Force Fields for Classical Molecular Dynamics simulations of Biomolecules

Emad Tajkhorshid

Beckman Institute
Departments of Biochemistry
Center for Biophysics and Computational Biology
University of Illinois at Urbana-Champaign
Classical Force Field Parameters

- Topology and structure files
- Parameter files
- Where do all the numbers needed by an MD code come from?
- Where to find these numbers and how to change them if needed.
- How to make topology files for ligands, cofactors, special amino acids, ...
- How to develop / put together missing parameters.
Classical Molecular Dynamics

\[ U(r) = \frac{1}{4\pi\varepsilon_0} \frac{q_i q_j}{r_{ij}} \]

Coulomb interaction

\[ U(r) = \epsilon_{ij} \left[ \left( \frac{R_{\text{min},ij}}{r_{ij}} \right)^{12} - \left( \frac{R_{\text{min},ij}}{r_{ij}} \right)^6 \right] \]
Classical Molecular Dynamics

Bond definitions, atom types, atom names, parameters, ...
Energy Terms Described in

- Bond
- Dihedral
- Angle
- Improper
The Potential Energy Function

\[
U(\vec{R}) = \sum_{\text{bonds}} k_{i}^{\text{bond}} (r_{i} - r_{0})^2 + \sum_{\text{angles}} k_{i}^{\text{angle}} (\theta_{i} - \theta_{0})^2 + \sum_{\text{dihedrals}} k_{i}^{\text{dihedrals}} [1 + \cos (n_{i}\phi_{i} + \delta_{i})] + \sum_{i} \sum_{j \neq i} 4\epsilon_{ij} \left[ \left( \frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left( \frac{\sigma_{ij}}{r_{ij}} \right)^{6} \right] + \sum_{i} \sum_{j \neq i} \frac{q_{i}q_{j}}{r_{ij}}
\]

\(U_{\text{bond}}\) = oscillations about the equilibrium bond length
\(U_{\text{angle}}\) = oscillations of 3 atoms about an equilibrium bond angle
\(U_{\text{dihedral}}\) = torsional rotation of 4 atoms about a central bond
\(U_{\text{nonbond}}\) = non-bonded energy terms (electrostatics and Lenard-Jones)
Interactions between bonded atoms

\[ V_{\text{angle}} = K_\theta (\theta - \theta_o)^2 \]

\[ V_{\text{bond}} = K_b (b - b_o)^2 \]

\[ V_{\text{dihedral}} = K_\phi (1 + \cos(n\phi - \delta)) \]
\[ V_{bond} = K_b (b - b_o)^2 \]

<table>
<thead>
<tr>
<th>Chemical type</th>
<th>(K_{bond})</th>
<th>(b_o)</th>
</tr>
</thead>
<tbody>
<tr>
<td>C-C</td>
<td>100 kcal/mole/Å (^2)</td>
<td>1.5 Å</td>
</tr>
<tr>
<td>C≡C</td>
<td>200 kcal/mole/Å (^2)</td>
<td>1.3 Å</td>
</tr>
<tr>
<td>C≡C</td>
<td>400 kcal/mole/Å (^2)</td>
<td>1.2 Å</td>
</tr>
</tbody>
</table>

Bond angles and improper terms have similar quadratic forms, but with softer spring constants. The force constants can be obtained from vibrational analysis of the molecule (experimentally or theoretically).
Dihedral Potential

\[ V_{\text{dihedral}} = K_\phi (1 + \cos(n\phi - \delta)) \]

\[ \delta = 0^\circ \]
Nonbonded Parameters

\[
\sum_{\text{non-bonded}} \frac{q_i q_j}{4\pi D r_{ij}} + \epsilon_{ij} \left[ \left( \frac{R_{\text{min},ij}}{r_{ij}} \right)^{12} - \left( \frac{R_{\text{min},ij}}{r_{ij}} \right)^{6} \right]
\]

- \( q_i \): partial atomic charge
- \( D \): dielectric constant
- \( \epsilon \): Lennard-Jones (LJ, vdW) well-depth
- \( R_{\text{min}} \): LJ radius (\( R_{\text{min}}/2 \) in CHARMM)

Combining rules (CHARMM, Amber)

\[
R_{\text{min},ij} = R_{\text{min},i} + R_{\text{min},j}
\]

\[
\epsilon_{i,j} = \sqrt{\epsilon_i \epsilon_j}
\]
Note that the effect is long range.

From MacKerell
Charge Fitting Strategy

CHARMM- Mulliken* AMBER(ESP/RESP)

Partial atomic charges

*Modifications based on interactions with TIP3 water
\[ U(\vec{R}) = \sum_{bonds} k_i^{bond} (r_i - r_0)^2 + \sum_{angles} k_i^{angle} (\theta_i - \theta_0)^2 + \sum_{dihedrals} k_i^{dihedral} \left[ 1 + \cos(n_i \phi_i + \delta_i) \right] + \sum_{i \neq j} 4\varepsilon_{ij} \left[ \left( \frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left( \frac{\sigma_{ij}}{r_{ij}} \right)^6 \right] + \sum_{i \neq j} q_i q_j \]
File Format/Structure

- The structure of a pdb file
- The structure of a psf file
- The topology file
- The parameter file
- Connection to potential energy terms
Structure of a PDB file

---

>>> It is an ascii, fixed-format file <<<

"No connectivity information"
Looking at File Structures

- PDB file
- Topology file
- PSF file
- Parameter file
Parameter Optimization Strategies

Check if it has been parameterized by somebody else

- Literature
- Google

**Minimal optimization**
- By analogy (direct transfer of known parameters)
- Quick, starting point

**Maximal optimization**
- Time-consuming
- Requires appropriate experimental and target data

**Choice based on goal of the calculations**

- **Minimal**
  - database screening
  - NMR/X-ray structure determination

- **Maximal**
  - free energy calculations, mechanistic studies,
  - subtle environmental effects
Getting Started

- Identify previously parameterized compounds
- Access topology information – assign atom types, connectivity, and charges – annotate changes

CHARMM topology (parameter files)

top_all22_model.inp (par_all22_prot.inp)
top_all22_prot.inp (par_all22_prot.inp)
top_all22_sugar.inp (par_all22_sugar.inp)
top_all27_lipid.rtf (par_all27_lipid.prm)
top_all27_na.rtf (par_all27_na.prm)
top_all27_na_lipid.rtf (par_all27_na_lipid.prm)
top_all27_prot_lipid.rtf (par_all27_prot_lipid.prm)
top_all27_prot_na.rtf (par_all27_prot_na.prm)
toph19.inp (param19.inp)

NA and lipid force fields have new LJ parameters for the alkanes, representing increased optimization of the protein alkane parameters. Tests have shown that these are compatible (e.g. in protein-nucleic acid simulations). For new systems is suggested that the new LJ parameters be used. Note that only the LJ parameters were changed; the internal parameters are identical.

www.pharmacy.umaryland.edu/faculty/amackere/force_fields.htm
A Brief Overview of The Force Field Toolkit (ffTK)

Dr. Christopher G. Mayne
Tajkhorshid Group
February 13th, 2012
### Available Methods for Obtaining Parameters

**Analogy**  
(Re-use of parameters from similar structures)

<table>
<thead>
<tr>
<th>Method</th>
<th>Website</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>SwissParam</td>
<td><a href="http://swissparam.ch/">http://swissparam.ch/</a></td>
<td></td>
</tr>
</tbody>
</table>

**Development**

<table>
<thead>
<tr>
<th>Method</th>
<th>Website</th>
</tr>
</thead>
</table>
An Example: Acetaminophen

Tyrosine

NMA or ACE-patch

New Types
An Example: Acetaminophen

Tyrosine

New Charges

NMA or ACE-patch

New Types
ffTK Facilitates the Parameterization Workflow

PSF/PDB

- System Preparation
- Geometry Optimization (QM)
- Water Interaction En. (QM)
- Charge Optimization
- Frequency Calculation (QM)
- Bonds & Angles
- Transform Hessian
- Torsion Scan (QM)
- Find Missing Parameters
- Torsion Optimization
- Geometry Optimization (QM)
- update PDB
- update PSF
- update PAR
- update PAR
- build init PAR

PAR File

Calculation

Action
**ffTK Interface**

- Tasks divided into separate tabs
- File dialog buttons
- Entry boxes to hold variables
- Treeview boxes to hold lists
- Action buttons
- Action menus
- Arrows/triangles indicate collapsable elements
ffTK 1.0 is Available in VMD 1.9.1

- Setup necessary QM calculations
- Visualize calculation input/output
- Multidimensional optimization of developing parameters
- Read/Write files (pdb, par, log, gau)

Full documentation online: [http://www.ks.uiuc.edu/Research/vmd/plugins/fftk/](http://www.ks.uiuc.edu/Research/vmd/plugins/fftk/)

Tutorial is under development
Partial Charge Assignment

- Most important aspect for ligands

- Different force fields might take different philosophies
  - AMBER: RESP charges at the HF/6-31G level
    - Overestimation of dipole moments
    - Easier to set up
  - CHARMM: Interaction based optimization
    - TIP3P water representing the environment
    - Could be very difficult to set up

- Conformation dependence of partial charges
- Lack of polarization

- Try to be consistent within the force field

- pKa calculations for titratable residues
Parameterization of unsaturated lipids

- All C=C bonds are cis, what does rotation about neighboring single bonds look like?
DHA conformations from MD

- rotational barriers are extremely small
- many conformers are accessible with short lifetimes

Courtesy of Scott Feller, Wabash College
Dynamics of saturated vs. polyunsaturated lipid chains

- $sn_1$ stearic acid = blue
- $sn_2$ DHA = yellow
- 500 ps of dynamics

Movie courtesy of Mauricio Carrillo Tripp

Courtesy of Scott Feller, Wabash College
Lipid-protein interactions

- Radial distribution around protein shows distinct layering of acyl chains
Lipid-protein interactions

- Decomposition of non-bonded interaction shows rhodopsin is strongly attracted to unsaturated chain
- All hydrophobic residues are stabilized by DHA

<table>
<thead>
<tr>
<th>resname</th>
<th>$U_{DHA}$</th>
<th>$U_{stearic}$</th>
<th>ratio</th>
</tr>
</thead>
<tbody>
<tr>
<td>PHE</td>
<td>-44.9</td>
<td>-22.6</td>
<td>2.0</td>
</tr>
<tr>
<td>ILE</td>
<td>-30.0</td>
<td>-10.1</td>
<td>3.0</td>
</tr>
<tr>
<td>VAL</td>
<td>-24.0</td>
<td>-9.6</td>
<td>2.5</td>
</tr>
<tr>
<td>LEU</td>
<td>-23.1</td>
<td>-13.0</td>
<td>1.8</td>
</tr>
<tr>
<td>MET</td>
<td>-22.8</td>
<td>-9.7</td>
<td>2.4</td>
</tr>
<tr>
<td>TYR</td>
<td>-18.6</td>
<td>-10.4</td>
<td>1.8</td>
</tr>
<tr>
<td>ALA</td>
<td>-11.4</td>
<td>-3.0</td>
<td>3.8</td>
</tr>
<tr>
<td>TRP</td>
<td>-10.3</td>
<td>-2.4</td>
<td>4.2</td>
</tr>
</tbody>
</table>

Courtesy of Scott Feller, Wabash College
Origin of protein:DHA attraction

- Flexibility of the DHA chain allows solvation of the rough protein surface to occur with little intra-molecular energy cost

Courtesy of Scott Feller, Wabash College
Major Recent Developments

• New set of lipid force field parameters for CHARMM (CHARMM32+)
  – Pastor, B. Brooks, MacKerell

• Polarizable force field
  – Roux, MacKerell