B.Tech. – VIEP – COMPUTER SCIENCE AND ENGINEERING (BTCSVI)

Term-End Examination

00675

June, 2019

BICSE-008 : BIO-INFORMATICS

Time : 3 hours　　　　　　　　*Maximum Marks : 70*

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

1. (a) What is bio-informatics ? Describe its scope in modern biology.　　*5*

    (b) What is Gene Prediction ?　　*5*

2. (a) Write the MUSTA algorithm for geometric hashing.　　*5*

    (b) Explain the natural language processing and its limitations.　　*5*

3. (a) Discuss progressive alignment method employed in multiple sequence alignment problems.　　*5*

    (b) How can Hidden Markov Model framework be applied for Gene Prediction problem ?　　*5*

4. (a) How can micro array data analysis be done ? Explain in detail. *5*

(b) Define Protein – Protein docking algorithms. *5*

5. (a) Discuss in detail about genetic networks. *5*

(b) Write about Hidden Markov Model of multiple sequence alignment. *5*

6. Explain computational methods for identification of polypeptides from mass spectrometry. *10*

7. (a) What are the sequence-based database searches ? *5*

(b) What are the different types of bio-informatics databases ? *5*

8. Explain Critical Assessment of Structure Prediction (CASP) and structures of aligomeric proteins. *10*

9. With the help of suitable example, demonstrate Needleman-Wunsch algorithm. *10*

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

(a) Genome Aligment

(b) RNA Secondary Structure

(c) Multiple-threading Algorithms