00115

# B.Tech. - VIEP - ELECTRONICS AND COMMUNICATION ENGINEERING

## (BTECVI)

## Term-End Examination, 2019

### BIELE-017 : BIO-INFORMATICS

Time : 3 Hours]                    [Maximum Marks : 70

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

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1.   (a)   Explain Kinemages for biological structure.  [5]

     (b)   State the role of MUSTA algorithm in geometric hashing.                          [5]

2.   (a)   Explain phylogenetic algorithms in detail.   [5]

     (b)   What is DNA sequencing ? Explain with suitable diagram.                          [5]

3.   Explain FASTA algorithm. Why is it more rigorous data base search than BLAST ?        [10]

4. What do you understand by multiple sequence alignment ? Write it's application in bio-informatics and also explain different types of sequence alignment.[10]

5. (a) Describe how you would build a HMM (Hidden Marker Model). [5]

   (b) Explain the prediction of epitomes on a genomic scale. [5]

6. (a) Describe vector machine. Explain its principle.[5]

   (b) What are the application of vector machine in bio-informatics ? [5]

7. (a) Explain K. mean clustering in bio-informatics.[5]

   (b) Write short-gun approach for genome sequencing. [5]

8. What is folding problem ? Classify the protesian on the basis of their structure. Write about secondary structure prediction techniques. [10]

9. Discuss the complexity of an algorithm to reconstruct a genetic network from micro array perturbation data. Also write the limitation of genetic network. [10]

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

    (a)    Genetic Networks

    (b)    3D Motifs

    (c)    Xtallography

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