

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

Term-End Examination

00286

June, 2014

BIELE-017 :BIO-INFORMATICS

Time : 3 hours

Maximum Marks : 70

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

1. What is RNA ? Explain the structure prediction method of RNA. Write the representation of secondary structure of RNA. 10
2. Describe the various applications of bio-informatics. Why is it important ? Write the working principle of BLAST and FASTA. 10
3. What is Bio-informatics ? What are the three divisions of Bio-informatics ? Write the names of some important softwares used in Bio-informatics. Why is it important ? 10
4. What do you mean by multiple sequence alignment ? Explain about different types of sequence alignment. Write the application of multiple sequence alignment in Bio-informatics. 10

5. Write short notes on any *two* of the following : $2 \times 5 = 10$
- (a) Final Thoughts
 - (b) Natural Language Processing
 - (c) Vector Machine applications in Bio-informatics
 - (d) Genome Sequencing
6. Explain Genetic Networks. Write in brief about secondary structure prediction techniques. 10
7. Write the overview of MUSTA algorithm for geometric hashing and multiple alignment. Write its application with brief description. 10
8. Explain about phylogenetic algorithms. Write the method of Join Phylogenetic alignment. 10
9. Describe how you would build a Hidden Markov Model (HMM) to predict protein secondary structure. 10
10. Explain microarray clustering with its complete classification. 10
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