Molecular Dynamics Simulations
SS 2007

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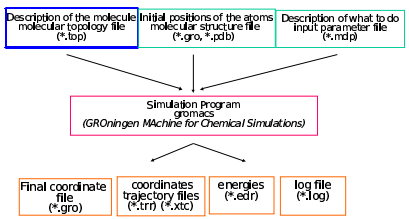
Molecular Topology File

Running a simulation



Molecular Topology File

What does it contain?

- list of all atoms and residues including names
- a complete description of all interactions in system
- lists of all bonds, bond angles, dihedral angles etc.
- partial charges of all atoms
- Lennard-Jones parameters for all atoms
- special interactions (exclusions, 1-4 interactions, constraints)

How is it generated?

- by hand
  or
- automatically from an amino acid sequence and predefined building blocks

Example of topology file (*.top)

```
#include "ffG43a1.itp"

[ moleculetype ]
; Name            nrexcl
Protein             3

[ atoms ]
;   nr       type  resnr residue  atom   cgnr     charge      mass  typeB    chargeB    massB
    1         NL     1    LYSH     N      1      0.129     14.0067 ; comments
    2          H     1    LYSH     H1     1      0.248     1.008
    3          H     1    LYSH     H2     1      0.248     1.008   ;
    4          H     1    LYSH     H3     1      0.248     1.008   ;
    5        CH1     1    LYSH     CA     1      0.127     12.019  ;

.....

[ bonds ]
;  ai    aj funct         c0         c1         c2         c3
   1     2     2     0.1000  1.8700e+07

.....

[ angles ]
;  ai    aj    ak funct         c0         c1         c2         c3
   2     1     3     2     109.50     380.00

[ dihedrals ]
;  ai    aj    ak    al funct         c0         c1         c2         c3         c4         c5
    2     1     5    14     1      0.000      3.77          3

.....

#include "spc.itp"

.....

[ molecules ]
; Compound        #mols
Protein             1
SOL               78
```

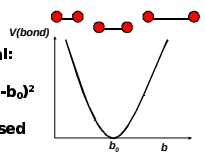
MD Unit in GROMACS

Quantity	Symbol	Unit
length		
distance	r	nm
mass	m	u (atomic mass unit)
time	t	ps
charge	q	e = electronic charge
temperature	T	K
energy	E, V	kJ/mol
Force	F	kJ/mol*nm
pressure	p	kJ/mol*nm^3 = 16.6054 Bar
velocity	v	nm/ps
dipole moment	μ	e*nm

Bond stretching

V(bond)

In topology file:
function number = 1



- **Harmonic potential:**

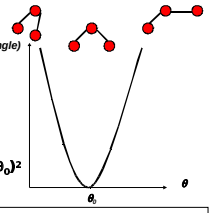
V(bond) =1/2 K_b $(b-b_o)^2$

- **Most commonly used**

Other bond potential: Morse potential
In topology file: function number = 3

Angle bending

V(angle)



In topology file:
function number = 1

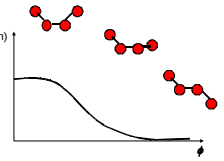
- **Harmonic potential:**

V(angle) = 1/2 K_θ $(\theta- \theta_0)^2$

Other angle potential: Cosine based potential
In topology file: function number = 2

Torsion terms

V(torsion)



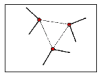
In topology file:
function number = 1
order = n ; K_ϕ; δ

Cosine expansion:

V(torsion)= K_ϕ [1+ cos(nϕ+δ)]

Other dihedral potential: Ryckaert-Bellemans potential
In topology file: function number = 3

Non-Bonded Interactions



Lennard-Jones (6-12) potential

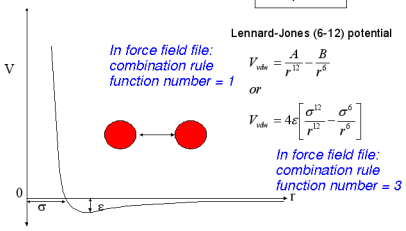
In force field file:
combination rule
function number = 1

$$V_{vdw} = \frac{A}{r^{12}} - \frac{B}{r^6}$$

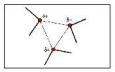
or

$$V_{vdw} = 4\varepsilon\left[\frac{\sigma^{12}}{r^{12}} - \frac{\sigma^6}{r^6}\right]$$

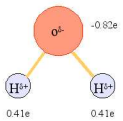
In force field file:
combination rule
function number = 3



Non-Bonded Interactions



water



partial charge (z) distributions

Coulomb Interactions

$$V = \frac{z_i z_j}{4\pi \ _0 r_{ij}}$$

Understand a topology file: part 1

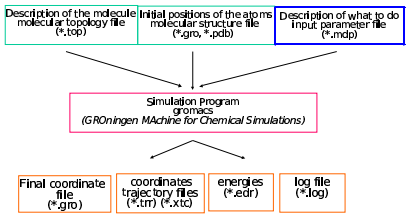
- Take (copy) the file butane.pdb and example.top from
Mdcourse directory
- Visualize the file butane.pdb (using vmd or rasmol)
- Look at the topology file example.top
- Understand which analytical function and which parameter are
used.
- Check the topology file: there are missing interactions, type
error, etc for a total of 10 *errors*.

- Write a topology using an united-atom force field for the
molecule in mol1.pdb

Understand a topology file: part 2

- Take (copy) the file butane_uni.pdb from Mdcourse directory
- Visualize the file butane_uni.pdb (using vmd or rasmol)
- Choice the best dihedral function and parameter for the C-C-C-C torsion potential given in file cccc.agr
  - use the command "xmgrace cccc.agr" to visualize the file
  - fit the function by hand/by using the function "non linear curve fitting" under Data-> transformation
  - In the formula window type (for example): "Y= a0+(1+cos(a1*X*180/pi))"; set the parameters value "2"; apply;
  - Look the values on the parameters in the new window and in the graph the plot of your functions.
- Write a topology using an united-atom force field for the molecule in butane_uni.pdb using the torsional potential you have found.

Running a simulation



Input Parameter File

What does it contain?

- Title (description of the run).
- parameters describing what run is to be performed.
  - MD or EM
  - temperature
  - nature of box
  - time step
  - length of run
  - how often to write out the results
  - etc.

How is it generated?

- by hand from a template file

Parameter files: em.mdp

```
;LINES STARTING WITH ; ARE COMMENTS

title    =  Minimization of Hen Egg White Lysozyme       ;Title of run
; The following lines tell the program standard locations where to find
certain files
cpp                 = /lib/cpp              ;Preprocessor
include             = -I../top              ;Directories to include in
the topology format

; Parameters describing what to do, when to stop and what to save.
integrator   = steep      ;Algorithm (steep = steepest decent minimization)
emtol        = 1.0        ;Stop minimization when the maximum force < 1.0 kJ/mol
nsteps   = 200        ;Maximum number of (minimization) steps to perform
nstenergy    = 10         ;Write energies to disk every nstenergy steps
nstxtcout    = 10         ;Write coordinates to disk every nstxtcount steps
xtc_grps = Protein        ;which coordinate group(s) to write to disk.
energygrps   = Protein         ;which energy group(s) to write to disk

; Parameters describing how to find the neighbors of each atom and how to
calculate the interactions.
nstlist  = 5          ;Frequency to update the neighbor list and long range forces.
ns_type  = simple     ;Method to determine neighbor list (simple, grid).
rlist    = 1.0        ;cutoff for making neighbor list (short range forces).
coulombtype = cut-off      ;treatment of long range electrostatic interactions
rcoulomb= 1.0         ;long range electrostatic cutoff
rvdw= 1.0             ;long range van der Waals cutoff

constraints  = none       ;Bond types to replace by contraints
pbc  = no         ;Periodic Boundary Conditions (yes/no)
```

Parameters for Energy Minimization in Vacuo

```
;LINES STARTING WITH ; ARE COMMENTS
title    =  Minimization of butane      ;Title of run
; Parameters describing what to do
integrator   = steep      ;Algorithm (steep = steepest decent
minimization)
emtol        = 2.0        ;Stop minimization when the maximum force < 2.0 kJ/mol
; Parameters describing when to stop.
nsteps       = 7777   ;Maximum number of (minimization) steps to perform
; Parameters describing what to save.
nstenergy    = 1          ;Write energies to disk every nstenergy steps
energygrps   = BUT        ;which energy group(s) to write to disk
; Parameters describing how to find the neighbors of each atom and how to
calculate the interactions.
nstlist  = 0
ns_type  = simple
rlist    = 0.0
coulombtype = cut-off
rcoulomb= 0.0
rvdw= 0.0

constraints= none       ;Bond types to replace by contraints
pbc  = no         ;Periodic Boundary Conditions (yes/no)
```

Mimimize a molecule: Running simulation with GROMACS

grompp makes a run input file

grompp -f *parameter_file* -c *geometry_file* -p *topology_file* -o *TPR_file*

*.mdp *.gro *.top

mdrun performs a simulation

mdrun -v -s *TPR_file* (-deffnm *name*)