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BIELE-017

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

00523

Term-End Examination

December, 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. (a) What do you understand by Bio-informatics ? How is it related to sequences and genomes ? 3

   (b) Describe the sequence analysis in detail considering Genome annotation and Computational evolutionary biology. 4

   (c) Explain about the kinemages for biological structures. 3

2. (a) What is the need of Biological databases ? What is its use in the context of Bio-information ? 3

   (b) Explain the dot matrix and diagram method for comparing sequences. 3

   (c) How are sequences aligned by dynamic programming method ? 4

3. (a) How do you predict RNA secondary structure ? Explain its method. 5

(b) How do you predict protein secondary structure ? Explain with a suitable diagram. 5

4. (a) What is DNA sequencing ? Explain with a suitable diagram. 4

(b) How are sequences stored in a computer ? Which format is used ? 3

(c) How are conversions done from one sequence format to another ? What are the methods available ? 3

5. (a) Describe the methods of sequence alignment. Draw its flow chart and explain briefly. 6

(b) What do you mean by Xtallography ? Explain in brief. 4

6. (a) Explain the vector machine applications in Bio-informatics. 4

(b) Discuss Microarray Clustering and its classification. 4

(c) Describe structural genomics used in Bio-informatics. 2

7. (a) Explain MUSTA algorithm for geometric hashing and multiple alignment. 5

(b) What are 3D Motifs ? Explain in context with Bio-informatics. 5

8. (a) Describe the terminologies and ontologies used in Bio-informatics. 5

(b) Explain the Hidden Markov models to generate an alignment of a set of sequences. 5

9. (a) Give some insight on gene finding algorithms. 4

(b) Explain about molecular energetics and dynamics. 3

(c) What do you mean by Genome Alignment ? 3

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

(a) BLAST and FASTA

(b) NMR

(c) Natural Language Processing

(d) Proteomics