

NPTEL 2024 Assignment Questions
Bioinformatics: Algorithms and Applications

Week 1

1. In a protein sequence, amino acids are linked together through _____ bonds
 - a. Phosphodiester bond
 - b. Peptide bond**
 - c. Hydrogen bond
 - d. Disulfide bond
2. The GC content of the DNA sequence “ACGCGAATGC” is _____ %
60
3. Purines have
 - a. No aromatic rings
 - b. One aromatic ring
 - c. Two aromatic rings**
 - d. Both one and two aromatic rings
4. What is the composition of negatively charged amino acid residues in the sequence MKMLGKKLDPIILXEKKLLL?
 - a. 5%
 - b. 10%**
 - c. 0%
 - d. 25%
5. What is the contribution of information technology in bioinformatics?
 - a. Draw structures
 - b. Evaluate the statistical significance
 - c. Understand the structure and function of biological macromolecules
 - d. Develop databases and web servers**
6. Average hydrogen bonding energy for the sequence GTACC is (GT: -6; TA: -8; AC: -7; CC: -9; CG: -12) _____
 - a. -8.75
 - b. -7.5**
 - c. -14
 - d. -17.5
7. Which of the following is the stop codon?
 - a. UCU
 - b. UAA**
 - c. UUU
 - d. UAU
8. In DNA binding proteins, the interface residues have the preference for _____
 - a. Hydrophobic amino acids
 - b. Positively charged amino acids**
 - c. Negatively charged amino acids
 - d. Sulphur containing amino acids

9. Difference between DNA and RNA is observed at
- a. Sugar level only
 - b. Base level only
 - c. Both a and b**
 - d. None of the above
10. How many trinucleotide codons can be formed from DNA bases (A, T, G, C)?
- a. 64**
 - b. 32
 - c. 16
 - d. 20

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Week 2

1. Rank the amino acids, V, D, L, A, and T in the increasing order of polarity
 - a. **L, V, A, T, D**
 - b. T, A, V, L, D
 - c. D, V, L, A, T
 - d. T, A, L, V, D
2. The major functional role of insulin is _____
 - a. Enhancing catalytic activity
 - b. Transport of molecules
 - c. **Regulating sugar metabolism**
 - d. All the above
3. The presence of a gap in an alignment refers to
 - a. Only Insertions
 - b. Only Deletions
 - c. **Both insertions and deletions**
 - d. Substitutions
4. For the following alignment (match score: 2; mismatch score: 0, gap: -2) what is the net score?

AGGTGTG
ACGA--G

 - a. **2**
 - b. 3
 - c. 4
 - d. 1
5. Which among the following PAM matrix is the most appropriate for aligning closely related sequences?
 - a. **PAM-1**
 - b. PAM-250
 - c. PAM-500
 - d. PAM-1000
6. Which of the following group contains only aromatic amino acids?
 - a. Trp, Tyr and Thr
 - b. Phe, Met and Cys
 - c. **Trp, Phe, and Tyr**
 - d. Gly, Val, and Ile
7. _____ is an enzyme that facilitates the conversion of ethanol to acetaldehyde.
 - a. Carbonic anhydrase
 - b. **Alcohol dehydrogenase**
 - c. DNA polymerase

- d. Amylase
8. How many major classes of enzymes are typically recognized in biochemistry?
- a. 2
 - b. 4
 - c. 6**
 - d. 8
9. _____ are membrane proteins that selectively allow ions to pass through the membrane.
- a. Receptors
 - b. Channels**
 - c. Adhesion proteins
 - d. Pumps
10. _____ enhances the complexity of sequence alignment by increasing the number of possible alignments.
- a. Mutations
 - b. Substitutions
 - c. Insertions and Deletions**
 - d. None of the above

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Week 3

1. In PAM 250 matrix, which of the following mutations is acceptable?
 - a. **Glu to Asp**
 - b. Lys to Cys
 - c. Glu to Arg
 - d. Glu to Val
2. Which of the following is/are true for FASTA format?
 - a. **It starts with '>'**
 - b. It ends with a '\$'
 - c. It contains uppercase letters only
 - d. Both (a) and (b) are true
3. The sequence identity of the following sequence alignment is ____ %

AVEGTDFKLI
ATLGIDHKAY

40

4. Which of the following software is used for multiple sequence alignment?
 - a. **MAFFT**
 - b. AL2CO
 - c. BLAST
 - d. FASTA
5. What is the similarity (positives) between Homo sapiens (human) and Lagothrix lagotricha (monkey) myoglobin?
 - a. 69.8%
 - b. 89.6%
 - c. **92.9%**
 - d. 60.2%
6. In the given Needleman-Wunsch alignment matrix, the value of X is _____.
Match: 4; Gap: -2; Mismatch: -1.

		A	T	C
	0	-2	-4	-6
A	-2	4	2	
G	-4	2	X	
T	-6			

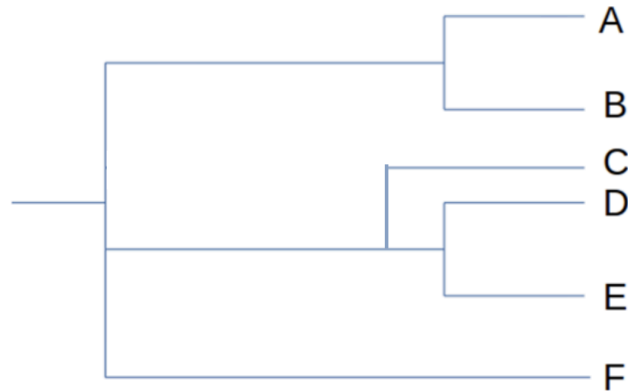
7. The conservation score at position 1 for the following multiple sequence alignment obtained with unweighted frequency and entropy-based measure is
- ```
 123456789
MVLSPLDKT
AVLSPADKT
MVLSPVDKT
CSAADKTNV
MVLSPADKT
```
- a. 0.95  
**b. -0.95**  
c. -0.32  
d. 0.31
8. If  $n$  is the number of sequences and  $m$  is the length of sequences, the order of complexity in multiple sequence alignment is
- a.  $M+n$   
b.  $m/n$   
**c.  $m^n$**   
d.  $Mn$
9. Local alignment is used for identifying
- a. Overall alignment efficiency  
**b. Similar sub-sequences**  
c. Number of gaps  
d. Number of mismatches
10. Which of the following software is used for calculating the conservation score?
- a. Clustal  
b. CD-HIT  
**c. AL2CO**  
d. BLAST

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**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



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**Week 5**

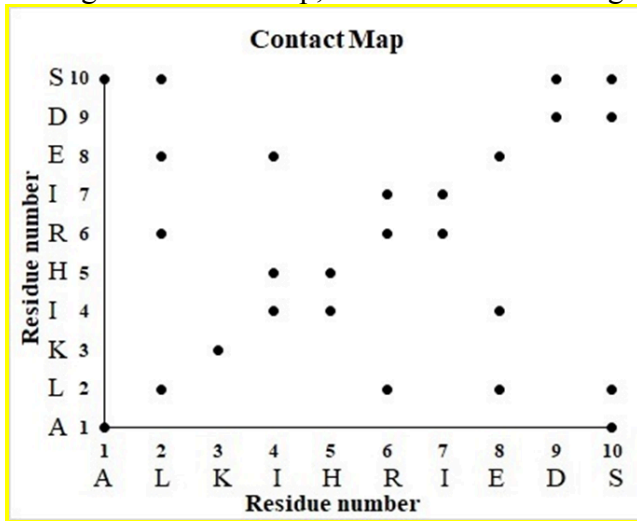
1. What is the Euclidean distance between the sequences, ADIKLAAIKL and LKDAAIAIKL using amino acid composition?
  - a. 0.1
  - b. 0.4
  - c. **0.0**
  - d. 0.2
  
2. Protein secondary structures are formed by \_\_\_\_
  - a. **Hydrogen bonds**
  - b. Hydrophobic interactions
  - c. Electrostatic interactions
  - 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  $\alpha$ -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 ( $\Phi$ ) and psi ( $\Psi$ ) 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**

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**Week 6**

1. In Protein Data Bank, most of the known three-dimensional structures of proteins are determined by the method, \_\_\_\_\_
  - a. Circular Dichroism
  - b. NMR spectroscopy
  - c. X-ray crystallography**
  - d. Cryo-Electron microscopy
2. Temperature factors of less than 75 in a protein structure shows that the atom is \_\_\_\_\_
  - a. Rigid
  - b. Flexible**
  - c. Located in a fixed position
  - d. None of the above
3. From the given contact map, which of the following residues form long-range contacts?



- a. I4 and E8
  - b. D9 and S10
  - c. K3 and S10
  - d. L2 and E8**
4. Which method provides the information on atomic level solvent accessibility?
    - a. HBPLUS
    - b. NACCESS**
    - c. DSSP
    - d. ASAview
  5. Which of the following is not a protein visualization software?
    - a. Pymol
    - b. Rasmol
    - c. Jmol
    - d. None of the above**
  6. Proteins with segregation of alpha helices and beta strands belong to \_\_\_\_ class

- a. All alpha class
  - b. All beta class
  - c. Alpha+Beta class**
  - d. Alpha/Beta class
7. If the atoms of a particular residue have an occupancy of less than 1, it implies that
- a. The residue is said to assume alternate conformations.**
  - b. The residue is missing in some cases.
  - c. The residue is flexible.
  - d. The residue is not conserved.
8. Which databases contain information on structural classes of proteins?
- a. SCOP and UniProt
  - b. CATH and EMBL
  - c. SCOP and CATH**
  - d. DALI and CATH
9. Extended state accessible surface area (ASA) of a residue X can be obtained from the ASA of tripeptides,
- a. Gly-X-Gly**
  - b. Gly-X-Ala
  - c. Lys-X-Lys
  - d. Ala-X-Gly
10. X-ray crystallography provides information on \_\_\_\_\_ to determine protein three-dimensional structures?
- a. Electron density map**
  - b. X, Y, Z coordinates
  - c. Alpha helices and beta strands
  - d. Sequence alignment

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**Week 7**

1. The free energy change between folded and unfolded states of a protein is in the range of
  - a. 0-5 kcal/mol
  - b. 5-25 kcal/mol**
  - c. 50-100 kcal/mol
  - d. 100-500 kcal/mol
2. Which of the following method is used for measuring the folding free energy?
  - a. Circular dichroism**
  - b. Isothermal calorimetry
  - c. X-ray crystallography
  - d. All of these
3. Side chain modelling is generally performed using
  - a. Available rotamer libraries**
  - b. Random search
  - c. Systematic search
  - d. None of the above
4. Comparing solid, liquid and gas, which medium has the minimum entropy?
  - a. Solid**
  - b. Liquid
  - c. Gas
  - d. All the states have the same entropy
5. PDBparam provides information on
  - a. Protein 3D structure based parameters**
  - b. Protein sequence based parameters
  - c. DNA 3D structure based parameters
  - d. DNA sequence based parameters
6. The amount of heat used or released in a system at constant pressure is termed as \_\_\_\_\_
  - a. Internal Energy
  - b. Volume
  - c. Enthalpy**
  - d. Entropy
7. What is the nature of a process when the value of  $\Delta G$  (Gibbs free energy) is positive?
  - a. Spontaneous
  - b. Non-Spontaneous**
  - c. Equilibrated
  - d. None of the above
8. Hydrophobic free energy is related to \_\_\_\_\_
  - a. Contact between amino acid residues
  - b. Solvent accessibility**
  - c. Center of mass

- d. Relative mutability
9. If N-H...O forms a hydrogen bond, identify the hydrogen bond donor:
- N
  - H
  - O
  - N-H
10. Consider atomic mass for C, N and O as 12, 14 and 16, respectively, what is the center of mass for Gly with the following X, Y and Z coordinates?

|      |     |    |     |   |    | X   | Y   | Z   |
|------|-----|----|-----|---|----|-----|-----|-----|
| ATOM | 457 | N  | GLY | A | 58 | 6.3 | 4.5 | 8.7 |
| ATOM | 458 | CA | GLY | A | 58 | 6.1 | 3.5 | 8.6 |
| ATOM | 459 | C  | GLY | A | 58 | 7.4 | 2.8 | 9.1 |
| ATOM | 460 | O  | GLY | A | 58 | 7.4 | 1.6 | 9.5 |

- 6.8, 3.0, 9.0**
- 6.8, 2.8 and 8.0
- 7.1, 2.1 and 7.8
- 6.5, 2.5 and 6.2