Biophysics - BIO361
Rubrics - Optional Quiz

Total Marks : 20
Duration : 1h

Part1- Multiple Choice Questions

Total marks - 15*1=15 marks

Each Question is for one mark. No negative marking. Correct answers are written in BOLD letters.

1. A dynamical simulation is performed by carrying out a certain number of structural updates using the Verlet method of equation. Assuming that the simulated phenomenon takes 200 fs to occur, and that a timestep of 0.1 fs is used, how many timesteps are needed?
a) 2,000
b) 200
c) 10
d) 4,000

2. Biomolecular simulation using molecular dynamics or Monte Carlo methods is one of the major fields of computational science nowadays. Which of the following statements is correct?
a) Modelling proteins is harder than modelling simpler systems such as liquid water, as the normal molecular dynamics method cannot be applied to biomolecules.
b) Only small proteins such as crambin can be simulated, given the huge number of solvent and protein atoms present in larger proteins.
c) **Using state-of-the-art codes and computers, it is possible to carry out simulations of systems containing many millions of atoms.**
d) Proteins are modelled using special forcefields describing secondary structure elements such as α-helices instead of the atoms making up the protein.

3. Molecular dynamics approaches use classical mechanics in the form of Newton's laws of motion because:
a) Quantum mechanics only applies to light particles such as electrons.
b) Scientists have not yet developed any methods able to describe motion of atoms using quantum mechanics.
c) Vibrational frequencies of proteins are so incredibly small that it would be dangerous to attempt a quantum mechanical description of them.
d) Given the relatively high mass of atoms, it is often an acceptable approximation to neglect quantum mechanical effects when describing their motion.

4. Which GROMACS command is given to create the following: The topology for the molecule, A position restraint file and a post-processed structure file:
a) editconf
b) pdb2gmx
c) grompp

d) trajconv

5. An MDP file is needed for which of the following steps?
a) Removing water of crystallization from PDB
b) Generating a unit cell for the simulation
c) **Adding ions to the unit cell having the protein and solvent**
d) Removing PBC

6. During the solvation step in the lysozyme in water tutorial, here is the information before solvation:

```
[ molecules ]
; Compound        #mols
Protein_A           1
```

and here is the information after solvation:

```
[ molecules ]
; Compound  #mols
Protein_A       1
SOL         10832
```

, the following changes are being recorded in which file?

a) solv.gro
b) topol.top
c) moleculetype.tpr
d) em.log

7. What is the function of the 'grompp' command in GROMACS?
a) **To generate input files for molecular dynamics simulations**
b) To visualize molecular structures
c) To perform energy minimization
d) To calculate RMSD values

8. Which of the following statements regarding molecular mechanics is untrue?
a) It treats atoms as spheres.
b) It treats bonds as rigid features.
c) It is a computational method.
d) It uses equations that obey the laws of classical physics.

9. In MDsim, what is the role of the force field?
a) Measure molecular weights
b) Describe the magnetic properties of molecules
c) **Model interatomic forces to simulate molecular motion**
d) Determine static molecular structures

10. What is the primary goal of Molecular Dynamics Simulation (MDsim)?
a) Studying static molecular structures
b) **Simulating molecular motions over time**
c) Identifying magnetic properties of molecules
d) Determining molecular weights in dynamic environments

11. What is the purpose of the "equilibration" phase in a GROMACS simulation?
a) To calculate the potential energy of the system
b**) To adjust the simulation temperature and pressure**
c) To visualize the trajectory
d) To generate the final simulation report

12. In MD sim, what is the purpose of a "trajectory"?
a) A specific type of force field
b) A list of neighboring atoms
c) **The path traced by a molecule over time**
d) A method for calculating free energy differences

13. Which factor is NOT typically considered when setting up an MDsim?
a) Temperature
b) Pressure
c**) Gravity**
d) Force field parameters

14. The entropy of a system reaches its minimum at
a) 0 K
b) 303 K
c) 323 K
d) 1000 K

15. What is the correct definition of temperature?
a) Temperature is a physical quantity that expresses quantitatively the attribute of hotness or coldness
b) Temperature is a physical quantity that expresses the attribute of hotness or coldness
c) Both A & B
d) None

Part 2 - Short Answer-type Questions (2.5 marks each)
Total marks - 2.5*2 = 5 marks

1. What is molecular dynamic simulation, why do we need it. Explain what is PBC (0.5+1+1)
   MDS is a computational method that calculates the time-dependent behavior of a molecular system. It helps in exploration of the macroscopic properties of a system through microscopic simulations. It is used to study both thermodynamic properties and for understanding the physical basis of the structure and function of biological macromolecules. Biological molecules exhibit a wide range of time scales over which specific processes occur; for example
   - Local Motions (0.01 to 5 Å, 10^{-15} to 10^{-1} s) – Atomic fluctuations, Sidechain Motions, Loop Motions

- Rigid Body Motions (1 to 10Å, 10^{-9} to 1 s) – Domain Motions(hinge bending), Subunit motions
- Large-Scale Motions (> 5Å, 10^{-7} to 10^{4} s) – Helix-coil transitions, Dissociation/Association, Folding and Unfolding

Periodic boundary condition (PBCs) are a set of boundary conditions which are often chosen for approximating a large (infinite) system by using a small part called a unit cell.

2. What are the ways to check if the protein model is good or not? Name and explain all the steps to improve the accuracy of a protein model? (1+0.5+1)

- Making DOPE score profile using modeller,
- RMSD using pymol and
- Free energy calculations using spdbv. (Any two points are enough)

Advanced Modelling techniques are used to improve the accuracy of the model, which consists of loop modelling, multi template modelling and Modeling using ligand bound to a binding site.