Molecular Mechanics



- **Definition of the force field**
- **Bonding terms**
- **Non-bonded terms**
- Parametrization

Force Field = Potential Energy of Molecular System



Force Field = Functional Form + Parametrization

Example: acetamide



3N-6 = 21 internal coordinates

vs. redundant internals

8 bonds 12 valence angles 10 torsions

Simplicity vs. complexity universal parametrization derivatives

Bonding Terms

Bond stretching



$$U(r_{\rm AB}) = \frac{1}{2}k_{\rm AB}(r_{\rm AB} - r_{\rm AB,eq})^2$$

Typical values of *k* (in kcal.mol⁻¹.Å⁻²)

C-C ~300 C=C ~650 C=O ~780

Bond Stretching



Good description of chemical

NOT efficient computation

Harmonic potential $V(r) = \frac{k}{2}(r - r_e)^2$

Angle Bending

$$V(\Theta) = \frac{k}{2} (\Theta - \Theta_e)^2$$

Typical values of *k* (in kcal.mol⁻¹.deg⁻²)

C-C-C ~0.01

Higher-order terms can be used (cubic, quartic)

Torsions

$$V(\omega) = \sum_{n=0}^{N} \frac{V_n}{2} [1 + \cos(n\omega - \gamma)]$$

AMBER One or two terms

MM2 Mostly 3 terms



Figure 2.2 Definition and sign convention for dihedral angle ω . The bold lines are the projections of the AB and CD bonds into the bisecting plane. Note that the sign of ω is independent of whether one chooses to view the bisecting plane from the AB side or the CD side

Improper Torsions or Out-of-Plane Bending

For cyclic or conjugated systems

To keep atoms in plane (e.g. cyclobutanone)



Figure 2.5 Alternative molecular coordinates that can be used to compute the energetics of distortions from planarity about a triply substituted central atom

Cross-terms in force fields

Bond-bond, bond-stretch, bend-bend-torsion, ... e.g.

$$V(r_1, r_2, \Theta) = \frac{k_{r_1, r_2, \Theta}}{2} [(r_1 - r_{1, e}) + (r_2 - r_{2, e})](\Theta - \Theta_e)$$

Non-Bonding Terms

Van der Waals interactions

Dispersive interactions (London force, 1930)

Two Drude Oscillators

$$V(r) = -\frac{\alpha^4 \hbar \omega}{2(4\pi\varepsilon_0)^2 r^6}$$

Drude particles are model oscillators used to simulate the effects of electronic polarizability in the context of a classical molecular mechanics force field. They are inspired by the Drude model of mobile electrons and are used in the computational study of proteins, nucleic acids, and other biomolecules.



Figure 2.6 Non-attractive hard-sphere potential (straight lines) and Lennard–Jones potential (curve). Key points on the energy and bond length axes are labeled

Electrostatic Interactions

Coulomb's law

$$V_{el} = \sum_{i < j} \frac{q_i q_j}{4\pi\varepsilon_0 r_{ij}}$$

Central multipole expansion

Charge-charge

Charge-dipole



Methods for deriving partial atomic charges

Atomic charge ... not observable!

QM: Mulliken, Lowdin, Bader AIM, ESP

Rapid Methods: partial equalisation of orbital electronegativity

ESP: Electrostatic Potential Fits

Solvent dielectric models

Solvent Effects

Water Models

Polarized FFs

United Atoms Force Field (Coarse-Grained Models)

Force Field Parametrization (Transferability, Heterocompounds, Inorganic Molecules)

MM/MD (force field) methods: molecular simulations

Molecular mechanics (MM): optimization of molecular geometry **Molecular dynamics (MD):** dynamical trajectory (t, T, ...p, V, PBC)



(Dis)advantages: universal parametrization

- Systems: 100.000 atoms can be studied conveniently (more on the coarse-grained level
- Limitations: standard force fields are not able to describe chemical reactions; heterocompounds poorly described