Elements of Biophysics

Saul Pierotti

October 28, 2019

21/10/19

- The course is made of elements, it is not a complete course
- We want to understand biomolecules
- Structure-function relationship
- The scale of things
- I don't know something if I cannot describe it with a model
  - A model is an equation
- Laser time dependent X ray cristallography allows to see a molecule "breathing"
- The deeper you go in resolution, the more you have to increase the perturbation
  - Bragg diffraction theorem
- Life makes sense only in the light of thermodynamics
- A cell is held together by London forces
- Freeze fracturing
- Atomic force microscope
- rita.casadio@unibo.it
- Complexity means that there are emergent proprieties
  - We do not have models that can predict a cell from its components
- Mitosis, meiosis, apoptosis, developmental biology
- Protein synthesis
- In a cell there are at least 240k different proteins
  - Their relative concentration is of paramount importance
- We are able to label all the neurons in a mouse brain

22/10/19

- I came late
- Bonds can be polar
- Ionic bonds are 2.7/3Å long, and around -5 to -10 Kcal/mol
- Covalent bonds are around 100 Kcal/mol and they show an optimal nuclear distance, which is the bond lenght $(1 - 1.4Å)$
  - The typical C-C bond is 1.4Å
- Bond lenghts are calculated by X-ray diffraction studies, bond strenghts with calorimetry
- Disulphide bond are around -40 Kcal/mol, 2.07Å
  - This bond is stable in an oxydized ambient
- Redox ambient potential describes the tendency of molecules in an environment to lose or acquire electrons
- Steric hindrance
- Bond resonance
- Peptide bond is around 1.5Å (?) and is polar,
  - A long protein chain is highly polar end to end 2-4 Kcal/mol

- A Debye is the unit of measure of permanent dipoles
- A water molecule has a dipole
- The C-H bond is not polar (!)
- The OH_3^+ structure is called hydronium ion
  - One O atom generally interacts with 4 H, binding 2 at a time in a covalent way
- An H bond can be completely explained only with quantomechanics, it is 3-5 Kcal/mol and 1.5Å
- Cell membrames

23/10/19

- The dipolar interaction energy can be derived from the dipol moments
- The London force is the most dependent on distance
- The hydrophobic effect is the tendency of nonpolar molecules to aggregate in a polar solvent so to minimize the surface exposed to the solvent
- DNA
- We do not know the structure of mRNA
- The width of the DNA helix depends on salt concentration
  - The more salt the more compact it is
- The information content of DNA is in AT CG base pairing (so she wants)
- Transcribed regions are called loci
- Trascription is controlled by DNA methylation

24/10/19

- The relative dielectric constant comes from condensers
- A biological process is a series of chemical reactions catalized by enzymes
- Protein biosynthesis is a biological process that transfer information from DNA to ribosomes
- The receiver of information is the ribosome
- Every protein has an half-life: there is turnover
- The genetic code is redundant

28/10/19

- A protein is a biopolymer made of repeating peptide bonds, which form the backbone
- When an aminoacid enters in the structure of a protein, it becomes an amino-residue
- An aminoacid has a carboxil group and an aminic group bonded to a C_α
  - The side chain R can be one of 20 varieties
  - The carboxil group has a $pK_a \approx 4.2$
  - The amino group has a $pK_a \approx 9$
- The formation of the peptide bond is a condensation process where a water molecule is expelled
- The peptide bond is planar and has a dipole moment of around x debye
  - The bond is subjected to resonance because the C_α is bound to 2 electronegative atoms, O and N
  - It is shorter than a single bond, and the bond with O is longer than a double bond
  - The plane is defined by O, C_α and N
- Can every sequence be a protein?
- The bond between C_α and N is called Φ, the bond between C_α and COOH is called Ψ
  - Rotation is possible around these bonds
- Amino acids are zwitterionic, meaning that they have at phisiological pH both positive and negative charge
- The protein structure is the golden standard of proteomics
  - It allows the best predictions on function
- Functional genomics is the use of available data to infer information about unknown genes and proteins

- The secondary structure derives from the stabilisation of the protein by hydrogen bonding
- SCOP categorizes protein domains
  - The class of a protein is the way in which the backbone is organised (secondary structure)
    - An all-alpha or all-beta protein have more than 90% of the residues in that conformation
    - Alpha+beta proteins have a linker connecting the 2 domains
    - Alpha/beta proteins have a mixing of the structures
  - A fold is the topological arrangment of a portion of secondary structure
  - A superfamily has a probable common ancestor
  - A family is a collection of proteins that have similar function and structure
    - They can also have very different sequences (!)
- To categorize proteins, we have to do a structural alignment