

**B.Tech. – VIEP – ELECTRONICS AND
COMMUNICATION ENGINEERING
(BTECVI)**

Term-End Examination

December, 2014

00336

BIELE-017 : BIO-INFORMATICS

Time : 3 hours

Maximum Marks : 70

Note : Attempt any **seven** questions. Each question carries equal marks.

1. What is NMR ? Write the possible representation of secondary structure of RNA. Write RNA structure prediction method with explanation. 10
2. What is Microarray ? Write the classification of Microarray. Write in brief the steps involved in a Microarray experiment. 10
3. What is 3D structure alignment ? Explain in brief the different types of 3D structure alignments. Write the use of 3D structure alignment in Bio-Informatics. 10
4. Write in brief a description of the area where MUSTA is used. Explain about MUSTA algorithm for multiple alignment. 10

5. Write short notes on any *two* of the following : $2 \times 5 = 10$
- (a) ID Motifs
 - (b) NLP
 - (c) Genome sequencing
 - (d) Phylogenetic algorithms
6. Explain Hidden Markov Model (HMM). Also describe a bio-informatics application of Hidden Markov Model (HMM). 10
7. Write the working principle of BLAST and FASTA. Also describe the output of a BLAST search. 10
8. What is Bio-Informatics ? What are the three divisions of Bio-Informatics ? Describe the various applications of Bio-Informatics. 10
9. Explain in detail Phylogenetic algorithms. 10
10. Discuss the complexity of an algorithm to reconstruct a genetic network from Microarray Perturbation data. Also write the limitation of genetic networks. 10
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