Quiz2 2025
Biophysics(BIOP)
(24. Nov. 25)

Total Marks:20

Time: 45 min

Section-A (MCQ 1*10 Marks)

1. **The alignment file in MODELLER (.ali) requires which of the following formats?**

A. Pure FASTA
B. PIR format with template/target metadata
C. XML metadata plus FASTA
D. Clustal formatted blocks

2. **Which parameter in MODELLER controls how many alternative conformations are generated during a loop-modeling run?**

A. alnfile
B. starting_model / ending_model
C. md_level
D. loop.assess_methods

3. **The purpose of running gmx grompp before minimization is:**

A. To generate a topology file for the protein
B. To preprocess inputs and convert them into a binary portable run file (.tpr)
C. To analyze short-range Coulomb interactions
D. To check for errors during trajectory integration

4. **During a permanent hair-curling process, the reducing agent is used primarily to:**

A. Break hydrogen bonds between keratin strands
B. Convert disulfide bonds (–S–S–) into sulfhydryl groups (–SH)
C. Remove water molecules from keratin helices
D. Oxidize cysteine residues into cystine

5. **Which groups only contain amino acids with nonpolar side chains?**

A. Valine, Glycine, Isoleucine
B. Tyrosine, glycine, Serine
C. Arginine, asparagine, Histidine
D. Asparagine, valine, Glutamic acid

6. The .gro file generated after solvation contains:

A. Parameter definitions for force fields
B. Processed topology metadata
C. Atomic coordinates and box vectors
D. Bond constraints for hydrogen atoms

7. Which MD simulation analysis commands is correct for its function:

A. gmx Rmsf: per-residue flexibility, gmx gyrate: backbone deviation vs time
B. gmx Rmsf: per-residue flexibility, gmx rms: backbone deviation vs time
C. gmx gyrate:folding status, gmx rmsf: backbone deviation vs time
D. Gmx mdrun:for running simulation, gmx gyrate:per residue flexibility

8. Which of the following is TRUE regarding the functional enzyme?

A. Chymotrypsin is active as a single polypeptide chain, while chymotrypsinogen requires three chains to function.
B. Chymotrypsin and chymotrypsinogen both function as a single polypeptide chain.
C. Chymotrypsin requires three polypeptide chains for activity, while chymotrypsinogen is synthesized as one inactive polypeptide chain.
D. Chymotrypsinogen requires two polypeptide chains, while chymotrypsin requires one.

Please read the information given below to answer questions 9 & 10

A ligand binds to a receptor that interconverts between three conformations (C_1, C_2, C_3).
Unbound energies:

- $G_1 = 0$ kJ/mol
- $G_2 = +5$ kJ/mol
- $G_3 = +10$ kJ/mol

Upon ligand binding, only C_2 is stabilized by 8 kJ/mol, giving:

- $G_1 = 0$ kJ/mol (unchanged)
- $G_2 = -3$ kJ/mol (5 − 8)
- $G_3 = +10$ kJ/mol (unchanged)

9. At T = 300 K, which statement is most accurate?

A. C_2 becomes the dominant conformation because its free energy becomes the lowest among all three states.
B. C_1 remains the dominant conformation since it was the lowest-energy state before ligand binding.
C. C_3 becomes significantly populated due to entropic stabilization at 300 K.
D. All three conformations will occur equally once the ligand binds.

10. Given the same system, which statement best reflects the expected equilibrium populations after ligand binding?

A.C_2 becomes overwhelmingly favored because a 3 kJ/mol difference at 300 K corresponds to a strong Boltzmann bias.
B. C_1 and C_2 will remain equally populated because their free energies are within 10 kJ/mol of each other.
C.C_3 will become nearly as populated as C_2 because ligand binding increases conformational entropy.
D. C_3 becomes the dominant state because the ligand does not change its free energy.

Section B

1. The command **"gmx trjconv -pbc mol -center"** is applied to the production trajectory before analysis. Why is this step necessary?

Ans: It recenters the protein and reconstructs broken molecules across periodic boundaries, ensuring that RMSD, radius of gyration, and hydrogen-bond analysis are performed on intact, properly positioned structures rather than fragmented images.

2. Torsion (dihedral) angles are highlighted as the "**most important degrees of freedom**" in proteins. Based on the chemical structure of the peptide backbone, explain why the rotation around the dihedral angle **phi** and **psi** is significantly easier to alter than the peptide bond omega angle.

Ans: The rotation around the dihedral angle phi and psi is relatively easy because they involve **single** C-C **or** C-N **bonds**, allowing free rotation that is only limited by steric clashes between the side chains and the backbone atoms. In contrast, the **peptide bond** omega **has significant partial double-bond character** due to resonance between the carbonyl oxygen and the amide nitrogen. This partial double-bond character makes the peptide bond highly rigid, restricting rotation and enforcing an almost planar conformation (typically *trans*), requiring much higher energy to alter.

3. In a GROMACS md.mdp file, the following parameters are set: **dt = 0.002 ps** and **nsteps = 500000.**

a. Calculate the total simulation time in **picoseconds (ps)** and **nanoseconds (ns)**.

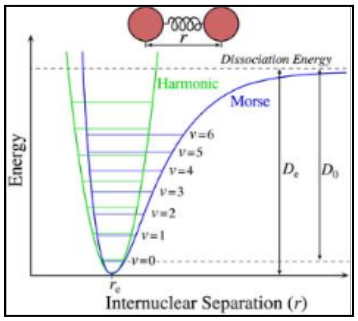
Ans: Total time=nsteps×dt =500000×0.002 ps =1000 ps

Convert to nanoseconds: 1000 ps=1 ns

b. Explain why choosing an appropriate combination of nsteps and dt is crucial in MD simulations.

Ans: A too-short simulation may not capture conformational changes, while too long increases computational cost unnecessarily. If dt is too large, bond vibrations cannot be resolved → simulation may "blow up."

4. The energy vs. internuclear separation graph shows that the Harmonic potential and the Morse potential diverge at large separations. Explain the



crucial physical difference the Morse potential captures that the Harmonic approximation fails to represent.

Ans: **The Morse potential includes bond breaking**, because it flattens out at large distances, meaning the bond can actually separate and the energy stops increasing once the bond is broken.

The Harmonic potential cannot show bond breaking, because it increases energy forever as the atoms move apart. It only works well when atoms vibrate close to the equilibrium bond length.

5. If a computational biologist is primarily interested in performing a sequence alignment to find homologs and calculate the structural property like Radius of gyration, which format is preferred in both case and why?

Ans: **For Sequence Alignment (Homolog Search):** The FASTA format is preferred because it contains only the amino acid sequence, which is the sole input needed for algorithms like BLAST

.ali and .pir format

For Radius of Gyration Calculation: The PDB format,gro,tpr files are required because they contain the **spatial coordinates** (X, Y, Z values) for every single atom. This geometric information is essential to measure the distribution of mass and calculate the radius of gyration.