(Following Paper ID and Roll No. to be filled in your Answer Book)

PAPER ID : 9592 Roll No.

B.Tech.

(SEMESTER-IV) THEORY EXAMINATION, 2011-12

BIOINFORMATICS–I

Time : 3 Hours] *[Total Marks : 100*

Note : Answer **all** the Sections.

Section – A

1. Attempt **all** of the following : **10 × 2 = 20**

(a) What is Secondary Database, how is it different from Primary Database ?

(b) What is e-value and how to interpret e-value of a query sequence ?

(c) What is the significance of end-free sequence alignment ?

(d) How PSI-Blast is different from BLAST ?

(e) What are the heuristics which make FASTA algorithm efficient ?

(f) How the scores in Dayhoff's amino acid substitution matrix were being computed ?

(g) Explain Chous-Fasman steps for predicting secondary structure of protein.

(h) What is "Structurally Conserved Region" in homology modelling ?

(i) What do you mean by print-tip normalization in Microarray data analysis ?

(j) Explain one method to align three dimensional structure of protein.

Section – B

2. Attempt any **three** of the following : **3 × 10 = 30**

   (a) Explain the steps involved in Edmund degradation method of protein sequencing.

   (b) Enumerate steps involved in BLAST algorithm with detailed note on e-value of the score.

   (c) Describe briefly the steps of comparative modelling of protein three dimensional structures.

   (d) Differentiate PAM and BLOSSUM. Explain about PAM 250 and how it is different from BLOSSUM 62.

   (e) Explain the Lowess normalization of Microarray data.

Section – C

Attempt **all** questions : **5 × 10 = 50**

3. For given sequences find the score of alignment by Needleman and Wunsch dynamic approach

   Seq 1 : ACCTCG

   Seq 2 : CTGGC

OR

For above given sequences find the score of alignment by Smith Waterman dynamic approach.

4. Give detailed steps of chemical chain termination method of DNA sequencing.

OR

Di-deoxy chain termination method of DNA sequencing.

5. Give steps of K-Mean clustering of Microarray data analysis.

OR

Give Self Organizing Map (SOM) method for Microarray data analysis.

6. Name any three primary databases, with a detailed note on its query engine. How secondary datasets are annotated from primary databases ?

OR

Differentiate the working of SRS and ENTREZ. Give detailed note on Pfam, PROSITE and BLOCK.

7. What do you mean by de-novo-docking and how is it different from structure based drug designing ?

OR

What is torsion angle ? How to find the following torsion angle from given coordinate information of a three dimensional polypeptide chain ?

(a) Omega torsion angle

(b) Phi torsion angle

(c) Psi torsion angle

(d) Chi torsion angle and

(e) Zeta torsion angle