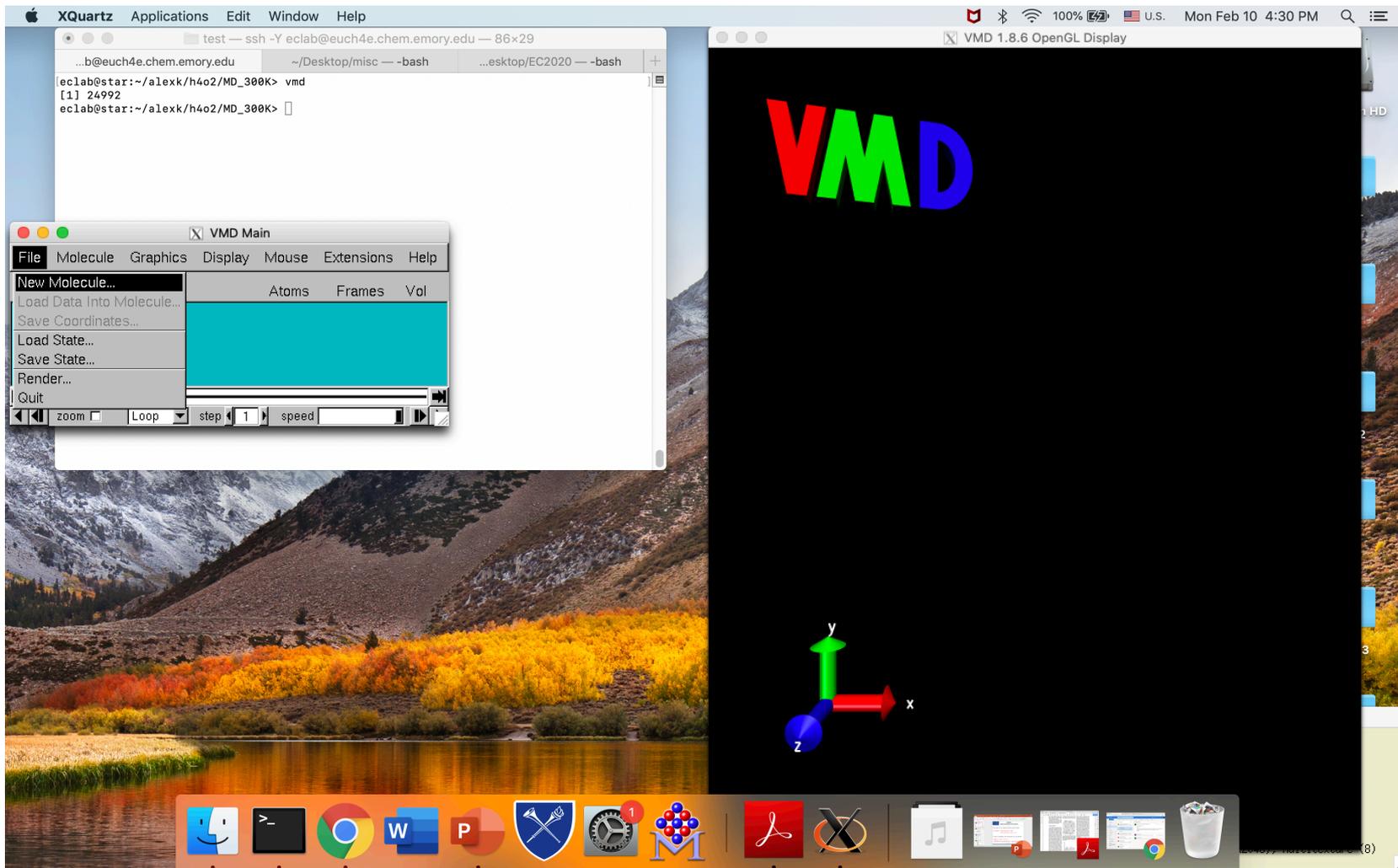
- MAC users: Xquartz 2.7.8 recommended

www.xquartz.org/releases/index.html

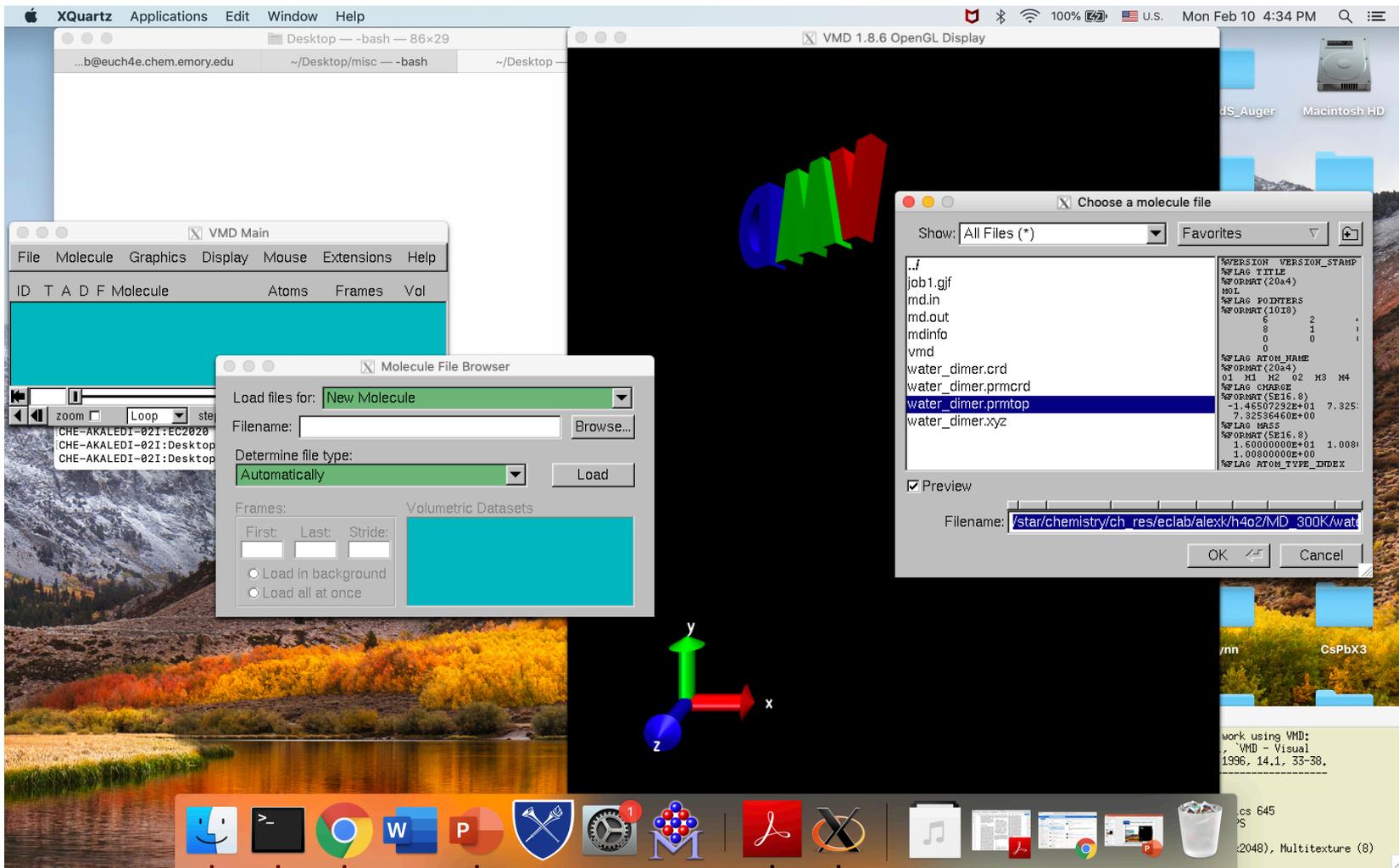
- PC users: Xlaunch or Xming

> vmd

VMD Session on STAR defining a New Molecule



VMD Session on STAR loading parameters



The screenshot displays a VMD (Visual Molecular Dynamics) session on a Mac OS X desktop. The main window, titled "VMD 1.8.6 OpenGL Display", shows a 3D molecular model of a water dimer. A "Choose a molecule file" dialog is open, showing a list of files with "water_dimer.prmrtp" selected. A "Molecule File Browser" dialog is also open, showing the "Load files for:" field set to "New Molecule" and the "Determine file type:" dropdown set to "Automatically". The desktop background is a scenic landscape with a lake and mountains. The dock at the bottom contains various application icons including Finder, Terminal, Chrome, Word, PowerPoint, and VMD.

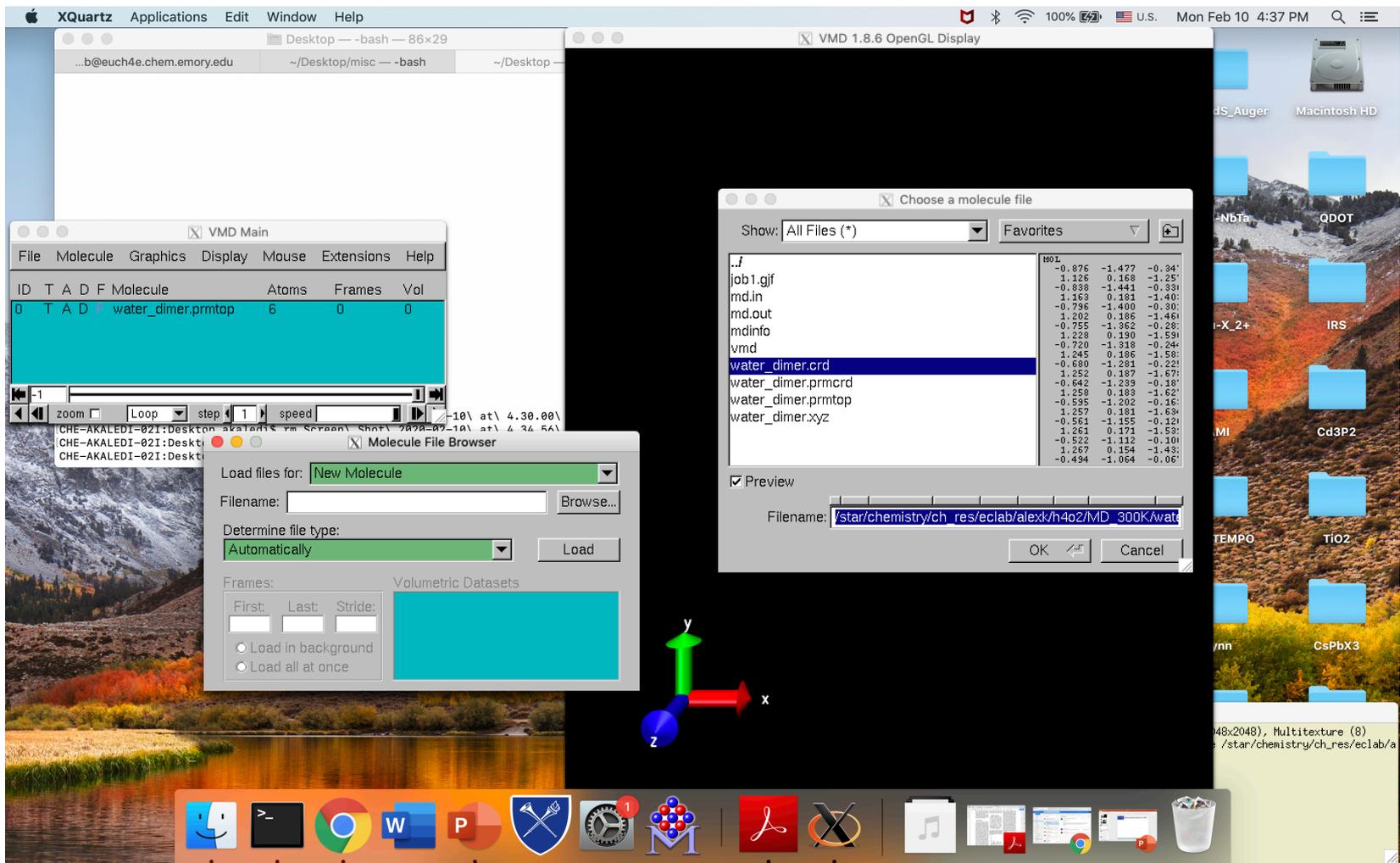
The "Choose a molecule file" dialog shows the following file list:

File Name	File Type
job1.gif	%VERSION VERSION_STAMP
md.in	%FLAG TITLE
md.out	%FORMAT (2044)
mdinfo	%FLAG POINTERS
vmd	%FORMAT (1018)
water_dimer.crd	%FLAG ATOM_NAME
water_dimer.pmcrcd	%FORMAT (2044)
water_dimer.prmrtp	01 H1 H2 O2 H3 H4
water_dimer.xyz	%FLAG CHARGE
	%FORMAT (5E16.8)
	-1.46507232E+01 7.325E
	7.32536460E+00
	%FLAG MASSES
	%FORMAT (5E16.8)
	1.60000000E+01 1.000E
	1.00800000E+00
	%FLAG ATOM_TYPE_INDEX

The "Molecule File Browser" dialog shows the following fields:

- Load files for: New Molecule
- Filename: (empty)
- Determine file type: Automatically
- Frames: First, Last, Stride (empty)
- Volumetric Datasets: (empty)
- Load in background (selected)
- Load all at once (unselected)

VMD Session on STAR loading trajectory



VMD Main

ID	T	A	D	F	Molecule	Atoms	Frames	Vol
0	T	A	D	F	water_dimer.prmtpop	6	0	0

Choose a molecule file

Show: All Files (*) Favorites

File	MOLE
./	-0.876 -1.477 -0.341
job1.gjf	1.126 0.168 -1.257
md.in	-0.838 -1.441 -0.331
md.out	1.163 0.181 -1.401
mdinfo	-0.796 -1.400 -0.301
mdinfo	1.202 0.186 -1.461
vmd	-0.755 -1.362 -0.281
water_dimer.crd	1.228 0.190 -1.531
water_dimer.prmcrd	-0.720 -1.318 -0.241
water_dimer.prmcrd	1.245 0.186 -1.581
water_dimer.prmtpop	-0.600 -1.291 -0.221
water_dimer.xyz	1.252 0.187 -1.671
	-0.642 -1.239 -0.181
	1.258 0.189 -1.621
	-0.595 -1.202 -0.161
	1.257 0.181 -1.631
	-0.561 -1.155 -0.121
	1.261 0.171 -1.531
	-0.522 -1.112 -0.101
	1.267 0.154 -1.431
	-0.494 -1.064 -0.061

Molecule File Browser

Load files for: New Molecule

Filename: Browse...

Determine file type: Automatically Load

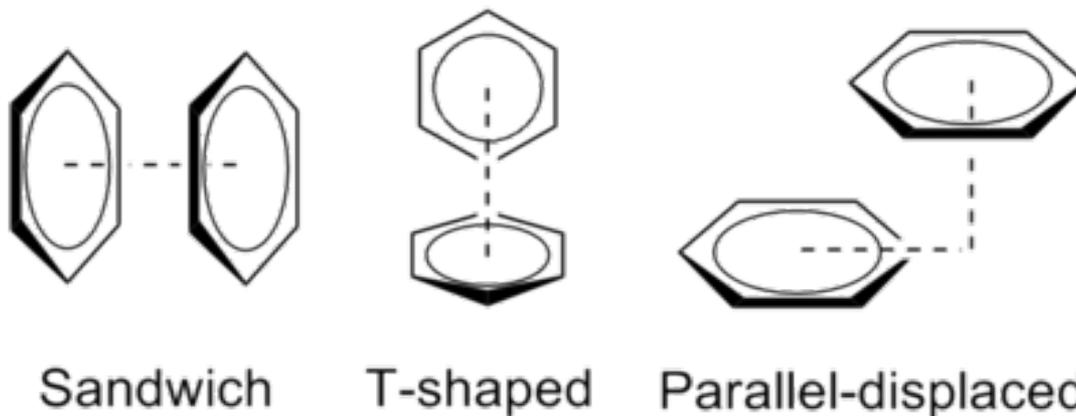
Frames: First: Last: Stride:

Load in background Load all at once

Part II: other applications

- The challenge of π - π stacking interactions
- Advanced Methods of Structure search

Exemplary π - π stacking interactions



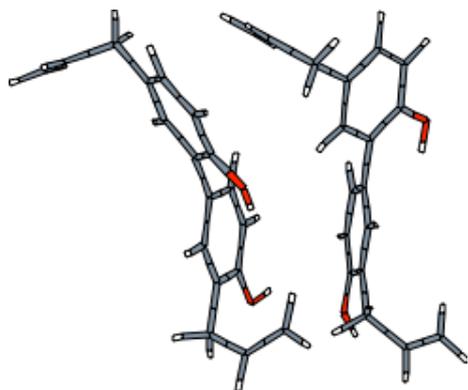
The dominant component of fragment interaction energy is the dipole induction, also known as electrostatic dispersion.

These interactions are described by dynamically correlated methods (CI/MP2) while a generic DFT fails to yield a correct description.

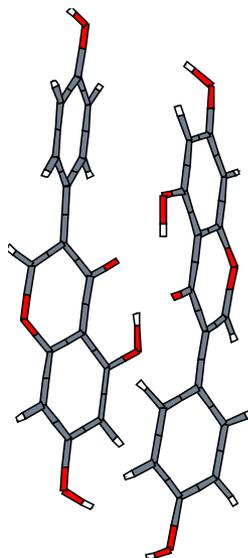
On the other hand, the **non-bonding** potentials parameterized in AMBER provide a remarkably accurate description of the above systems.

examples of π - π stacking systems calculated with AMBER

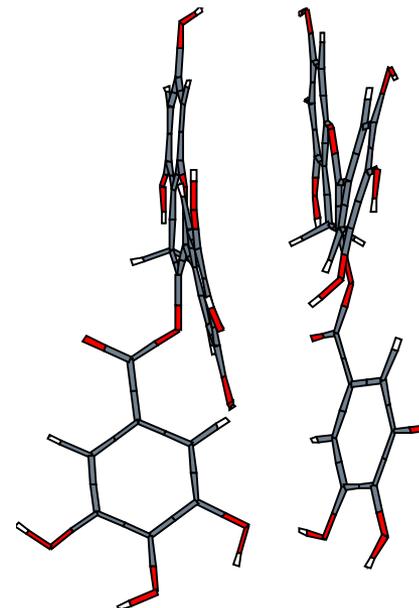
dimer-A



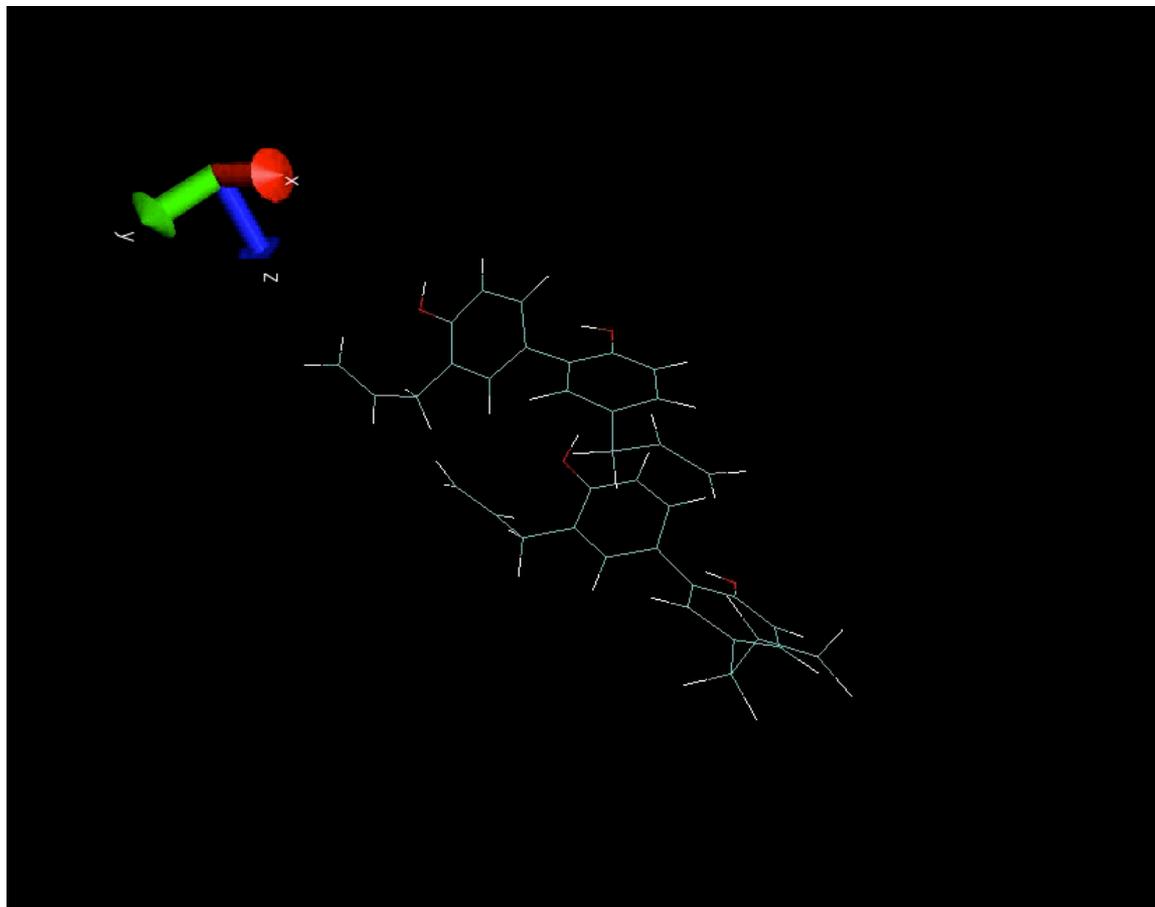
dimer-B



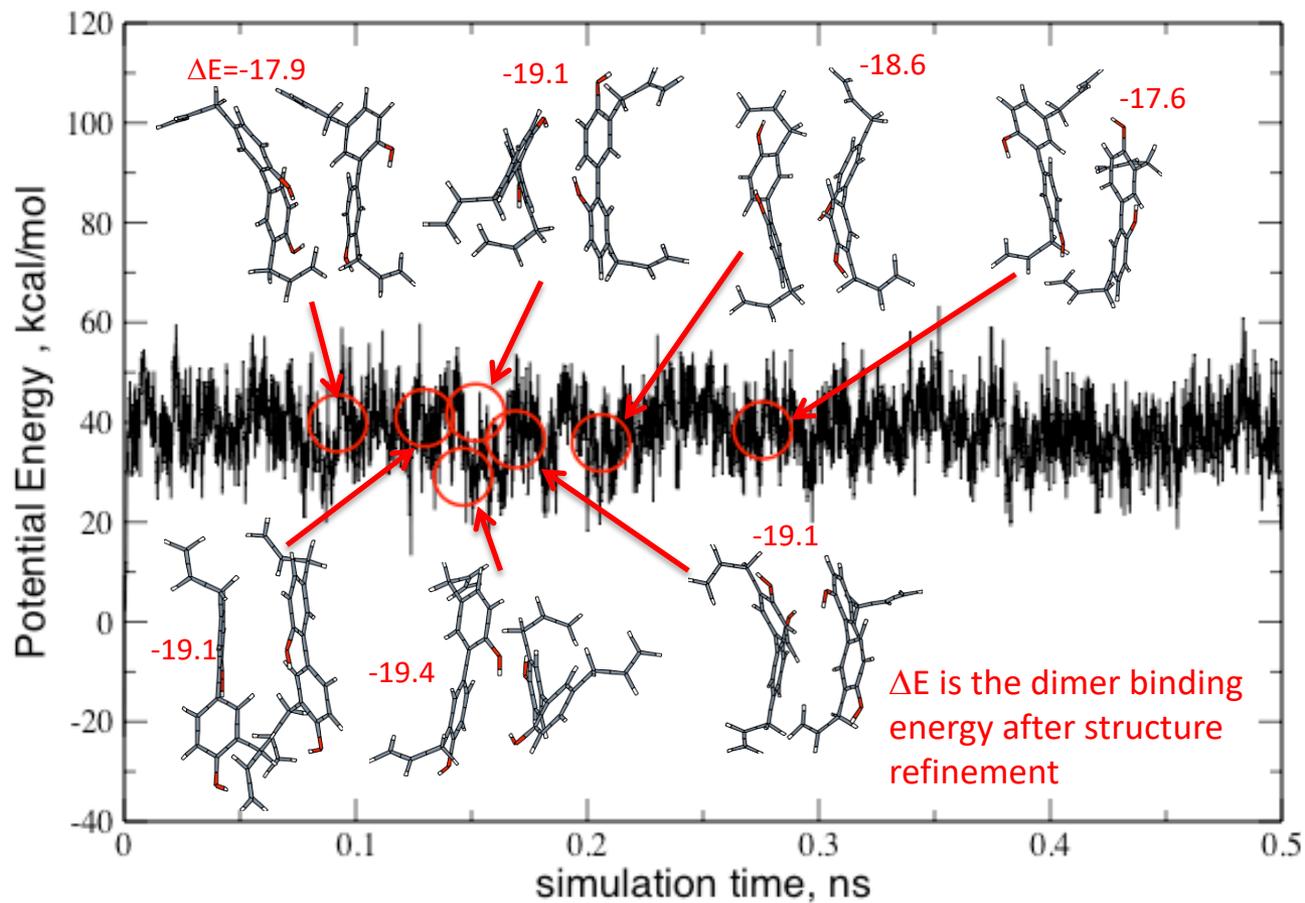
dimer-C



visualization of the molecular dynamics of of dimer-C in gas phase at 300K



Analysis of the molecular dynamics of dimer-C in gas phase at 300K

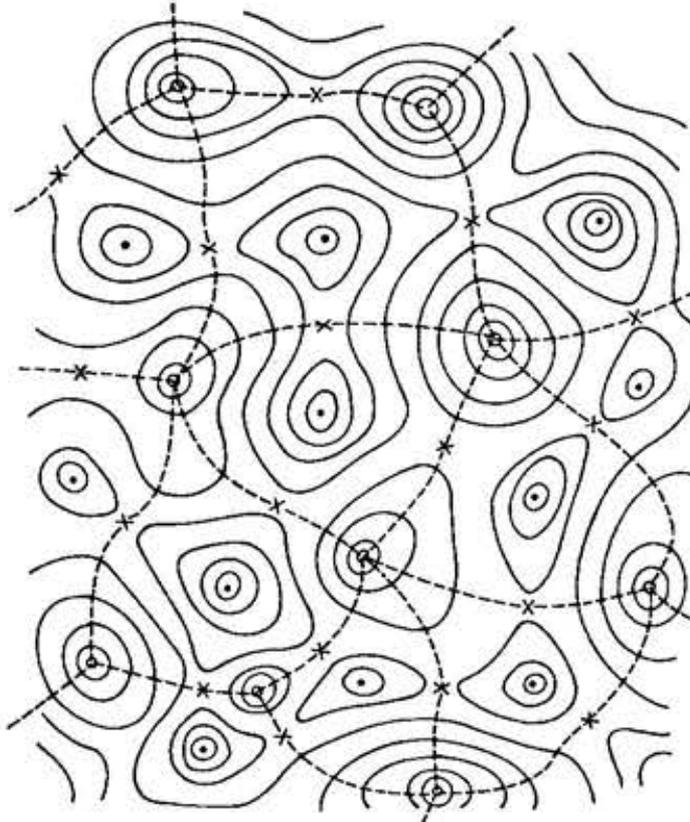


Improved search techniques

- MD trajectories tend to "fly over" low energy structures due to inertia (kinetic energy)
- Thus, long time propagation is required to find low energy structures
- Long-time MD may be computationally prohibitive
- What other methods may avoid this problem?



Potential Energy “Landscape”



Schematic representation of the potential energy surface for an N-atom system.

Minima are shown as filled circles and saddle points as crosses.

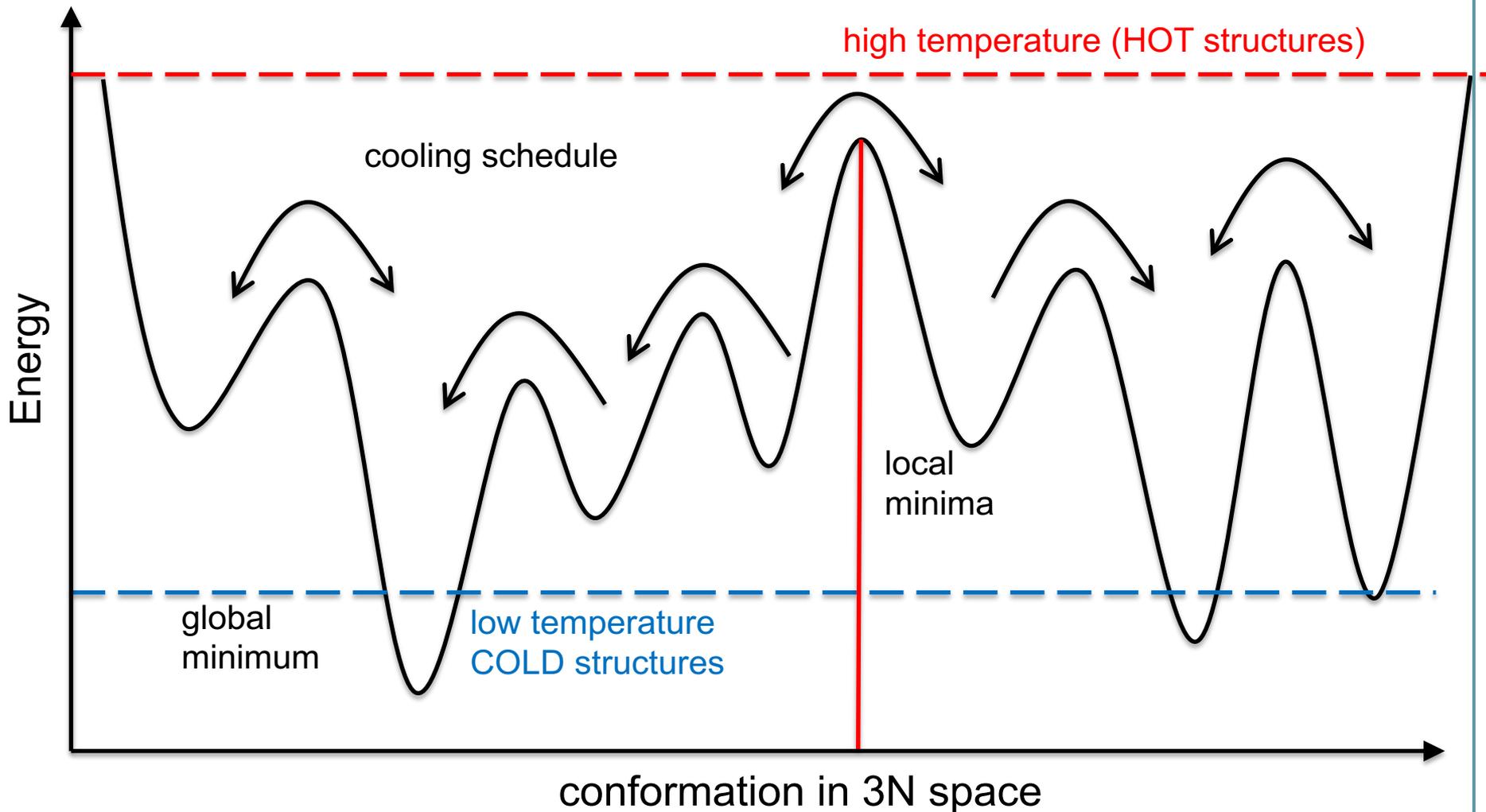
Potential energy is constant along the continuous curves.

Regions belonging to different minima are indicated by dashed curves.

F. H. Stillinger, T. A. Weber “Packing Structures and Transitions in Liquids and Solids” *Science* 225, 983-989, 1984.

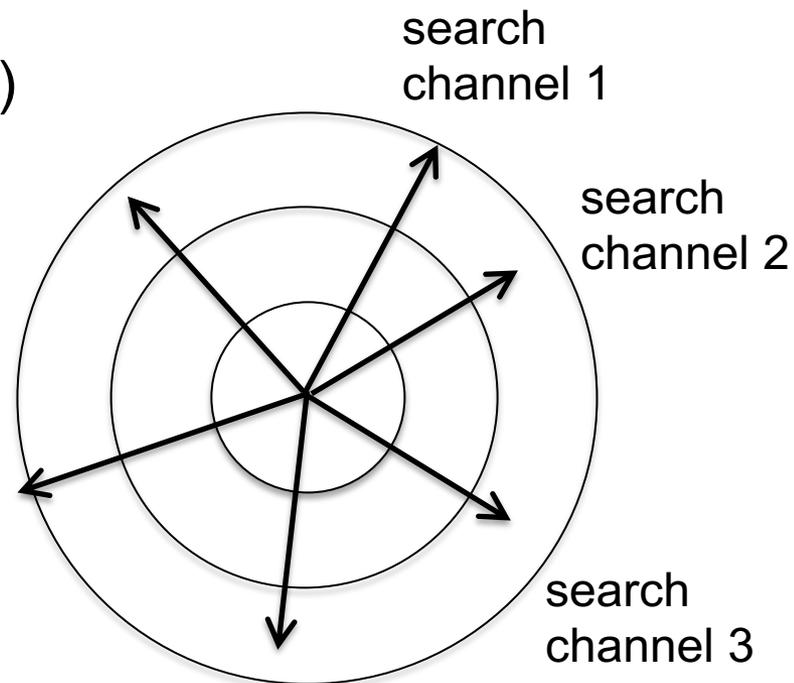


Monte Carlo (MC) methods: simulated annealing (SA) MD search



multichannel SA-MD MC search

- 1) start at some initial (high E) structure
- 2) send out a random trajectory (arrow)
- 3) heat system to 500 - 600K
- 4) cool gradually to 0K
- 5) a final set of structures will be a good sample of low energy minima



Summary of Amber MM tools

- AMBER's versatile definitions allow to set up calculations of general molecular systems
- MD simulations are easily run for all typical ensembles
- Systems of 10^4 - 10^5 order of atoms are possible to model
- Visualization and analysis is performed with VMD
- Advanced Monte Carlo techniques allow for extensive Energy Landscape exploration