STELLA MARIS COLLEGE (AUTONOMOUS) CHENNAI –600 086
(For candidates admitted during the academic year 2008-09 & thereafter)

SUBJECT CODE: BY/PC/BF24

M. Sc. DEGREE EXAMINATION, APRIL 2009
BIOTECHNOLOGY
SECOND SEMESTER

COURSE : MAJOR CORE
PAPER : BIOINFORMATICS
TIME : 3 HOURS **MAX. MARKS: 100**

SECTION – A (20 MARKS)

I CHOOSE THE CORRECT ANSWER: (1 x 5 = 5)

1. Which Heat Shock Protein' (HSP) family is involved in forming a 'folding cage'.
   a) HSP 60 b) HSP 70 c) HSP 80 d) HSp 65
2. A model which shows the amino acid probability distribution for each position in the family.
   a) matrix b) statistical profile c) patterns d) Regular expressions
3. The SMILES notation for acetic acid is
   a) CCOO b) COC c) CC (=O) O d) None of the above
4. A sequence database with annotated collection of all publicly available nucleotide sequences and their protein translations.
   a) Gen Bank b) PIR c) TAIR d) none of the above
5. The most widely used RNA secondary structure programme.
   a) M P Fold b) M Fold c) Motif d) none of the above

II FILL IN THE BLANKS WITH THE APPROPRIATE ANSWER: (1 x 5 = 5)

6. The simplest and commonest format for DNA / protein sequence is a _____ _____.
7. _____ and _____ are primary protein sequence database.
8. In scaled trees, each _____ _____ is proportional to the number of changes.
9. Structural domains are also known as _____.
10. In haploid organisms, the genome size refers to the total amount of _____ in the genome.

III EXPAND THE FOLLOWING: (1 x 3 = 3)

11. OFAGE
12. UPGMA
13. SCOP

..2

IV STATE WHETHER TRUE OR FALSE: (1 x 5 = 5)

14. Kyte – Doolittle algorithm is employed in MSA.
15. Resolvase enzyme acts on the unprocessed copies of transposons.
16. Retrotransposons are mobile elements that transpose via RNA intermediate.
17. NMR is used to detect metabolites.
18. The first genetic map was created by Morgan and Sturtevant.

V. DEFINE IN ONE OR TWO SENTENCES (2 x 1 = 2)

19. 1 Pam:
20. kTUP:

SECTION – B

ANSWER ANY FOUR OF THE FOLLOWING QUESTIONS IN NOT MORE THAN 600 WORDS. All QUESTIONS CARRY EQUAL MARKS. DRAW DIAGRAMS WHEREVER NECESSARY. (4 x 10 = 40)

21. Present the aim of Blast software: i) Describe in words how the algorithm works ii) Describe the output of a Blast search.
22. Explain the different methods of reconstructing phylogenetic trees.
23. Describe the various steps used in Multiple Sequence Alignment.
24. Sequences alignment can be local or global. Discuss with suitable examples.
25. Write notes on: a) A bioinformatics application of Hidden Markov Models
    b) Swiss Prot
    c) NCBI
26. How does one find specific genes in a Eukaryotic Genome? TrEMBL
27. Elaborate on the different types of DNA microarrays.

SECTION – C

ANSWER ANY TWO OF THE FOLLOWING QUESTIONS IN NOT MORE THAN 1200 WORDS. All QUESTIONS CARRY EQUAL MARKS. DRAW DIAGRAMS WHEREVER NECESSARY. (2 x 20 = 40)

28. a) Discuss the various DNA sequencing technologies that you have studied.
    (OR)
    b) Describe with one example the Needleman-Wunsch algorithm. How would you construct a BLOSUM matrix?

29. a) Describe the various mechanisms for predicting RNA secondary structure
    (OR)
    b) Describe the various steps involved in designing and developing a drug for commercial use.

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