Force Fields for MD simulations

• Topology/parameter files
• Where do the numbers an MD code uses come from?
• How to make topology files for ligands, cofactors, special amino acids, …
• How to obtain/develop missing parameters.

• QM and QM/MM force fields/potential energy descriptions used for molecular simulations.
The Potential Energy Function

\[ U(\vec{R}) = \sum_{\text{bonds}} k_i^{\text{bond}} (r_i - r_0)^2 + \sum_{\text{angles}} k_i^{\text{angle}} (\theta_i - \theta_0)^2 + \]

\[ \sum_{\text{dihedrals}} k_i^{\text{dihedral}} [1 + \cos (n_i \phi_i + \delta_i)] + \]

\[ \sum_{i} \sum_{j \neq i} 4\varepsilon_{ij} \left[ \left( \frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left( \frac{\sigma_{ij}}{r_{ij}} \right)^6 \right] + \sum_{i} \sum_{j \neq i} \frac{q_i q_j}{\varepsilon r_{ij}} \]

\( U_{\text{bond}} = \) 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)
Energy Terms Described in the CHARMM Force Field

- Bond
- Angle
- Dihedral
- Improper
Classical Molecular Dynamics

\[ r(t + \delta t) = r(t) + v(t)\delta t \]

\[ v(t + \delta t) = v(t) + a(t)\delta t \]

\[ a(t) = F(t) / m \]

\[ F = -\frac{d}{dr} U(r) \]
Classical Molecular Dynamics

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

Coulomb interaction

\[
U(r) = \varepsilon_{ij} \left[ \left( \frac{R_{\text{min},ij}}{r_{ij}} \right)^{12} - 2 \left( \frac{R_{\text{min},ij}}{r_{ij}} \right)^6 \right]
\]

van der Waals interaction
Classical Molecular Dynamics
Classical Molecular Dynamics

Bond definitions, atom types, atom names, parameters, ....
What is a Force Field?

In molecular dynamics a molecule is described as a series of charged points (atoms) linked by springs (bonds).

To describe the time evolution of bond lengths, bond angles and torsions, also the non-bonding van der Waals and electrostatic interactions between atoms, one uses a force field. The force field is a collection of equations and associated constants designed to reproduce molecular geometry and selected properties of tested structures.
**Energy Functions**

\[
U(\vec{R}) = \sum_{\text{bonds}} k_i^{\text{bond}} (r_i - r_0)^2 + \sum_{\text{angles}} k_i^{\text{angle}} (\theta_i - \theta_0)^2 + \sum_{\text{dihedrals}} k_i^{\text{dihedrals}} \left[ 1 + \cos (n_i \phi_i + \delta_i) \right] + \sum_{i \neq j} 4\epsilon_{ij} \left[ \left( \frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left( \frac{\sigma_{ij}}{r_{ij}} \right)^6 \right] + \sum_{i \neq j} \frac{q_i q_j}{\epsilon r_{ij}}
\]

- \( U_{\text{bond}} \) = 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)
Parameter optimization of the CHARMM Force Field

Based on the protocol established by

Alexander D. MacKerell, Jr , U. Maryland

See references: www.pharmacy.umaryland.edu/faculty/amackere/force_fields.htm

Interactions between bonded atoms

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

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

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

From MacKerell
Bond energy versus bond length is given by the equation:

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

<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=O</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

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

\[ \delta = 0^\circ \]

From MacKerell
Nonbonded Parameters

\[ \sum_{\text{nonbonded}} \frac{q_i q_j}{4 \pi D r_{ij}} + \varepsilon_{ij} \left[ \left( \frac{R_{\text{min},ij}}{r_{ij}} \right)^{12} - 2 \left( \frac{R_{\text{min},ij}}{r_{ij}} \right)^{6} \right] \]

q<sub>i</sub>: partial atomic charge
D: dielectric constant
\varepsilon: Lennard-Jones (LJ, vdW) well-depth
R<sub>min</sub>: LJ radius (R<sub>min</sub>/2 in CHARMM)
Combining rules (CHARMM, Amber)

\[ R_{\text{min},i,j} = R_{\text{min},i} + R_{\text{min},j} \]
\[ \varepsilon_{i,j} = \sqrt{\varepsilon_i \times \varepsilon_j} \]

From MacKerell
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
van der Waals interaction

\[ \varepsilon_{ij} \left[ \left( \frac{R_{\text{min},ij}}{r_{ij}} \right)^{12} - 2 \left( \frac{R_{\text{min},ij}}{r_{ij}} \right)^6 \right] \]

From MacKerell

Lennard-Jones Energy versus Distance

Interaction Energy, kcal/mol

Distance, Å

\[ e=0.2, R_{\text{min}}=2.5 \]
CHARMM Potential Function

\[ U(\vec{R}) = \sum_{\text{bonds}} k_i^\text{bond} (r_i - r_0)^2 + \sum_{\text{angles}} k_i^\text{angle} (\theta_i - \theta_0)^2 + \sum_{\text{dihedrals}} k_i^\text{dihedral} [1 + \cos(n_i \phi_i + \delta_i)] + \sum_{i \neq j} 4 \epsilon_{ij} \left[ \left( \frac{\sigma_{ij}}{r_{ij}} \right)^{12} - \left( \frac{\sigma_{ij}}{r_{ij}} \right)^6 \right] + \sum_{i \neq j} \frac{q_i q_j}{r_{ij}} \]

- **PDB file** for geometry
- **Parameter file** for parameters
- **PSF file** for topology
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

<table>
<thead>
<tr>
<th>Index</th>
<th>Name</th>
<th>Residue</th>
<th>Chain</th>
<th>Residue</th>
<th>X</th>
<th>Y</th>
<th>Z</th>
<th>Segname</th>
</tr>
</thead>
<tbody>
<tr>
<td>22</td>
<td>N</td>
<td>ALA</td>
<td>A</td>
<td>3</td>
<td>-4.073</td>
<td>-7.587</td>
<td>-2.708</td>
<td>BH</td>
</tr>
<tr>
<td>23</td>
<td>HN</td>
<td>ALA</td>
<td>A</td>
<td>3</td>
<td>-3.813</td>
<td>-6.675</td>
<td>-3.125</td>
<td>BH</td>
</tr>
<tr>
<td>24</td>
<td>CA</td>
<td>ALA</td>
<td>A</td>
<td>3</td>
<td>-4.615</td>
<td>-7.557</td>
<td>-1.309</td>
<td>BH</td>
</tr>
<tr>
<td>25</td>
<td>HA</td>
<td>ALA</td>
<td>A</td>
<td>3</td>
<td>-4.323</td>
<td>-8.453</td>
<td>-0.704</td>
<td>BH</td>
</tr>
<tr>
<td>26</td>
<td>CB</td>
<td>ALA</td>
<td>A</td>
<td>3</td>
<td>-4.137</td>
<td>-6.277</td>
<td>-0.676</td>
<td>BH</td>
</tr>
<tr>
<td>27</td>
<td>HB1</td>
<td>ALA</td>
<td>A</td>
<td>3</td>
<td>-3.128</td>
<td>-5.950</td>
<td>-0.907</td>
<td>BH</td>
</tr>
<tr>
<td>28</td>
<td>HB2</td>
<td>ALA</td>
<td>A</td>
<td>3</td>
<td>-4.724</td>
<td>-5.439</td>
<td>-1.015</td>
<td>BH</td>
</tr>
<tr>
<td>29</td>
<td>HB3</td>
<td>ALA</td>
<td>A</td>
<td>3</td>
<td>-4.360</td>
<td>-6.338</td>
<td>0.393</td>
<td>BH</td>
</tr>
<tr>
<td>30</td>
<td>C</td>
<td>ALA</td>
<td>A</td>
<td>3</td>
<td>-6.187</td>
<td>-7.538</td>
<td>-1.357</td>
<td>BH</td>
</tr>
<tr>
<td>31</td>
<td>O</td>
<td>ALA</td>
<td>A</td>
<td>3</td>
<td>-6.854</td>
<td>-6.553</td>
<td>-1.264</td>
<td>BH</td>
</tr>
<tr>
<td>32</td>
<td>N</td>
<td>ALA</td>
<td>A</td>
<td>4</td>
<td>-6.697</td>
<td>-8.715</td>
<td>-1.643</td>
<td>BH</td>
</tr>
<tr>
<td>33</td>
<td>HN</td>
<td>ALA</td>
<td>A</td>
<td>4</td>
<td>-6.023</td>
<td>-9.463</td>
<td>-1.751</td>
<td>BH</td>
</tr>
<tr>
<td>34</td>
<td>CA</td>
<td>ALA</td>
<td>A</td>
<td>4</td>
<td>-8.105</td>
<td>-9.096</td>
<td>-1.934</td>
<td>BH</td>
</tr>
<tr>
<td>35</td>
<td>HA</td>
<td>ALA</td>
<td>A</td>
<td>4</td>
<td>-8.287</td>
<td>-8.878</td>
<td>-3.003</td>
<td>BH</td>
</tr>
<tr>
<td>36</td>
<td>CB</td>
<td>ALA</td>
<td>A</td>
<td>4</td>
<td>-8.214</td>
<td>-10.604</td>
<td>-1.704</td>
<td>BH</td>
</tr>
<tr>
<td>37</td>
<td>HB1</td>
<td>ALA</td>
<td>A</td>
<td>4</td>
<td>-7.493</td>
<td>-11.205</td>
<td>-2.379</td>
<td>BH</td>
</tr>
<tr>
<td>38</td>
<td>HB2</td>
<td>ALA</td>
<td>A</td>
<td>4</td>
<td>-8.016</td>
<td>-10.861</td>
<td>-0.665</td>
<td>BH</td>
</tr>
<tr>
<td>39</td>
<td>HB3</td>
<td>ALA</td>
<td>A</td>
<td>4</td>
<td>-9.245</td>
<td>-10.914</td>
<td>-1.986</td>
<td>BH</td>
</tr>
<tr>
<td>40</td>
<td>C</td>
<td>ALA</td>
<td>A</td>
<td>4</td>
<td>-9.226</td>
<td>-8.438</td>
<td>-1.091</td>
<td>BH</td>
</tr>
<tr>
<td>41</td>
<td>O</td>
<td>ALA</td>
<td>A</td>
<td>4</td>
<td>-10.207</td>
<td>-7.958</td>
<td>-1.667</td>
<td>BH</td>
</tr>
</tbody>
</table>

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

“No connectivity information”
(name CA CB) and (resid 1 to 4) and (segname BH)

protein and rename LYS ARG GLU ASP

water and within 5 of (protein and resid 62 and name CA)

water and within 3 of (protein and name O and z < 10)
Checking 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 (i.e. direct transfer of known parameters)
- Quick, starting point - dihedrals??

**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
Roadmap Charmm27 Optimization*

- Initial Geometries Model Compounds?
  - Partial Atomic Charges
  - VDW Parameters
    - Bonds, Angles, Torsions, Improper
    - Condensed Phase MD Simulations
  - Parameterization Complete

Related: QM/MP2/6-31G* Barriers, bonds,…
HF/6-31G* hydrated groups, TIP3W
Self-consistent iteration

Exp. Data IR, X-ray,…
Stat. Var.

*based on MacKerell, JCC v21, 86,105 (2000)
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](http://www.pharmacy.umaryland.edu/faculty/amackere/force_fields.htm)
When creating a covalent link between model compounds move the charge on the deleted H into the carbon to maintain integer charge (i.e. methyl ($q_C=-0.27, q_H=0.09$) to methylene ($q_C=-0.18, q_H=0.09$))
Top_all22_model.inp contains all protein model compounds. Lipid, nucleic acid and carbohydrate model compounds are in the full topology files.

HG will ultimately be deleted. Therefore, move HG (hydrogen) charge into CG, such that the CG charge becomes 0.00 in the final compound.

Use remaining charges/atom types without any changes.

Do the same with indole
Comparison of atom names (upper) and atom types (lower)

From MacKerell
Creation of topology for central model compound

Start with alanine dipeptide. Note use of new aliphatic LJ parameters and, importantly, atom types.

NR1 from histidine unprotonated ring nitrogen. Charge (very bad) initially set to yield unit charge for the group.

Note use of large group to allow flexibility in charge optimization.
HG1 deleted from CYS and the charge was moved to SG (-0.23 +0.16=0.07) so that the SG charge becomes 0.07 in final compound and the group remains neutral

Changes annotated!
Partial Atomic Charge Determination

Method Dependent Choices

1. RESP: HF/6-31G overestimates dipole moments (AMBER)

2. Interaction based optimization (CHARMM)

For a particular force field do NOT change the QM level of theory. This is necessary to maintain consistency with the remainder of the force field.

From MacKerell
Starting charges??
Mulliken population analysis
Analogy comparison

peptide bond
methyl
imidazole (N-N=C)?

**Final charges** (methyl, vary $q_C$ to maintain integer charge, $q_H = 0.09$)
interactions with water (HF/6-31G*, monohydrates!)

From MacKerell
Comparison of analogy and optimized charges

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Analogy</th>
<th>Optimized</th>
</tr>
</thead>
<tbody>
<tr>
<td>C1</td>
<td>CT3</td>
<td>-0.27</td>
<td>-0.27</td>
</tr>
<tr>
<td>H11</td>
<td>HA3</td>
<td>0.09</td>
<td>0.09</td>
</tr>
<tr>
<td>H12</td>
<td>HA3</td>
<td>0.09</td>
<td>0.09</td>
</tr>
<tr>
<td>H13</td>
<td>HA3</td>
<td>0.09</td>
<td>0.09</td>
</tr>
<tr>
<td>C2</td>
<td>C</td>
<td>0.51</td>
<td>0.58</td>
</tr>
<tr>
<td>O2</td>
<td>O</td>
<td>-0.51</td>
<td>-0.50</td>
</tr>
<tr>
<td>N3</td>
<td>NH1</td>
<td>-0.47</td>
<td>-0.32</td>
</tr>
<tr>
<td>H3</td>
<td>H</td>
<td>0.31</td>
<td>0.33</td>
</tr>
<tr>
<td>N4</td>
<td>NR1</td>
<td>0.16</td>
<td>-0.31</td>
</tr>
<tr>
<td>C5</td>
<td>CEL1</td>
<td>-0.15</td>
<td>-0.25</td>
</tr>
<tr>
<td>H51</td>
<td>HEL1</td>
<td>0.15</td>
<td>0.29</td>
</tr>
<tr>
<td>C6</td>
<td>CT3</td>
<td>-0.27</td>
<td>-0.09</td>
</tr>
<tr>
<td>H61</td>
<td>HA</td>
<td>0.09</td>
<td>0.09</td>
</tr>
<tr>
<td>H62</td>
<td>HA</td>
<td>0.09</td>
<td>0.09</td>
</tr>
<tr>
<td>H63</td>
<td>HA</td>
<td>0.09</td>
<td>0.09</td>
</tr>
</tbody>
</table>
Dihedral optimization based on QM potential energy surfaces (HF/6-31G* or MP2/6-31G*).

From MacKerell
Potential energy surfaces on compounds with multiple rotatable bonds

1) Full geometry optimization
2) Constrain n-1 dihedrals to minimum energy values or trans conformation
3) Sample selected dihedral surface
4) Repeat for all rotatable bonds dihedrals
5) Repeat 2-5 using alternate minima if deemed appropriate

From MacKerell
QM development of force field parameters for retinal

Used for rhodopsin and bacteriorhodopsin simulations
Retinal Proteins -- Rhodopsins

- Covalently linked to a lysine
- Usually protonated Schiff base
- all-trans and 11-cis isomers
Unconventional chemistry
Isomerization Barriers in retinal

DFT/6-31G**

TABLE 2 The parameter set B used for the torsional potentials of the main polyene chain of the retinal Schiff base

<table>
<thead>
<tr>
<th>$\phi_i$</th>
<th>$k_i$ (kcal/mol)*</th>
<th>$n_i$</th>
<th>$\delta_i$ (deg)</th>
</tr>
</thead>
<tbody>
<tr>
<td>$C_5=\equiv C_6=\equiv C_7=\equiv C_8$</td>
<td>11.24</td>
<td>2.0</td>
<td>180.00</td>
</tr>
<tr>
<td>$C_6=\equiv C_7=\equiv C_8=\equiv C_9$</td>
<td>39.98</td>
<td>2.0</td>
<td>180.00</td>
</tr>
<tr>
<td>$C_7=\equiv C_8=\equiv C_9=\equiv C_{10}$</td>
<td>17.03</td>
<td>2.0</td>
<td>180.00</td>
</tr>
<tr>
<td>$C_8=\equiv C_9=\equiv C_{10}=\equiv C_{11}$</td>
<td>37.28</td>
<td>2.0</td>
<td>180.00</td>
</tr>
<tr>
<td>$C_9=\equiv C_{10}=\equiv C_{11}=\equiv C_{12}$</td>
<td>22.50</td>
<td>2.0</td>
<td>180.00</td>
</tr>
<tr>
<td>$C_{10}=\equiv C_{11}=\equiv C_{12}=\equiv C_{13}$</td>
<td>35.08</td>
<td>2.0</td>
<td>180.00</td>
</tr>
<tr>
<td>$C_{11}=\equiv C_{12}=\equiv C_{13}=\equiv C_{14}$</td>
<td>28.30</td>
<td>2.0</td>
<td>180.00</td>
</tr>
<tr>
<td>$C_{12}=\equiv C_{13}=\equiv C_{14}=\equiv C_{15}$</td>
<td>29.46</td>
<td>2.0</td>
<td>180.00</td>
</tr>
<tr>
<td>$C_{13}=\equiv C_{14}=\equiv C_{15}=\equiv N_{16}$</td>
<td>30.43</td>
<td>2.0</td>
<td>180.00</td>
</tr>
<tr>
<td>$C_{14}=\equiv C_{15}=\equiv N_{16}=\equiv C_{16}$</td>
<td>28.76</td>
<td>2.0</td>
<td>180.00</td>
</tr>
</tbody>
</table>

Tajkhorshid et al., 1999.

$E_{\text{dihedral}} = (1/2)k_i[1 + \cos(n_i\phi_i - \delta_i)]$. 
Coupling of electronic excitation and conformational change in bR
Inducing isomerization

500 nm
~50 kcal/mole
Retinal Charge Distribution

QM/MM derived partial atomic charges
Classical Retinal Isomerization in Rhodopsin

Twist Propagation
\[ \hat{H} = \sum_i \frac{1}{2} p_i^2 + \sum_i \sum_A \frac{Z_A}{r_{iA}} + \sum_{i>j} \frac{1}{r_{ij}} + \sum_{A>B} \frac{Z_A Z_B}{r_{AB}} + \sum_i \sum_p \frac{q_p}{r_{ip}} + \sum_A \sum_p \frac{Z_A q_p}{r_{Ap}} + V_{QM-MM}^{MM} + V_{QM-MM}^{MM} \]
Ab Initio QM/MM Excited State MD Simulation

Quantum mechanical (QM) treatment of the chromophore, and force field (MM) treatment of the embedding protein.
QM/MM calculation of ATP hydrolysis
ATP hydrolysis in $\beta_{TP}$
Coarse grain modeling of lipids

150 particles

9 particles!
Modeling the active-complex: today’s tutorial.
VMD to Attach the substrate GLN to the active site of hisH
Creating a new topology file entry

HG1 deleted from CYS and the charge was moved to SG (-0.23 + 0.16 = 0.07) so that the SG charge becomes 0.07 in final compound and the group remains neutral

Changes annotated!
Creating new parameters

**EBOHDS**

\[ V(bond) = k_b (b - b_0)^2 \]

\[ k_b: \text{ kcal/mole/Å}^2 \]

\[ b_0: \text{ Å} \]

<table>
<thead>
<tr>
<th>atom type ( k_b ) ( b_0 )</th>
</tr>
</thead>
<tbody>
<tr>
<td>Modified for CYG residue after 6-31G* geometry optimization</td>
</tr>
<tr>
<td>S CC 240.000 1.7814 ! ALLOW ALI SUL IDN</td>
</tr>
</tbody>
</table>

**ANGLES**

\[ V(\text{angle}) = k_{theta}(\text{Theta} - \text{Theta}_0)^2 \]

\[ k_{theta}: \text{ kcal/mole/ rad}^2 \]

\[ \text{Theta}_0: \text{ degrees} \]

\[ k_{\text{Urey-Bradley}}: \text{ kcal/mole/Å}^2 \]

<table>
<thead>
<tr>
<th>atom types K_{theta} Theta0 Kub SO</th>
</tr>
</thead>
<tbody>
<tr>
<td>Modified for CYG residue after 6-31G* geometry optimization</td>
</tr>
<tr>
<td>CT2 S CC 34.000 100.2000 ! ALLOW ALI SUL IDN</td>
</tr>
<tr>
<td>CT2 CC S 50.000 114.5000 ! ALLOW ALI SUL IDN</td>
</tr>
<tr>
<td>U CC S 75.000 122.2000 ! ALLOW ALI SUL IDN</td>
</tr>
</tbody>
</table>

**DIHEDRALS**

\[ V(\text{dihedral}) = k_{chi}(1 + \cos(n(\text{chi}) - \delta)) \]

\[ k_{chi}: \text{ kcal/mole} \]

\[ n: \text{ multiplicity} \]

\[ \delta: \text{ degrees} \]

<table>
<thead>
<tr>
<th>atom types K_{chi} n delta</th>
</tr>
</thead>
<tbody>
<tr>
<td>HA CT2 S CC 0.2500 3 0.00</td>
</tr>
<tr>
<td>CT2 S CC CT2 2.05 2 180.00</td>
</tr>
<tr>
<td>CT2 S CC U 2.05 2 180.00</td>
</tr>
</tbody>
</table>
Semi-empirical Parameter Estimation Using SPARTAN

Main Spartan Window

You build a part of CYG

Be careful with the dihedral drive section!