

**Note :—** Attempt ALL questions.

1. Explain the following terms :
  - (a) BLOSUM
  - (b) Progressive alignment
  - (c) E-value
  - (d) FASTA
  - (e) Promoter
  - (f) Motif
  - (g) Phylogeny
  - (h) Cladogram
  - (i) Emission Probability
  - (j) Perceptron. 10×1½=15

2. Align following sequences using Needleman Wunsch algorithm. Use identity matrix for scoring :

Sequence 1 : TTGCCGGCATT

Sequence 2 : TGCCGCATTA.

**OR**

Mention tools used for searching homologous sequences in database. Discuss different types of BLAST and their application. 15

3. Explain methods used for genome sequence assembly.

**OR**

Discuss methods used for prediction of gene. 15

4. What is a neural network ? Explain its application in bioinformatics.

**OR**

What is Hidden Markov Model ? Explain one application of HMM. 15

5. What are molecular markers ? Explain molecular clock theory.

**OR**

What is clustering ? Explain different types of evolutionary tree. 15

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