Outline:

Intermolecular Interactions \( (F = -∇U) \)
- repulsive \( U \sim 1 / r^{12} \)
- attractive, dispersive \( U \sim 1 / r^{6} \)
- electrostatic \( U \sim 1 / r, 1 / r^{2}, 1 / r^{3}, \ldots \)

Intermolecular Interactions and solution structures
- proteins
- DNA

Intermolecular Forces

These interactions lead to deviations from ideality that are of great interest: water properties, solid desk, keeps DNA in nice double helix – focus of the whole course.

We will now investigate the details of these interactions with an eye towards explaining not only real gas behavior, but also how these effects can influence structure and dynamics in solution phase biochemical systems. This is where the action is.

Remember from Monday, that simplest interaction between two atoms (like argon-argon) has this Lennard-Jones shape.

\[
\begin{align*}
U(R) & = \\
1: & \text{Attractive} \\
2: & \text{Repulsive} \\
3: & \text{No interaction}
\end{align*}
\]

In this case, the potential energy between the two atoms depends only on the distance between them. Recall that we relate force to the potential:

\[
F = -∇U \quad \text{dimension} \quad \frac{dU}{dR}
\]

Region 3: We can see at very long distances, there is no potential energy between the two atoms -> ideal gas limit
**Region 1**: At very short distances, the potential energy is very positive and atoms are repulsed by one another.

**Repulsion Forces**

The Pauli exclusion principle forbids that any two electrons may occupy the same space. So as molecules closely approach each other, there is a strong rise in potential energy which indicates the repulsive effect of the interacting electrons. The distance dependence of this effect is usually represented as follows:

\[ U(r) \propto \frac{1}{r^{12}} \quad \text{or} \quad U(r) \propto e^{-r} \]

**Region 2**: At intermediate distances, the potential energy is negative and atoms are attracted to one another. This is our focus for much of this course.

**Dispersion or London Forces** (Fritz London 1930)

Dispersion forces can also be thought of in terms of the interaction of instantaneous and temporary dipole moments. The existence of the dipole is solely due to instantaneous fluctuations of the charge distribution (quantum mechanical in nature). The sequence that leads to this effect can be pictured:

1) An **instantaneous** dipole is formed in one molecule
2) An **induced** dipole is formed on the second molecule

These are particularly strong in atoms with big, soft sloshy electron densities (e.g. Iodine)

**Sketch some sloshing charge distributions**

Dispersion forces therefore exist in all molecules and the potential energy function has the following **distance dependence**:

\[ U(r) \propto -\frac{1}{r^6} \quad \text{longer ranged than repulsion} \]

Strength of this interaction depends on: # electrons and polarizability (spatial extent)

For instance, put in order:

methane (CH₄), propane (C₃H₈), hexane (C₆H₁₄) and benzene (C₆H₆).

**Lennard-Jones** – puts repulsion and attraction together

Based on these two contributions to the potential energy, it has been found that the **Lennard-Jones Potential** often provides a good description of the potential energy for atoms and non-polar molecules:
\[ U(r) = 4\varepsilon \left[ \left( \frac{\sigma}{r} \right)^{12} - \left( \frac{\sigma}{r} \right)^6 \right] \]

repulsion dispersion

Where \( \varepsilon \) and \( \sigma \) are adjustable parameters that depend on the identity of the system. (Also written in other forms, sometimes even other powers.)

For interactions between polar molecules (such as H\(_2\)O-H\(_2\)O) there exists another kind of intermolecular interaction that arises from the asymmetric charge distribution.

**Electrostatic Forces (not considered in MT – important for polar molecules & ions)**

**Coulomb’s law:** charges repel or attract \[ U \propto \frac{q_1 q_2}{R_{12}} \]

**electric dipole:** consists of two electric charges \( q \) and \(-q\) separated by a distance \( l \) and represented by a vector \( \mu \) that points from the negative charge to the positive charge. The magnitude of the vector is \( q*l \) and is called the electric dipole moment.

\[ -q \quad +q \]

\[ \mu \]

\[ l \]

\[ |\mu| = q \times l \]

Debye unit (D): \( 1 \text{ D} = 3.336 \times 10^{-30} \text{ C m} \)

A molecule possesses a nonzero electric dipole moment if it has an asymmetrical charge distribution:

- H-F nonzero
- N-N zero (symmetrical)

Thus, we refer to HF as a **polar** molecule. What about CO\(_2\), CCl\(_4\), CH\(_3\)Cl

Larger molecules are more complicated sums of charges and positions. Usually reasonably correct to take vector sums of individual little dipoles. (show \( \alpha \)-helix with carbonyl and amine dipoles pointing in same direction)
Most molecules have complicated charge distributions that are not well described by a dipole moment alone.

**What should we do?** Expand. Another expansion to describe complicated charge distribution with fairly simple terms.

charge distribution = monopole (charge) + dipole moment + quadrupole moment + octupole moment + …

**monopole (n=0):** one point charge (Na\(^+\))

**dipole (n=1):** two point charges that has no monopole (\(\delta^+ \text{H} - F^\delta\))

**quadrupole (n=2):** four point charges that has no dipole (\(\delta^- \text{O} = +2\delta \text{C} = O^\delta\))

**octupole (n=3):** eight point charges that has no dipole or quadrupole (CH\(_4\))

and so on

Note that large molecules are rarely described by any 1 term, but usually a sum of many terms (an expansion!)

**Show 22.11**

**Distance Dependence of Electrostatic Forces**

Interactions between these charge descriptions (using Coulomb’s law and some geometry) are found by summing over the multipoles for each molecule (where m and n are the respective multipole indices for the interacting molecules):

\[ U(r) \propto \frac{1}{r^{m+n+1}} \text{ (can be positive or negative)} \]

monopole-monopole: \(q_1q_2 / r\)

dipole – dipole: \(\mu_1\mu_2 / r^3\)

quad-quad: \(\theta_1\theta_2 / r^5\)

**dipole – quad?**: \(\mu_1\theta_2 / r^4\)

(long range or short range??)

Note that electrostatic interactions have orientation dependence. They can be either attractive or repulsive. Draw aligned and anti-aligned and ask **which is attractive?**

This is a big difference between electrostatic and dispersion forces. Dispersion have no directionality (isotropic) and always are attractive.

Because of the shorter range of electrostatic forces, dispersion forces are much smaller than electrostatic forces in polar molecules such as H\(_2\)O (**show ice structure**). Therefore, dispersion forces are most often important in non polar systems such as benzene.
Approximate Magnitudes of the Chemical Bonding for Representative Systems

H-H: 500 kJ mol\(^{-1}\) (chemical bond)
H\(_2\)O - H\(_2\)O: 20 kJ mol\(^{-1}\) (intermolecular (electrostatic) bond)
Ar - Ar: 1 kJ mol\(^{-1}\) (intermolecular (dispersion) bond) (can be larger in bigger molecules)

It is the magnitude of these energies that determines the condensed phase properties of materials. Ether is a low-boiling compound because it is held together in the liquid phase by weak dispersion interactions and water is a high boiling compound because it is held together by strong electrostatic interactions (hydrogen bonds).

Influence of IM Forces on Macromolecular Structure in Solution

I have already alluded to some of the unique properties of liquid water as being a direct manifestation of the strong hydrogen bonding that occurs.

**What is the hydrogen-bonded structure of water (must take into account electrostatics and repulsion)?** wants to look like ice

Since water is strongly attracted to itself, it will also be attracted to other molecules in solution that have polar subunits.

Protein Structure

Proteins have very unique chemical properties that depend very sensitively on their three dimensional shape. Since proteins function in solution, their intermolecular interaction with water will strongly influence their shape.

Hydrophillic-hydrophobic considerations

We already mentioned the polar N-H and O-H groups in the protein backbone. Also polar sidechains which will prefer to interact with water or other polar groups via strong electrostatic interactions (hydrogen bonding). **We call them? hydrophillic**

The carbon chains which connect these polar groups (and many sidechains) are largely non-polar in nature and will not be strongly attracted to water - **hydrophobic**

Therefore, proteins will fold into three dimensional structures that maximize hydrophilic interaction with water and avoid hydrophobic interaction with water. Note that hydrophobic interaction in the interior is just less-bad, not good. If it stuck out, it would destroy the desirable ice-like water structure.

Show lysozyme. with polar units highlighted.
Show beta-sheet and alpha-helix → fantastic feat of Pauling and Corey to predict structure

Although electrostatics play an important role in these structures (forming hydrogen bonds), steric effects (repulsion forces) and dispersion forces are also very important.

The subject of protein structure and folding (transitions between structures of different biochemical activity) is a wonderful area of research.

**Structure of DNA**

As most of you know, the structure of DNA is that of a double helix. We can understand the rationale for this structure from an intermolecular force viewpoint. DNA is made up of nucleotide subunits, each of which have a phosphate group, a sugar group and a base group. *Show Zubay 1-8a*

The negatively charged phosphate groups prefer to interact with the water solvent while the base groups prefer to interact with each other (called base-pairing). Using these two pieces of information, we could predict the double helix structure. The phosphate groups are on the outside of the double helix and base pairing holds the two strands together on the inside. These forces are largely electrostatic. *Show Zubay 7-16a.*

However, just using these two constraints, we would find that the step ladder structure is just as likely. *Show Zubay 7-16b.*

Why is the double helix the preferred structure? The key is that in the double helix structure, adjacent base pairs can stack in such a way that an additional favorable interaction is created. Although this interaction is largely described by dispersion forces, it is of comparable magnitude to the electrostatic forces involved in the base pairing.