Total number of printed pages – 4

B. Tech

CPBT 8309 / PEBT 8301

Sixth Semester Examination – 2008

BIOINFORMATICS

Full Marks – 70

Time : 3 Hours

*Answer Question No. **1** which is compulsory and any **five** from the rest.*

The figures in the right-hand margin indicate marks.

1. Answer the following questions : 2×10

   (a) What is PSI-BLAST ? Why it is advantageous over BLAST ?

   (b) Expand EMBL. Which are the nucleotide databank of EMBL ?

   (c) Define gap penalty. What is its significance in the alignment of sequences ?

P.T.O.

(d) What is threading ? How threading play significant role in protein structure prediction ?

(e) Differentiate between BLOCKS and PROFILES.

(f) What is PAM matrix ? Show an out put for PAM Matrix.

(g) Differentiate between Lattice model and Continuous model of the polymer simulation.

(h) Which one is the potential database for metabolic and regulatory pathways?

(i) What basic tools of CAMD (Computer aided molecular design) you can adopt for ligand designing of protein ?

(j) Name three primary nucleotide sequence repositories along with their locations and functions.

2. (a) What is an 'E-value' ? You do a databank search using FASTA with an aminoacid

sequence as query. The only reported match has an E-value of 10. What does this mean for the similarity and homology of the sequences ? 5

(b) What are the major extensions of BLAST ? Discuss the algorithms used and applications of these programmes. 5

3. What are the sequence and structure databank of protein ? Briefly explain the PIR-PSD and SWIS-PROT database and their application in proteomics. 4+3+3

4. (a) What is sequence alignment ? Differentiate between the algorithms used for local and global alignment study. 5

(b) Calculate the dynamic programming matrix and optical alignment for two DNA sequence 'GAATTC' and 'GATTA', scoring '+2' for matching, '−1' for mismatch and '2' for linear gap penalty. 5

5. What is *In Sillico* secondary structure prediction of protein ? Discuss methods including

logic neural networking and Chao-Fasman algorithms for protein secondary structure prediction. 2+4+4

6. Differentiate between the following : 5×2

   (a) EST and SNP

   (b) SCOP and CATH.

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

   (a) Hidden Markov Model

   (b) Dynamic Programming using distance matrix

   (c) Molecular dynamics in drug designing

8. Define database and data type in bioinformatics. What are the different data types and databases are used for gene structure and gene product function prediction ? Show the out put format of nucleotide database in NCBI using ENTREZ search. 2+5+3