B. Tech. Biotechnology
(SEM. IV) EXAMINATION, 2006-07
BIOINFORMATICS - I

Time : 3 Hours] [Total Marks : 100

Note : Attempt all questions. All questions carry equal marks.

1 Attempt any two parts of the following:
   (a) Explain briefly about the primary sequence databases of nucleic acids.
   (b) Write short notes on:
      (i) UniGene
      (ii) Saccharomyces Genome database (SGD) and
      (iii) PIR
   (c) Write a note on Protein Data Bank (PDB)

2 Attempt any two parts of the following:
   (a) Write briefly about the Sequence Retrieval System (SRS) and ENTREZ
   (b) Write short notes on:
      (i) PROSITE
      (ii) BLOCKS and
      (iii) The Institute for Genome Research
3 Attempt any **four** parts of the following:
   (a) Explain briefly about the BLOSUM matrices.
   (b) Explain in detail about Smith-Waterman algorithm.
   (c) Distinguish global and local alignment with reference to alignment algorithm.
   (d) Explain how database similarity searches will be done by FASTA
   (e) What is progressive alignment? Describe multiple sequence alignment giving emphasis on CLUSTAL W.
   (f) Explain briefly about PSI-BLAST and PHI-BLAST.

4 Attempt any **two** parts of the following:
   (a) Explain Chou-Fasman and GOR methods for secondary structure analysis of proteins.
   (b) Explain about the Lattice models of protein folding.
   (c) Write a note on microarray data analysis.

5 Attempt any **two** parts of the following:
   (a) Explain briefly on classification of protein structures.
   (b) Write notes on :
       (i) CASP and
       (ii) LINUS.
   (c) Explain briefly about UPGMA and neighbour joining methods of tree building.

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