



- iv) HMM stands for
- a) Hidden Markov of Model
 - b) Hidden Material Method
 - c) Hidden Markov Model
 - d) None of these.
- v) Which one of the following does not match with the rest three ?
- a) PDB
 - b) NCBI
 - c) EMBL
 - d) ORF.
- vi) Similar sequences in two different organisms that have been derived from a common ancestor sequence is
- a) *Homologs*
 - b) *Orthologs*
 - c) *Paralogs*
 - d) *Xenologs*.
- vii) UPGMA stands for
- a) Unweighted Pair Group Method with Arithmetic Mean
 - b) Unpair Group Method with Arithmetic Mean
 - c) Unweighted Pair Group Method with Mean Arithmetic
 - d) None of these.
- viii) Which one of the following is the appropriate tool for a description of a sequence line with the symbol >
- a) FASTA
 - b) BLAST
 - c) MMD
 - d) None of these.

In Pursuit of Knowledge and Excellence

- In Pursuit of Knowledge and Excellence*

In Pursuit of Knowledge and Excellence

In Pursuit of Knowledge and Excellence

In Pursuit of Knowledge and Excellence

In Pursuit of Knowledge and Excellence

- In Pursuit of Knowledge and Excellence*



GROUP – C

(Long Answer Type Questions)

Answer any *three* of the following. $3 \times 15 = 45$

7. a) Briefly describe dynamic programming.
b) What is multiple sequence alignment ? What is the goal of multiple sequence alignment ?
c) Explain simultaneous methods and progressive methods for multiple alignments ? $5 + 5 + 5$
8. a) Write down the differences between PAM matrix and BLOSUM matrix with examples. Which one is better ? Justify your answer.
b) Write down steps of the FASTA. $8 + 7$
9. a) What is Gen Bank ? Explain the structure of Gen Bank entries.
b) Why do we create secondary databases ? $10 + 5$
10. a) Why is HMM required for symbol identification ? How is it used ?
b) Describe Vetervi algorithm in HMM. $(5 + 5) + 5$
11. a) Using the Smith Waterman algorithm, construct the partial alignment score table for the following two sequences. Assume the scoring parameters + 1 for match score, 0 for mismatch score and – 1 for gap penalty.
Sequence 1 : ATGCGCTACGTATT
Sequence 2 : ATGCGCT
b) Write the differences between Needleman - Wunsch algorithm and Smith Waterman algorithm with an example. $10 + 5$
12. Write short notes on any *three* of the following : $7\frac{1}{2} + 7\frac{1}{2}$
 - a) Protein folding
 - b) Chao-Fasman algorithm
 - c) Treading.