

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

**PAPER ID : 9592**

Roll No.

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**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 Edmond 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
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