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Total No. of Pages : 02

Total No. of Questions : 08

M.Tech. (Bio Tech.) (Sem.-3)
ADVANCED BIOINFORMATICS

Subject Code : MTBT-203

M.Code : 23018

Time : 3 Hrs.

Max. Marks : 100

INSTRUCTION TO CANDIDATES :

1. Attempt any FIVE questions out of EIGHT questions.
2. Each question carries TWENTY marks.

1.
 - a) Write a note on NCBI database and its applications.
 - b) Briefly describe PAM and BLOSUM matrices in pairwise alignment.
2.
 - a) Briefly describe different approaches used in multiple sequence alignment. Write a note on clustal W.
 - b) By using Smith and Waterman algorithm align the following sequences:
seq 1: CGTTCTA seq 2: AACGTTGG (Use 5 for match, -3 for mismatch and -4 for gap penalty).
3.
 - a) Briefly describe the CHIP analysis.
 - b) Briefly describe how do you find a motifs for a given protein sequence.
4.
 - a) What are molecular visualization softwares? Discuss about Pymol and its importance.
 - b) Briefly describe structural protein databases and their importance.
5.
 - a) What is QSAR? How does it help to predict activity for new compounds?
 - b) Briefly describe different chemistries involved in Real Time PCR.
6.
 - a) Write a note on Dynamic programming algorithm for sequence alignment.
 - b) Write a note on different phylogentic models used in reconstruction of phylogenetic trees.



7. a) Briefly describe how homology model building will be used in prediction of protein structure.
- b) By using the following distance matrix, reconstruct a phylogenetic tree with By using UPGMA, reconstruct a phylogenetic tree for the following distance matrix :

	A	B	C	D	E	F
B	19	-	-	-	-	-
C	27	31	-	-	-	-
D	8	18	26	-	-	-
E	33	35	41	31	-	-
F	18	1	32	17	35	-
G	13	13	29	14	28	12

8. a) Briefly describe the importance of 2D gel electrophoresis in proteomics.
- b) Briefly describe ^{13}C NMR based metabolic flux analysis.

NOTE : Disclosure of Identity by writing Mobile No. or Making of passing request on any page of Answer Sheet will lead to UMC against the Student.