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

SUBJECT CODE: BI/PC/BA35

M. Sc. DEGREE EXAMINATION, NOVEMBER 2008
BIOINFORMATICS
THIRD SEMESTER

COURSE : CORE
PAPER : BIOINFORMATICS
TIME : 1 ½ HOURS **MAX. MARKS: 35**

SECTION – A **3X5=15**

ANSWER ANY THREE OF THE FOLLOWING QUESTIONS IN 250 WORDS:

1. What is one PAM unit of evolutionary distance? Discuss the construction of PAM matrices.
2. Name any two protein folds from SCOP. Can two sequences with low sequence similarity adopt the same fold? Justify your answser. Can a protein fold form a scaffold for diverse functions?
3. What is hash table look up in FastA algorithm? Explain with an example.
4. Why do organisms have codon bias? Given the codon bias information of different species, suggest an application of this data.
5. What are the steps used for developing a homology model?

SECTION – B **2x10=20**

ANSWER THE FOLLOWING QUESTIONS IN 800 WORDS:

6. How does one perform a multiple sequence Alignment? Describe the use of ClustalW Add a note on the assessment of Alternative multiple sequence Alignment Algorithms.

(OR)

a) What are the resources available on the web for gene expression data and analysis.
b) What are the different clustering techniques used in microarray analysis.

7. a) A protein query sequence is searched against the non redundant database using BLAST. What is the effect of changing the scoring matrices?
b) PSIBLAST is used to find remote homologs. Explain the principle behind this.

(OR)

How do you do a Protein Expression Analysis of cells? Describe the process of mining data from yeast.

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