

(i) Printed Pages : 2

Roll No. ....

(ii) Questions : 9

Sub. Code :

0	9	8	4
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Exam. Code :

0	0	3	7
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B.Sc. (Hons.) Biotechnology 5<sup>th</sup> Semester

(2123)

BIOINFORMATICS (Common with Tools in Bioinformatic)

Paper : BIOT-503-T

Time Allowed : Three Hours]

[Maximum Marks : 67

Note :— Attempt *five* questions in all, including Question No. 1 which is compulsory and select *one* question from Units I—IV. All parts of a question should be done in continuation.

1. (a) Pairwise alignment.
- (b) PAUP.
- (c) Profiles.
- (d) Nucleotide Substitution.
- (e) Global alignment.
- (f) Q3score.
- (g) Bit score.
- (h) GenScan.
- (i) Tertiary structure of protein.
- (j) Consensus sequences.

10×1.5



## UNIT—I

2. (a) Discuss the significance of Bioinformatics technology. 6  
(b) Write a note on SCOP. 7
3. (a) Explain the structure of Pfam database. 5  
(b) Describe the construction and uses of PDB. 8

## UNIT—II

4. (a) Discuss the construction of BLOSUM matrices. 8  
(b) Write a note on the application of BLASTP. 5
5. (a) Explain any method used for pairwise sequence alignment. 8  
(b) Discuss the algorithm of BLAST. 5

## UNIT—III

6. Discuss the methods used for phylogenetic tree construction. 13
7. (a) Differentiate between Phylogram and Cladogram. 6  
(b) Explain the applications of Phylogenetic analysis. 7

## UNIT—IV

8. (a) Write a note on the significance of genome annotation. 6  
(b) Discuss the GOR method for protein secondary structure prediction. 7
9. (a) Elaborate on the use of RasMol for protein structure visualization. 6  
(b) How is Glimmer used for gene identification? 7