2316   20

Class–M.Sc.II Sem
Subject –Computational Methods for Sequence Analysis
Paper- BI-524

Time Allowed : 3 Hrs   Maximum Marks : 75

Section – A

Note :- **All the questions are compulsory. Each carries one and half marks.**

(a) What is Dot Matrix?

(b) Which algorithm is used in BLAST?

(c) Write about gene prediction tool used for Eukaryotes.

(d) Define Motif and Domain.

(e) Write about gap penality.

(f) What is Artifical Neural Network?

(g) Define PSI-BLAST.

(h) What is a promotor?

(i) Write about C_pG islands.

(j) What is PILE UP?

Section – B

Unit-I

1. Compare PAM and BLOSUM matrices. Discuss how you decide which matrix to be used during sequence alignment.   12

OR

2. Align ATTGCATGCGCT with ATTCCATGCGCT using Needleman Wunsch algorithm. Use score +1 for match, −1 for mismatch and −2 for gap penality. 12

Unit-II

3. Discuss algorithm of Clustal W and PILE UP. 12

OR

4. Write about BLAST, its various types and explain its algorithm. 12

Unit-III

5. What is multiple sequence alignment? Write about various methods of MSA. 12

OR

6. Explain promotor prediction in E. coli. 12

Unit-IV

7. What is Local and Global alignment? Explain the concept of substitution matrix used in both. 12

OR

8. What is Dynamic Programming? Write about Needleman Wunch algorithm. 12

Unit-V

9. Describe gene prediction in Eukaryotes with atleast two different methods. 12

OR

10. What is Domain? Explain how domain identified in protein structure. Discuss the significance of identifying Domain. 12

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