Molecular Simulation Research Projects

Intermolecular Interactions & Intramolecular

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Richard Feynman, Lectures in Physics



Richard P. Feynman Theoretical physicist



One-hour video, click here

When taking over the introductory course in physics in 1961 at Caltech.



One Sentence to Be Passed on to the Next Generation

"I believe it is the atomic hypothesis (or the atomic fact, or whatever you wish to call it)...

...In that one sentence, you will see, there is an enormous amount of information about the world, if just a little **imagination and thinking** are applied."

...this is what this course is about!

Adjusting the focus

We will look at the world from an atomistic perspective



From: <u>http://atomsinmotion.com/book/chapter1/atoms</u> Website contains some really nice explanations.

Ideal gas model – no interaction



http://www.falstad.com/gas/

This simulation corresponds to a hard-sphere potential which is similar to an ideal gas.

In nature molecules do interact ...

Coarse-grained molecular dynamic simulation of surfactants /water/air interface



Click <u>here</u> for a more details about this simulation

Humans do interact ...



E.A. Müller, HUMAN SOCIETIES A Curious Application of Thermodynamics, 1998 Chemical Engineering Education 32(3):230

Behaviour of the collective

How to compute the energy of a system



- U = energy. We are after the minimization of U!
- Chemical bonds are intramolecular interactions ranging from 150–1100 kJ/mol.
- Attractive and repulsive forces are intermolecular interactions ranging from 1–50 kJ/mol.

Intramolecular interactions: Bond stretching

 Often represented by simple harmonic potential

$$u_{stretch}(r_{ij}) = \frac{k_b}{2}(r_{ij} - r_0)^2$$

- Plays a big role e.g. for Infrared (or vibrational) spectroscopy of use to identify chemical substances.
- Not on the time scale of phenomena that we are interested in (VLE, LLE, adsorption, diffusion).

Intramolecular interactions: Molecule bending

 Represented by harmonic function around equilibrium angle θ₀

$$u_{bend}\left(\theta_{ijk}\right) = \frac{k_{\theta}}{2} \left(\theta_{ijk} - \theta_0\right)^2$$



- Force constant is significantly smaller than for bond stretching.
- Bond bending is taken into account for flexible molecules with three or more (pseudo) atoms

Intramolecular interactions: Torsion

 Depends on the dihedral angle Φ made by the two planes incorporating the first and last three atoms involved in the torsion

$$u_{tors}\left(\phi_{ijkl}\right) = \frac{k_{\phi}}{2} \left(1 + \cos 3\phi_{ijkl}\right)$$

- Torsional motions are generally hundreds of times less stiff than bond stretching motions.
- Needs to be taken into account for flexible molecules consisting of more than four (pseudo)atoms



Proper dihedral



Improper dihedral



Intermolecular distance

- The total potential energy is a function of the positions of all molecules of the system.
- It can be written as an infinite sum of two-body, threebody, etc. potentials.

$$U = \sum_{i < j} u(r_i, r_j) + \sum_{i < j < k} \Delta u_{ijk}(r_i, r_j, r_k) + \dots$$

Potential between two molecules i and j

Accounts for distortion of the pair potential due to the presence of the third molecule k.

Three-body and higher-body interactions are mostly ignored.

Hard sphere potential



- Simplest pair potential
- Takes volume exclusion into account (molecules can't come closer than their hard sphere diameter)
- Describes only repulsion, no attraction



Square well potential



- Somewhat more realistic
- Contains a region of attraction as well as the repulsive hard core.
- Although the square-well potential and the hard sphere potential are very simple they can provide valuable physical insight when used in molecular simulation.

Lennard Jones potential



- Very realistic representation of intermolecular interaction.
- Attractive term: 1/r⁶
- Repulsive term: 1/r¹²

LJ parameters are fitted to exp. data

Second virial coefficient

$$B_2(T) = -2\pi \int_0^\infty \left[\exp\left(-\frac{U(r)}{kT}\right) - 1 \right] r^2 dr$$

- Viscosity data
- Vapour Liquid Equilibria



- * Exp critical point
- Exp vapour liquid coexistence curve
- Simulation results

J. Phys. Chem. B, 1998, 102 (14), pp 2569–2577

Different values for LJ parameters exist

TABLE 1

Values of LJ parameters for Ar, Kr, CH_4 and N_2 from the second virial coefficient (a) and from the viscosity (b) taken from the literature.

System	σ (Å)	ε/k (K)	
Ar	3.504	117.7	(a)
	3.336	141.2	(a)
	3.400	122.0	(a)
	3.405	119.8	(a)
	3.465	116.0	(b)
	→ 3.418	124.0	(b)
3 3	3.542	93.3	(b)
		Mole 319-3	cular Engineering 6 325, 1996.

 Always check how LJ parameters were derived and if they are appropriate for the application

Electrostatic interactions



q: charge on ion, μ : dipole moment 17

Dependence of multipole interactions on the distance between two particles

ELECTRIC	Monopole	Dipole	Quadrupole	Octupole	Hexadecapole
Monopole	1/R	1/R ²	1/R ³	1/R ⁴	1/R ⁵
Dipole	1/R ²	1/R ³	1/R ⁴	1/R⁵	1/R ⁶
Quadrupole	1/R ³	1/R ⁴	1/R ⁵	1/R ⁶	1/R ⁷
Octupole	1/R ⁴	1/R⁵	1/R ⁶	1/R ⁷	1/R ⁸
Hexadecapole	1/R⁵	1/R ⁶	1/R ⁷	1/R ⁸	1/R ⁹





London Dispersion forces

- Part of the van der Waals forces (vdW), i.e., depend on the distance.
- Present in all molecules; temporary partial charges give temporary polarity.
- Weak interactions (0.05 2 kJ/mol) and their strength increases with the polarizability (the squishiness of the electron cloud)



What intermolecular forces are present?



Boiling point – measure for intermolecular interaction



Molecule	BP (°C)	Structure	MW (g/mol)
Pentane	36	CH ₃ CH ₂ CH ₂ CH ₂ —CH ₃	72
Diethyl ether	34	CH ₃ CH ₂ —O—CH ₂ CH ₃	74
Butanone	80	$CH_3CH_2 - C_{CH_3}$	72
Propanoic acid	141	O ∥ CH₃CH₂—C ◯OH	74

vdW and electrostatic interactions



 Responsible for protein folding and enzymatic recognition, i.e., sustaining live as you know it!

http://www.chembio.uoguelph.ca/educmat /phy456/456lec02.htm

...this interactions drive life in the universe!

References

 Ken A. Dill, Sarina Bromberg "Molecular Driving Forces", Garland Science, 2nd Ed. 2011

