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## 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 q 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.

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- 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 :

	Α	В	С	D	E	F
В	19	-	-	-	-	-
С	27	31	-	-	-	-
D	8	18	26	-	-	-
Е	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 13C NMR based metabolic flux analysis.

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## 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.