

Structural Elements of the Living Matter

- structure: - the periodic arrangement (order) of components of a system
 - components \longleftrightarrow arrangement
- living matter: - chemically, physically can be described in the same way as inorganic
 - their way of production, their composition (mostly organic), many polymers

① Water: - very abundant \longleftrightarrow irregular properties (anomalous properties)

abundant BUT not typical

- c - high specific heat capacity
- L_v - \sim latent heat of vaporization
- L_M - \sim \sim \sim \sim melting
- T_B - \sim boiling temperature
- T_F - \sim freezing temperature
- γ - \sim surface tension
- strange V-T function (p)
- ice is slippery

Structure of water at molecular level



- tetrahedral \bar{e} -pair arrangement

- V-shaped

- $r(H) \approx 90 \text{ pm} = 0,9 \text{ \AA}$

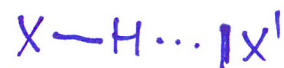
- $r(O) \approx 150 \text{ pm} = 1,5 \text{ \AA}$

- $d(H-O) \approx 120 \text{ pm} = 1,2 \text{ \AA}$

(primary interaction: covalent bonding)

- $d(H \cdots O) \approx 180 \text{ pm} = 1,8 \text{ \AA}$

(secondary interaction: H bonding)

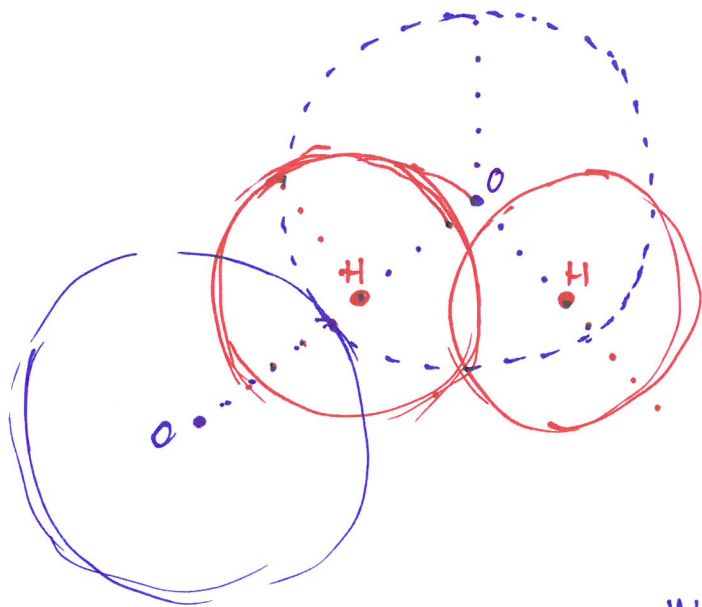


where: $X \& X' = N, O, F$

it is a weak dative covalent bond

weak primary bond?

strong secondary bond?



1.1 - Volume vs. temperature (1g water)

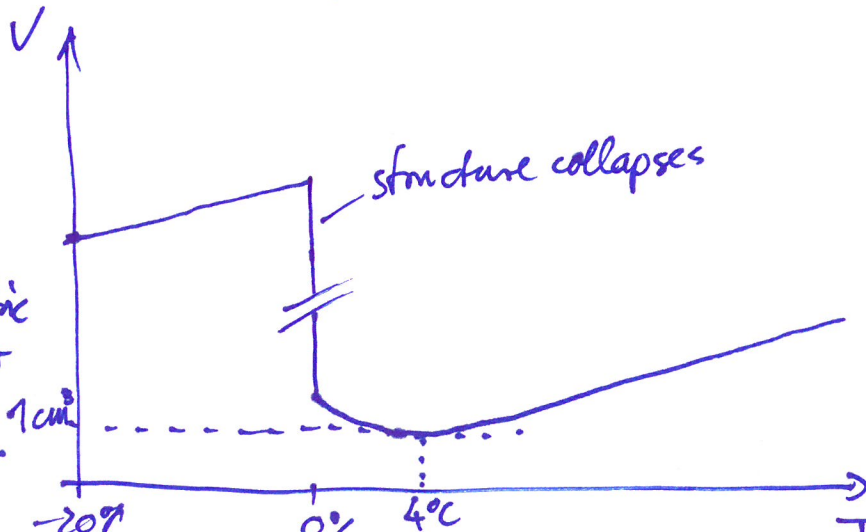
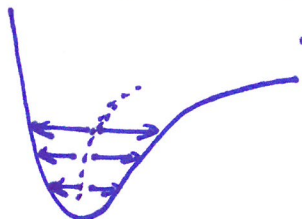
IDEAL (HOOKE)



100N \leftrightarrow 1cm \rightarrow 100N

150N \leftrightarrow 1,5cm \rightarrow 150N

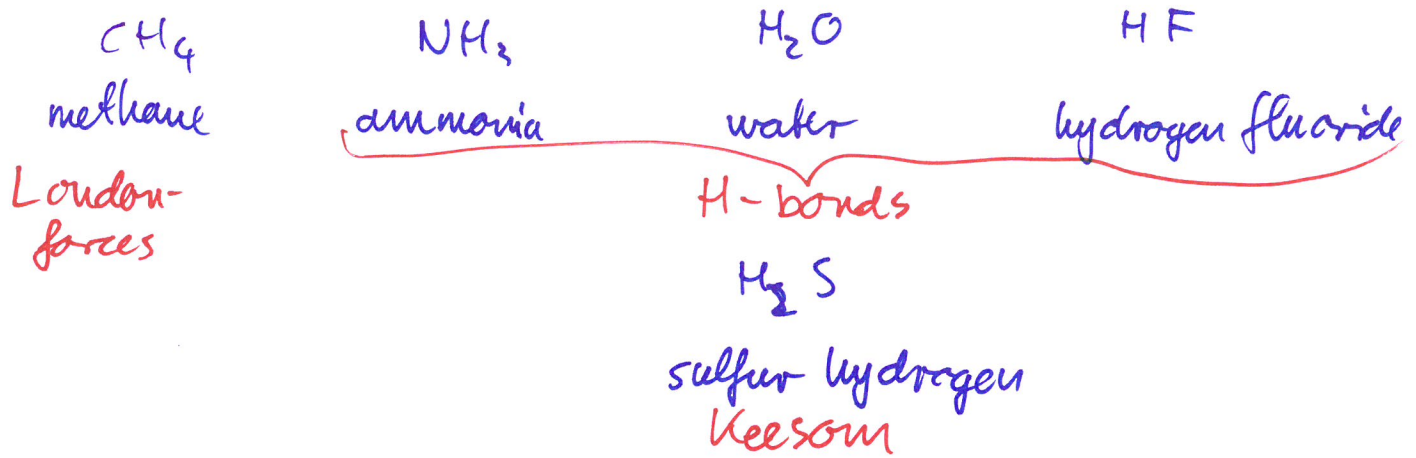
REAL: asymmetric non-linear



vibration
less order

* decreasing range of order

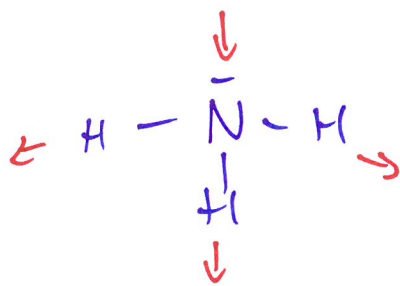
1.2 - Secondary interaction between water molecules in comparison with similar binary compounds



van der Waals interactions: dipole-dipole

- permanent dipole \leftrightarrow permanent dipole (KEESOM)
- permanent dipole \leftrightarrow induced dipole (DEBYE)
- London dispersion forces: transient dipole \leftrightarrow induced dipole

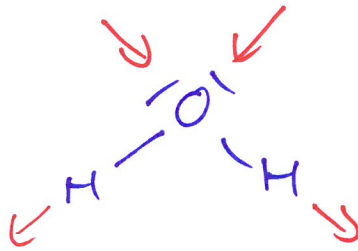
each of the following molecules are able to form 4 H-bonds:



donate: 3
receive: 1

consider 1000 molecules:
 $\frac{3000}{1000}$

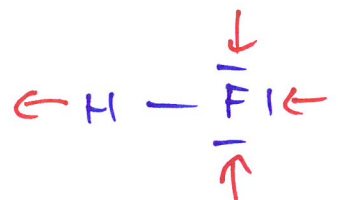
average number of H-bonds per molecule
chains



2
2

$\frac{2000}{2000}$

2
net
-3-



1
3

$\frac{1000}{3000}$

1
chains

- the high energy of an H-bond
 - the high bond/molecule ratio
- } strong intermolecular forces in H_2O

↓

$$C, L_V, L_M, T_F, T_B, \gamma$$

4.3 surface tension: the work required to create $1 m^2$ extra (new) surface • for a liquid

$$\gamma = \frac{W}{\Delta A} \quad [\gamma] = \frac{[W]}{[A]} = \frac{J}{m^2} = \frac{N}{m}$$

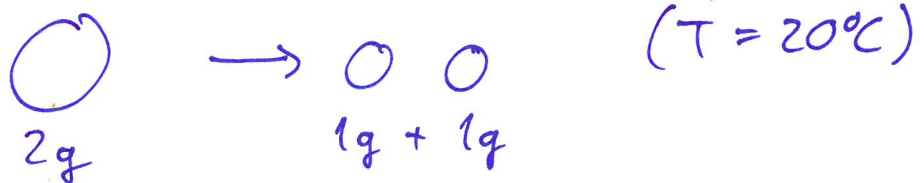
homework!

γ depends on: - chemical composition
- temperature
- etc. ...

$$\gamma(\text{water @ } 20^\circ C) = 72 \frac{mJ}{m^2}$$

homework: We have a spherical droplet of water of 2g.

a) What work is required to separate them into two 1g - spherical droplets?



b) By how many $^\circ C$ increases their temperature if they are reunited?

(suppose the released surface energy completely turns into heat)

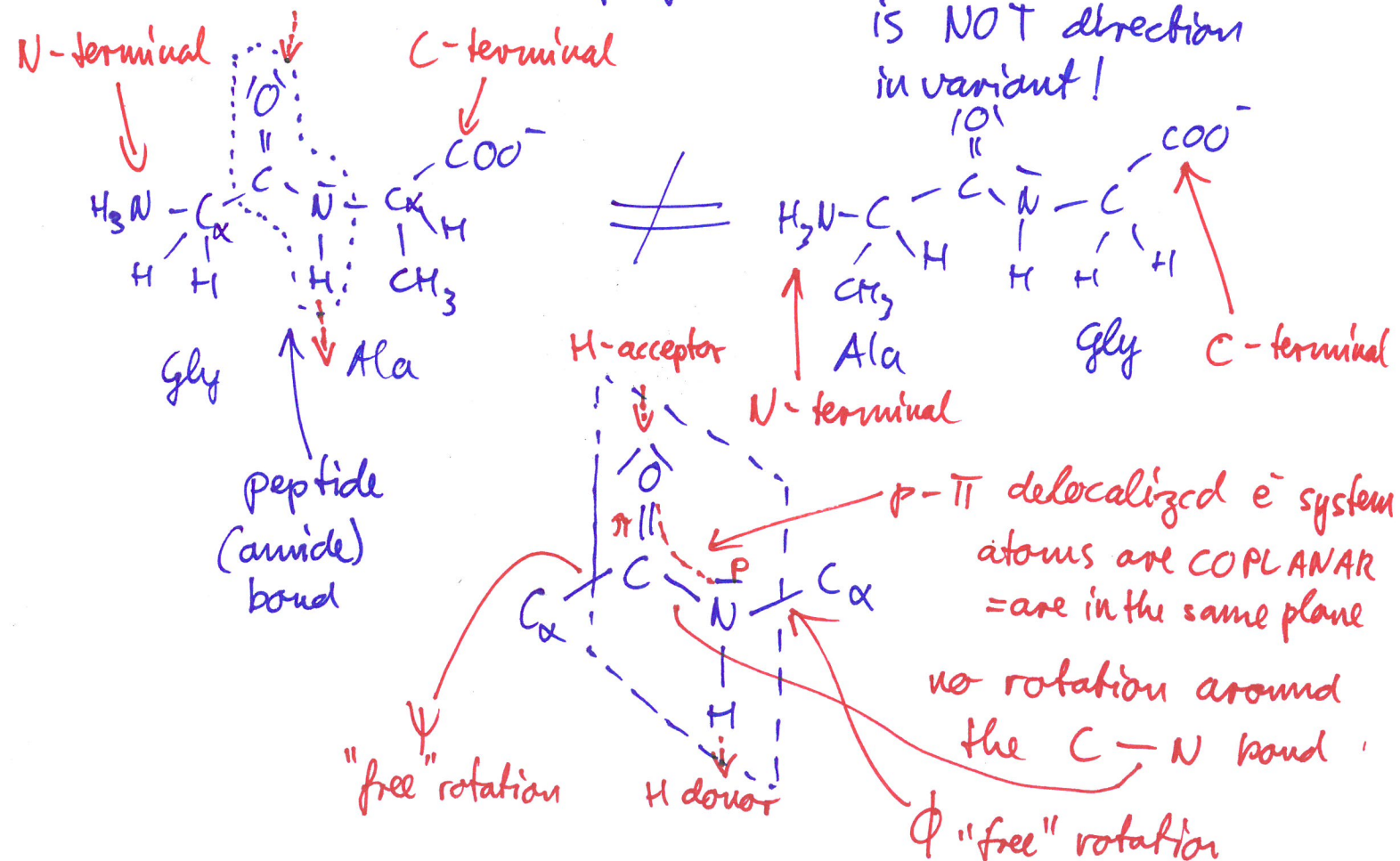


7.4. Why is water ^{ICE} slippery?

* "Classical" theory (WRONG!): ^{surface} becomes molten due to pressure (e.g. when standing on it)

* modern theory: - though bulk ice is organized as a crystalline structure
- on the surface it is less ordered more similar to liquid water

② Proteins: - polymers: consists of repeating units called monomers (in this case, amino acids = AA)
- copolymers: 20 different types of monomers (biogenic amino acids)
- directed copolymers: order of monomers is NOT direction in variant!



Proteins have a hierarchy of structures

- 2.1 Primary structure:
- the order of AA in the polypeptide chain
 - they are held together by covalent bonds
 - it can be determined using chemical analysis and X ray crystallography
 - every protein has it

- 2.2 Secondary structure:
- local order: repetition of ψ and ϕ bond angles for at least 3 AA units
 - they are stabilized by H bonds between peptide group O and N-H
 - they can be determined using spectroscopy
 - not all proteins have them there may be un-ordered sections
- types:
- α -helix
 - β sheet
 - parallel
 - antiparallel
 - β -turn

- 2.3 Tertiary structure:
- global order: the complete 3D conformation of a protein molecule
 - all proteins have it (few exceptions)
 - can be determined by
 - X-ray crystallography
 - NMR
 - electron microscopy
 - it is stabilized by hydrophobic interactions
- 6 -

- 2.4. Quaternary structure:
- global order of multiple ~~domains~~^{subunit} proteins
 - only characteristic of proteins with multiple polypeptide chains = subunits
 - otherwise similar to 3° structure