

NPTEL 2024 Assignment Questions
Bioinformatics: Algorithms and Applications

Week 5

1. What is the Euclidean distance between the sequences, ADIKLAAIKL and LKDAAIAIKL using amino acid composition?
 - a. 0.1
 - b. 0.4
 - c. **0.0**
 - d. 0.2

2. Protein secondary structures are formed by ____
 - a. **Hydrogen bonds**
 - b. Hydrophobic interactions
 - c. Electrostatic interactions
 - d. van der Waals interactions
3. Consensus predictions of protein secondary structures are based on
 - a. **Voting**
 - b. Hydrophobicity
 - c. Multiple Sequence Alignment
 - d. All of these
4. Which of the following amino acids is a helix breaker?
 - a. Lys
 - b. Leu
 - c. **Pro**
 - d. His
5. In α -helix, rise per residue is ____
 - a. 1 Å
 - b. **1.5 Å**
 - c. 42 Å
 - d. 2.5 Å
6. Which parameters are used to construct a Ramachandran plot?
 - a. **phi (Φ) and psi (Ψ) angles**
 - b. Protein sequence length and secondary structure content
 - c. Amino acid types and hydrophobicity
 - d. Hydrogen bond strength and solvent accessibility
7. In the command, blastclust -i infile -o outfile -p T -L .7 -b T -S 85, T stands for ____
 - a. DNA
 - b. RNA
 - c. **Protein**
 - d. Lipid
8. Hydrophobicity profile method identifies the secondary structures based on

- a. **Patterns**
 - b. Amino acid frequencies
 - c. Position conservation score
 - d. All of these
9. In Ramachandran plot, the allowed regions for alpha helix conformation are restricted to which quadrants?
- a. I & II
 - b. II & III
 - c. **III & I**
 - d. IV & II
10. Which of the following software is used for constructing non-redundant datasets?
- a. CD-HIT
 - b. Blastclust
 - c. PISCES
 - d. **All of the above**