

**B.Tech. – VIEP – COMPUTER SCIENCE AND  
ENGINEERING (BTCSVI)****Term-End Examination****December, 2015****BICSE-008 : BIO-INFORMATICS***Time : 3 hours**Maximum Marks : 70*

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

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1. (a) What are the current approaches for bio-informatics and the problems associated with them ? 5
- (b) What is Gene prediction ? 5
2. (a) What are multiple alignments ? 3
- (b) Describe the methods employed for multiple sequence alignment. 7
3. (a) Define a biological database and its importance. 5
- (b) What are sequence-based database searches ? 5

4. (a) Discuss genetic networks in detail. 5  
(b) How can micro-array data analysis be done ? Explain in detail. 5
5. (a) What is classical NMR spectroscopy ? 5  
(b) Explain integrated genomic maps in detail. 5
6. Explain the computational methods for identification of polypeptides from mass spectrometry. 10
7. (a) Describe dynamic programming for sequence alignment. 5  
(b) Write the MUSTA algorithm for geometric hashing. 5
8. (a) Explain natural language processing and its limitations. 5  
(b) What do you understand by micro-array clustering and classification ? Describe in brief. 5
9. (a) Define structural classification of proteins. 5  
(b) Differentiate between BLAST and FASTA tools for sequence alignment. 5
10. Write short notes on any **two** of the following :  $2 \times 5 = 10$
- (a) Hidden Markov Model  
(b) Xtallography  
(c) RNA Secondary Structure  
(d) 3-D Motifs and Final Thoughts
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