B. TECH.

(SEM. VIII) EXAMINATION, 2006-07

BIOINFORMATICS - III

Time : 3 Hours] [Total Marks : 100

Note : Attempt all questions.

1. Attempt any two parts of the following : 2\times10
   (a) Discuss Needleman and wunsch algorithm with suitable example.
   (b) Define Pairwise sequence alignment. Explain difference between global and local alignments and name the software tools used for the purpose.
   (c) Define Genome annotation. Explain sequence-to-structure-to-function paradigm.

2. Attempt any two parts of the following : 2\times10
   (a) Define the different computational methods of 3-D protein structure modeling and explain computational strategy for homology based 3-D protein structure modeling.
   (b) Explain briefly Genetic algorithm applied in biological system.
   (c) Discuss the applications of ANN in protein structure prediction.

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3 Attempt any two parts of the following: 2x10
(a) Enumerate protein databases with suitable examples.
(b) Discuss the merits and demerits of any tool(s) used for protein structure prediction.
(c) Discuss the concept of ab initio protein folding.

4 Attempt any two of the following: 2x10
(a) What is molecular modeling? Discuss with suitable examples.
(b) Explain various methods for protein-Ligand Docking in drug designing.
(c) Discuss the recent trends in computational Drug designing.

5 Attempt any two parts of the following: 2x10
(a) What is regulatory genomics? How it regulates the expression of desired protein?
(b) Define cDNA and ESTs sequences. Explain the procedure for ESTs library and database development, also give the application of ESTs.
(c) What are motifs? Discuss the purpose of motif finding and also name the suitable software tools required for the purpose.