STELLA MARIS COLLEGE (AUTONOMOUS) CHENNAI 600 086
(For candidates admitted from the academic year 2006-07)

SUBJECT CODE : BI/PC/BA35

M. Sc. DEGREE EXAMINATION, NOVEMBER 2007
BIOINFORMATICS
THIRD SEMESTER

COURSE : CORE
PAPER : BIOINFORMATICS AND ITS APPLICATIONS
TIME : 1½ HOURS **MAX. MARKS : 35**

SECTION – A **3X5=15**

ANSWER ANY THREE OF THE FOLLOWING QUESTIONS IN 250 WORDS:

1. What are the different types of gap penalties used in alignment programs?
2. Outline the steps in homology modeling. What is the minimum required sequence similarity between target and template sequences. How do you check for the quality of your model?
3. Explain the algorithms behind local & global alignments.
4. Differentiate between homology, similarity and identity. When two proteins are homologous what does it imply?
5. How do you use BLAST for functional annotation? What is the difference between P value and E value?

SECTION – B **2x10=20**

ANSWER THE FOLLOWING QUESTIONS IN 800 WORDS:

6. What are position specific scoring matrices? In what way does PSIBLAST make use of them?

OR

You are expected to find the differential expression profile of a tumor cell and a normal cell. Design a microarray experiment to do this. Name a web resource for microarray data.

7. How are metabolic pathways reconstructed for completed genomes? Which databases store such information?

OR

Describe FASTA algorithm.

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COURSE : CORE
PAPER : BIOINFORMATICS AND ITS APPLICATIONS – PRACTICAL

TIME : 2 HOURS **MAX. MARKS : 65**

1. Retrieve information pertaining to calcium binding motifs and domains from Prosite and Interpro respectively. Give some representative protein Ids from the results of the two searches. Check out if any of them have PDB structures and list out two PDB IDs. (10 marks)

2. Write a PERL program to accept a nucleotide sequence and a tetranucleotide motif from the user and count the number of occurrences of this motif along with positions of occurrence. (10 marks)

3. Write a PERL program to accept a protein sequence from the user. Validate that the input has no digits in it. Count the number of acidic residues in the sequence. (10 marks)

4. Retrieve the PDB structure with the PDB ID ICRL. What is its resolution and experimental method of determination? Does it have any ligands? If so what re they and what are the ligand protein interactions. Note the secondary structure of this protein and run a secondary structure prediction for the sequence. How does the prediction compare with the actual secondary structure as given by PDB. (15 marks)

5. Retrieve human p53 sequence and run PSIBLAST. You can go upto three iterations. Comment on your results. What was the best and the worst e-value and bit score in the third iteration. What disease(s) is this protein implicated in? (15 marks)

6. Viva 5 marks.

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