Molecular Forces in Biological Systems

- Electrostatic Interactions;
- Shielding of charged objects in solution





Electrostatic self-energy, effects of size and dielectric constant



Biological macromolecules are stabilized by physical interactions:

Strong

Weak

-200 - -800 kJ/mol (-50 - -200 kcal/mol)

Covalent bonds

-40 - -400 kJ/mol (-10 - -100 kcal/mol)

Ionic interactions

Ion-dipole interactions

Hydrogen bonds

Van der Waals interactions

Hydrophobic effect

Why care about electrostatics?

Longest-range biologicaly relevant interactions.

➤ A lot of biological molecules are charged. Amino acids: Asp⁻, Glu⁻, Lys⁺ Arg⁺, His⁺; DNA: phosphates⁻ in backbone, lipids, salt ions, etc.

dsDNA





Electrostatic force



$$\vec{F}(r) = \frac{q_A q_B}{4\pi\varepsilon\varepsilon_0 r^2} \frac{\vec{r}}{|r|}$$

Force on charge B due to charge A.



$$U = \frac{q_{\text{ref}}}{4\pi\varepsilon_0\varepsilon} \sum_i \frac{q_i}{|\mathbf{x}_i - \mathbf{x}_{\text{ref}}|}$$





A mean field theory replaces the interaction between elements in the system by the interaction of a single element with an effective field, which is the sum of the external field and the internal field.

Bjerrum length.



Flux of an electric field

Fluxes arise from

- Sources: positive charges
- Sinks: negative charges



Electric field flux: integral of electric displacement over a surface.





Gauss' law

The integral of field flux through a closed, $\Phi = \oint_{\partial \Omega} \varepsilon \mathbf{E}(\mathbf{s}) \cdot d\mathbf{s}$ simple surface is equal to the total charge inside the surface $= \frac{1}{\varepsilon_0} \int_{\Omega} \rho(\mathbf{x}) d\mathbf{x}$

This is true for *both* homogeneous and inhomogeneous dielectric media

Point charge in a sphere

- Point charge has spherically-symmetric field
- Field is constant on sphere surface
- Flux is independent of sphere diameter

$$\Phi = \varepsilon E(r) 4\pi r^2 = \varepsilon \frac{q}{4\pi\varepsilon_0 \varepsilon r^2} 4\pi r^2 = \frac{q}{\varepsilon_0}$$



Field from a line charge

13636666666

Assumptions: Homogeneous medium Line of length L, where L is "very big" (radial symmetry) Linear charge density of λ

L

 $\varepsilon \mathbf{E}(\mathbf{s}) \cdot d\mathbf{s}$ $\Phi =$ ∂ (cylinder)

$$= \int_{0}^{2\pi} \int_{0}^{L} \varepsilon E(r) r \, dz \, d\theta$$

$$= 2\pi r L \varepsilon E(r)$$







Field around DNA

B-DNA shape:

- 2 phosphates every 3.4 Å
- water dielectric constant of 80

What is the field 40 Å away from a "very long" B-DNA molecule?

$$E(r) = \frac{\lambda}{2\pi\varepsilon_{0}\varepsilon r}$$

$$= \frac{(1.60 \times 10^{-19} \text{ C})}{2\pi(8.854 \times 10^{-12} \text{ C}^{2} \text{ J}^{-1} \text{ m}^{-1})(80)(4 \times 10^{-9} \text{ m}^{-1})}$$

$$= 5.29 \times 10^{7} \text{ V m}^{-1}$$



Field from a charged plane $\Phi = \oint_{\partial (pillbox)} \varepsilon \mathbf{E}(\mathbf{s}) \cdot d\mathbf{s}$

Assumptions:

Homogeneous medium Surface of area A, Surface charge density of σ

$$= 2 \int_{0}^{2\pi} \int_{0}^{z} \varepsilon E(r) r \, dz \, d\theta$$
$$= 4\pi R^{2} \varepsilon E(r) = 2A\varepsilon E(r)$$





$$2A\varepsilon E(r) = \frac{\sigma A}{\varepsilon_0}$$

$$E(r) = \frac{\sigma}{2\varepsilon\varepsilon_0}$$

What is the field at distance r from the source?

Field around a membrane

POPS membrane

- -1 e charge per lipid
- 1 lipid per 55 Å²

What is the field 20 Å away from the membrane (in water)?

Bigger than DNA!



Mukhopadhyay P, et al. *Biophys J* **86** (3) 1601-9, 2004.

	lipole momen	<i>it</i>	
\vec{r}^{q}	$\vec{p} = q\vec{r}$	q_i $\vec{r_i}$	$\vec{p} = \sum_i q_i \vec{r_i}$

Interaction energy of a dipole with a field

 $U = -\vec{p}\cdot\vec{E}$

q +0.2 H

p = 0.4q = 0.2N = 0q = 0.4q = 0.4

p = 3.8 Debye

Molecule	Dipole moment
Water	1.9
Ethanol	1.7
Acetic acid (neutral)	1.7
Acetone	2.88
Acetamide	3.8

1 Debye = 0.2 electron-Angstroms = 3.3×10^{-23} Cm



Partial Charges



N-Acetyl-N' -Methylserinyl amide





Electrostatics of maromolecules

Electrostatically Accelerated Protein-Protein Association



McCammon Group - UCSD



^{© 1997, 1999} J. E. Wampler

Potential gradients around the Glu-Arg dipeptide



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A continuum dielectric medium

> Reduces the strength of electrostatic interactions relative to a vacuum.

➢ It has no atomic detail.

An *isotropic* dielectric continuum exhibits the same response in all directions

□ the dielectric tensor can be reduced to a scalar

for a homogeneous isotropic Coulomb's law takes a very simple, scaled form



$$-\nabla \cdot [\varepsilon(r)\nabla \varphi(r)] = \frac{\rho(r)}{\varepsilon_0}$$

$$-\nabla \cdot \nabla V(r) = \frac{\rho(r)}{\varepsilon_0 \varepsilon}$$

$$u(r) = \frac{q_1 q_2}{4\pi\varepsilon\varepsilon_0 r}$$

Dielectric Boundaries

• Boundary can be modeled as a step-function change in dielectric constant.

• The relevant form of the Poisson equation is:



$$-\nabla \cdot [\varepsilon(r)\nabla \varphi(r)] = \frac{\rho(r)}{\varepsilon_0}$$

• The dielectric discontinuity can serve as a source of **E**field lines even if there are no source charges there ($\rho = 0$).



Image Charges & Forces

When a charge approaches a dielectric discontinuity:

$$q_{image} = -\left(\frac{\varepsilon_2 - \varepsilon_1}{\varepsilon_2 + \varepsilon_1}\right)Q = kQ$$

(charge is in medium with ε_1)

Force = $kQ^2/(4\pi\epsilon_0\epsilon_1(2d)^2)$

k < 0 when $\varepsilon_1 < \varepsilon_2$ (charge in low dielectric) \rightarrow image charge of opposite sign, *force is attractive*.

k > 0 when $\varepsilon_1 > \varepsilon_2$ (charge in high dielectric) \rightarrow image charge of same sign, *force is repulsive*.



 α – polarizability of the molecule

Ion-induced dipole

Interaction energy between the induced dipole and the inducing field

$$U = -\int_{0}^{E} \vec{p} \cdot d\vec{E} = -\int_{0}^{E} \alpha \varepsilon_{0} \vec{E} d\vec{E} = -\frac{1}{2} \alpha \varepsilon_{0} E^{2}$$

Induced dipoles: dependent upon polarizability of molecule, how easily electrons can shuffle around to react to a charge

Induced dipoles and Van der Waals (dispersion) forces

Large planar assemblies of dipoles are capable of generating long-range interactions

van der Waals interactions

- this is a general term for the favorable interactions that occur between uncharged atoms
- van der Waals forces include:
 permanent dipole-permanent dipole interactions
 permanent dipole-induced dipole interactions
 dispersion interactions
- **all have energies that depend on 1/distance**⁶

Dispersion

 we consider London dispersion interactions here: these are common to <u>all</u> atoms even atoms that have no permanent dipoles (e.g. Ar)

- also known as 'temporary dipole-induced dipole' interactions
- 🔺 consider an argon atom
- on <u>average</u>, its electron distribution will be spherically symmetrical:
- but at any <u>instant</u>, it will not be perfectly symmetric, e.g.:

when the distribution is like this, there will be an electronic dipole:

4 now consider a second atom adjacent to the first:

it will be <u>polarized</u> by the first atom:

this will lead to a <u>favorable</u> dipole-dipole interaction between the two atoms

the interaction occurs because the electron distributions become <u>correlated</u>

- **4** London J Chem Soc <u>33,</u> 8-26 (1937)
- the magnitude of this effect depends on the distance between the two atoms:

it also depends on the atoms' <u>polarizabilities</u> (a):

 $E_{dispersion} \propto a_{atom1} x a_{atom2}$

a describes how much an electron distribution can fluctuate or respond to an applied electric field

a (of atoms and molecules) generally increases with more electrons:

4 the dispersion interaction between <u>many</u> atoms is usually approximated as a sum of London terms:

for N atoms, the total energy will be a sum of N(N-1)/2 terms

this is the <u>pairwise</u> <u>additivity</u> assumption

London dispersion + sterics

- we can now consider the sum of the two types of interactions that we've seen so far
- **4** consider approach of two uncharged atoms (e.g. Ar)

unfavorable electron overlap dominates at short distance

favorable dispersion interaction dominates at 'long' distance

Dispersion interactions & protein stability

so favorable interactions with close-packed atoms in the folded state

are partly balanced by: favorable interactions with water molecules in the unfolded state

4 the density of atoms is higher in a protein's folded state than in water (proteins are very tightly packed) so dispersion interactions <u>will</u> stabilize proteins

Dispersion interactions in nature

500 DOGO(01) coaratochaliys

Photo: M. Moffet

Geckos grip via van der Waals forces Optimizing rice yields reduces greenhouse gas emissions DNA topoisomerases: One step at a time Chloroplast ancestors found in host nuclear genomes Geckos get a grip using Van-der-Waalsforces

Autumn et al. PNAS <u>99,</u> 12252-12256 (2002)

The seta has 1000 nanohairs

The Gecko toe has 500000 microhairs (setae)

Nanostructure of the Gecko toe

If all of a gecko's setae were stuck to a surface at the same time it would be able to support 140 kg!

Spiders and lizards: Lots of pads (hair) per foot - but dry / no secretions

Gecko-Tape

Stanford University's Sticky Bot

Electrostatic Steering

System	Potential dependence on distance	Energy [kJ/mol]
ion-ion	r ⁻¹	250
ion-dipole	r ⁻²	15
dipol – dipol	r ⁻³	2
London	r -6	1

Dipole - dipole interactions

Interaction between ions and macromolecules

Non-specific screening effects

- Depends only on ionic strength (not species)
- Results of damped electrostatic potential
- Described by Debye-Hückel and Poisson-Boltzmann theory for low concentration

Site-specific binding

– Ionic specific (*concentration* of specific ion, not necessarily ionic strength)

– Site geometry, electrostatics, coordination, etc. enables favorable binding

– Influences

- Co-factors
- Allosteric activation
- Folding (RNA)

Polar solvation: Poisson equation

- Poisson equation
 - Classic equation for continuum electrostatics
 - Can be derived from hard sphere dipolar solvent
- Assumptions
 - No dielectric saturation (linear response)
 - No solvent-solvent correlation (local response)

 $-\nabla \cdot \varepsilon(\mathbf{x}) \nabla u(\mathbf{x}) = 4\pi \rho(\mathbf{x}) \quad \text{for } \mathbf{x} \in \Omega$ $u(\mathbf{x}) = u_0(\mathbf{x}) \quad \text{for } \mathbf{x} \in \partial \Omega$

Polar solvation: Boltzmann equation

- Mean field model
 - Include "mobile" charges
 - Boltzmann distribution
 - Ignore charge-charge correlations
 - Finite ion size
 - Weak ion-ion electrostatics
 - Low ion correlations
- Missing ion "chemistry"
 - No detailed ion-solvent interactions
 - No ion coordination, etc.

Poisson-Boltzmann equation The space – dielectric properies

The space – dielectric properies

Mobile ion charge distribution form:

Boltzmann distribution – no explicit ion-ion interaction
No detailed structure for atom (de)solvation

Result: Nonlinear partial differential equation

$$-\nabla \cdot \varepsilon(x) \nabla \phi(x) - 4\pi \sum_{m} Q_{m} \overline{n}_{m} e^{-\beta Q_{m} \phi(x) + V_{m}(x)} = 4\pi \sum_{i} q_{i} \delta(x - x_{i})$$
$$\phi(\infty) = 0$$

For not very high ion concentrations $\kappa a \ll 1$

$$V(r) = \frac{Z_{+}e}{4\pi\varepsilon\varepsilon_{0}r}e^{-\kappa r}$$

□ Viewed from beyond the counterion cloud, the macroion appears neutral.

□ Macroions will not feel each other until they' re nearby

Once they are nearby, the detailed surface pattern of charges can be felt by its neighbor, not just overall charge - streospecificity.

Hydrogen bonds

The hydrogen bonds is in the range of 3 - 40 kcal mol⁻¹.

The covalent bond between H and O in water is about 492 kJ mol⁻¹.

The van der Waals interaction is about 5.5 kJ mol^{-1} .

A hydrogen bond consists of a hydrogen atom lying between two small, strongly electronegative atoms with lone pairs of electrons (N, O, F).

Strength of an H-bond is related to the **D-H**---A

- Distance
- The D-H-A angle.

The hydrogen bond is stronger than typical electrostatic interactions between partial charges, but *it is easily disassociated by heat or by interaction with other atoms.*

Distance Van der Waals radius of O **1.5** Å. H: **1.1**Å, The closest approach should be **2.6** Å. Separation is about 1 Å less! It is 1.76 Å. Intermediate between VdW distance and typical O-H covalent Hydrogen bond of 0.96Å. bond =1.77 Å *The shorter the distance* Covalent bond =0.965 Å between D & A the stronger the interaction.

Hydrogen bond is directional

Hydrogen bond potential energy

$$U = \left(\frac{A}{r^{12}} - \frac{B}{r^6}\right)\cos\theta + \left(\frac{A'}{r^{12}} - \frac{B'}{r^6}\right)(1 - \cos\theta)$$

The hydrogen bonds define secondary structure of proteins.

Hydrogen bonds define protein binding specificity

