

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

Term-End Examination

December, 2017

00457

BIELE-017 : BIO-INFORMATICS

Time : 3 hours

Maximum Marks : 70

Note : Attempt any seven questions. All questions carry equal marks. Missing data, if any, may be suitably assumed. Use of scientific calculator is allowed.

1. (a) Discuss the applications and challenges in Bioinformatics. 5
- (b) Why is FASTA a more rigorous database search than BLAST ? Compare the algorithm in terms of speed and completeness. 5
2. (a) Discuss the various steps in dynamic programming to perform pair-wise sequence alignment. 5
- (b) What is PSI-BLAST ? Write down its various applications in Bioinformatics. 5

3. Define Microarray. Compare the SAGE with DNA-microarrays. 4+6

4. (a) Explain Xtallography process. 5
 (b) Describe the microarray clustering procedure with its classification. 5

5. (a) Compare 1D-motifs with 3D-motifs. 5
 (b) State the role of MUSTA algorithm in geometric hashing. 5

6. Explain the methodology involved in multiple sequence alignment. Also write down its advantages. 7+3

7. What are Genetic Networks ? How are they useful in predicting a gene-structure ? Write down its applications and advantages. 4+3+3

8. (a) Describe Hidden Markov models. 5
 (b) How will you predict epitomes on a genomic scale ? 5

9. (a) Discuss the phylogenetic algorithm with its various applications. 5
 (b) What are the various applications of comparative genomics algorithm in Bioinformatics ? 5



10. Write down short notes on any *two* of the following : ***2×5=10***

- (a) NMR
 - (b) Proteomics
 - (c) Gene-finding Algorithms
 - (d) 3D Structure Alignment
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