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# M. TECH. (BIOTECHNOLOGY)

THIRD SEMESTER EXAMINATION, 2009-10

## BIOINFORMATICS, GENOMICS AND PROTEOMICS

Time : 3 Hours

Total

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

1. (a) Explain the DNA microarray and its applications in de  
(b) Explain Protein-Protein interaction by different methods

2. Align the given two sequence globally by applying Needleman algorithm using the following inputs:

Match Score = +3

Mismatch Score = -1

Gap penalty = -2

Sequence 1: TAACGT

Sequence 2: AGTCAA

Back trace the matrix to show all the alignments. What is the optimal alignment?

3. Explain any Four in 80-100 words:

(a) Contigs

(b) Chromosome walking

(c) Shotgun sequencing

(d) Maxam Gilbert S

What is Drug and Target? Explain in detail the entire process of drug design in reference to use of latest Bioinformatics tools. 20

Describe various algorithms available for Tertiary structure prediction of proteins. Discuss the Homology Modeling methodology for tertiary structure prediction in detail. 20

Write short notes on the followings: 4 x 5 = 20

- (a) OMIM
  - (b) PROSITE
  - (c) Pfam
  - (d) EMP
- SWISS-PROT

