BIELE-017

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

00456 Term-End Examination

June, 2016

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.*

1. What is Bio-informatics ? Explain the relation between Bio-informatics and Computational genomics. What are the advantages and disadvantages of Bio-informatics in day-to-day life ? *10*

2. (a) What is dynamic programming sequence alignment ? Write its significance in relation to Bio-informatics.

   (b) Write the methods of preparation of biological databases. What is the use of these databases ? What are the types of biological databases available ? *5+5=10*

3. (a) What is 3D structure computation ? How is it done ? What is its use ?

    (b) What is NMR ? Enlist its usages. Explain in brief the process of NMR.   *5+5=10*

4. (a) What is Xtallography ? Explain in brief the process of Xtallography.

    (b) Explain in brief about the role of RNA secondary structure used in Bio-informatics.   *5+5=10*

5. What are microarrays ? What are the methods used for microarray clustering ? How do you classify microarrays ? What is the use of microarrays in Bio-informatics ?   *10*

6. (a) What are vector machine applications used in Bio-informatics ?

    (b) Explain the various terminologies and ontologies used in Bio-informatics.   *5+5=10*

7. What is 3D structure alignment ? Explain MUSTA algorithm for geometric hashing and multiple alignment.   *4+6=10*

8. (a) Discuss about Hidden Markov models used in Bio-informatics. What are its salient points ?

    (b) What do you mean by molecular energetic and dynamics ? Explain in brief.

    (c) How do you predict the structure of proteins ? Explain the methods involved.   *4+3+3=10*

9. (a) Discuss about Gene finding algorithms used in Bio-informatics.

(b) What do you mean by Natural Language Processing ? What is its use in Bio-informatics ? *5+5=10*

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

(a) BLAST and FASTA

(b) 1D Motifs

(c) Genetic Networks

(d) Proteomics