(i) Printed Pages : 2 Roll No. ....

(ii) Questions : 7 **Sub. Code :** | 1 | 0 | 0 | 2 |

Exam. Code : | 0 | 0 | 4 | 1 |

B.Sc. (Hons.) Bioinformatics 3rd Semester

(2122)

COMPUTATIONAL METHODS IN BIOMOLECULAR SEQUENCE AND PHYLOGENETIC ANALYSIS

Paper : BIN-3002

Time Allowed : Three Hours] **[Maximum Marks : 60**

Note :— Attempt **FIVE** questions in all. Q. No. **1** is compulsory. Select at least **TWO** questions from each unit.

1. Answer briefly :
   (a) Phylogram
   (b) UPGMA
   (c) Consensus
   (d) CDD
   (e) PSSM
   (f) Rooted tree
   (g) Pattern representations
   (h) Sequence profile. 8×1.5

UNIT—I

2. (a) How are Motifs different than Domains ? 6

   (b) Describe the definition and significance of sequence patterns. 6

3. Discuss the principle and applications of PSI-BLAST. 12

4. (a) Write short notes on :

   (1) PRATT

   (2) SMART. 6

   (b) How is InterPro used as a tool for searching patterns and profiles in protein ? 6

UNIT—II

5. (a) Define OTUs, Monophyletic Taxon and Dichotomy. 6

   (b) What are MEGA packages for Phylogenetic analysis ? 6

6. Discuss the character based methods for Phylogenetic Tree Construction. 12

7. Write notes on :

   (1) Bootstrapping

   (2) Jackknifing. 12