

(i) Printed Pages : 2

Roll No.

(ii) Questions : 7

Sub. Code :

1	3	8	2	7
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Exam. Code :

5	0	5	2
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B.Sc. (Hons.) (Bio-Technology) FYUP 2nd Semester

(2056)

FUNDAMENTALS OF BIO-INFORMATICS-II

Paper : BIFM201 (Common with B.Sc. Bio-Informatics

2nd Sem. FYUP)

Time Allowed : 3 Hours]

[Maximum Marks : 60

Note :— Attempt Five questions in all, selecting TWO questions from each UNIT. Question 1 is compulsory.

1. Short answer questions (Compulsory) : 2×6=12

- (1) What is the Sum of Pairs scoring function?
- (2) Block based alignment
- (3) Clustal Omega
- (4) Define Clade, Monophyletic taxon.
- (5) Newick format
- (6) Homoplasy.

UNIT—I

2. (a) Explain the Progressive Alignment method of Multiple Sequence Alignment (MSA). 7
- (b) What are the applications of Multiple Sequence Alignment? 5

3. (a) Is Dynamic programming feasible for Multiple sequence Alignment? Explain your answer briefly. 4
- (b) Describe briefly Heuristic algorithms for Multiple Sequence Alignment. 8
4. (a) Compare CLUSTAL Omega vs T-COFFEE. Which of these is more accurate and why? 3+2
- (b) Explain the concept of Iterative alignment in Multiple sequence alignment. 4
- (c) Phylogram vs. Cladogram. 3

UNIT—II

5. (a) What are rooted and unrooted trees? Calculate the number of unrooted trees when the number of taxa is four. 3+3
- (b) Explain the Maximum Parsimony method of tree construction. 6
6. (a) Name the different Distance based approaches used for Phylogenetic tree determination. Explain Neighbor Joining method in detail. 7
- (b) What is PHYLIP? Explain briefly. 5
7. (a) Write a short note on PDB database. 6
- (b) Explain the Hierarchical classification system of SCOP. 6