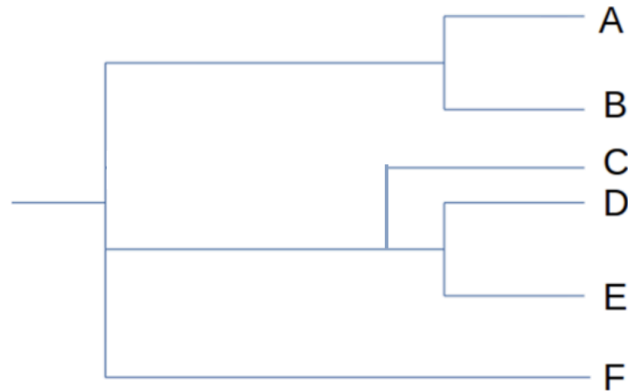


NPTEL 2024 Assignment Questions
Bioinformatics: Algorithms and Applications

Week 4

1. The closest pair of DNA sequences can be obtained from the _____
 - a. **Lowest number of nucleotide mismatches**
 - b. Highest number of nucleotide mismatches
 - c. Average number of nucleotide mismatches
 - d. Lowest number of nucleotide matches
2. Which of the following conditions define an amphipathic alpha helix?
 - a. **Four edges in which 1 & 2 have low and 3 & 4 have high hydrophobicity**
 - b. Four edges in which 1 & 3 have high and 2 & 4 have low hydrophobicity
 - c. Four edges in which 1 & 3 have low and 2 & 4 have high hydrophobicity
 - d. Two edges in which 1 has high and 2 has low hydrophobicity
3. Normalize the numbers 3, 6, 10, 15, 8 between 0 and 1
 - a. 0.0, 0.35, 0.58, 1.0, 0.42
 - b. **0.0, 0.25, 0.58, 1.0, 0.42**
 - c. 0.0, 0.25, 0.65, 1.0, 0.50
 - d. None of the above
4. The molecular weight of the peptide **LDEAQE** is [Ala: 85; Cys: 115; Asp: 130; Glu: 150; Phe: 160; Gly: 70; His: 150; Ile: 125; Lys: 145; Leu: 125; Met: 143; Asn: 130; Pro: 110; Gln: 140; Arg: 170; Ser: 100; Thr: 115; Val: 110; Trp: 200; Tyr: 175]
 - a. 780
 - b. 674
 - c. 870
 - d. **690**
5. What is the expansion of PSSM?
 - a. Point specific scoring matrix
 - b. **Position specific scoring matrix**
 - c. Position specific scanning matrix
 - d. Point specific scanning matrix
6. What is the average hydrophobicity of the peptide **CMPINFGREAT** (A,C,G,M,Y:1; F,I,L,V,W: 2; D,E,H,K,R: -2; N,P,Q,S,T: -1)?
 - a. **0.09**
 - b. -0.09
 - c. 1
 - d. -1

7. The Newick format for the following tree is _____



- a. ((A,B),(C,D),(E,F))
 - b. ((A,B,C),(D,(E,F)))
 - c. ((A,B),C,(D,(E,F)))
 - d. ((A,B),(C,(D,E)),F)**
8. How many unrooted trees can be obtained using 4 sequences?
- a. 1
 - b. 3**
 - c. 15
 - d. 47
9. Which of the following is a measure of the genetic distance between two species on a phylogenetic tree?
- a. Clade
 - b. Branch length**
 - c. Node
 - d. Root
10. _____ is a plot of hydrophobicity indices of residues against their sequence numbers
- a. Hydrophobicity profile**
 - b. Contact Map
 - c. Ramachandran plot
 - d. PAM