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M. TECH.**THIRD SEMESTER EXAMINATION, 2008-09****BIOINFORMATICS, GENOMICS & PROTEOMICS**Time : **3 Hours**Total Marks : **100**

- Note : (i) Attempt any **FIVE** questions.
(ii) Marks are indicated against each question.

1. Apply the Needleman – Wunsch Algorithm to determine the best alignment for the following amino acid sequences. 20

Seq 1 – TVVTGRVE

Seq 2 – TVATRIE

Use the match score = +3, mismatch score = -1 and gap penalty = -4
What is the score of the optimal alignment? Back trace the matrix to show all the optimal alignments possible.

2. (a) Explain in detail the shot gun sequencing methodology available for DNA sequencing. 10
(b) Briefly describe the principle and design of DNA microarray along with its specific applications. 10

3. List out the various algorithms available for the prediction of secondary structure of proteins. Discuss in detail the Chou-fasman and GOR algorithms for the same. What are the efficiencies of these methods? 20

4. Explain in detail the various insilico gene prediction strategies employed in the case of eukaryotes, along with their methodologies. 20

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5. (a) Define motif and profile. Given a set of multiple aligned sequences, how will you build a profile for the same? 10
- (b) Write short notes on the following 10
- (i) PROSITE
- (ii) Pfam
6. Discuss in detail the various experimental and the non-homology methods available for the study of protein-protein interactions. 20
7. Write short notes on any **Four** of the following : 5 x 4 = 20
- (a) PSI - BLAST
- (b) Human Genome Project
- (c) ExPASy Proteomics tools
- (d) Structure based approach to assignment of gene function.
- (e) KEGG

