NPTEL 2024 Assignment Questions
Bioinformatics: Algorithms and Applications

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