

STELLA MARIS COLLEGE (AUTONOMOUS) CHENNAI 600 086
(For candidates admitted during the academic year 2004– 05)

SUBJECT CODE: BT/MO/IB64

B.Sc. DEGREE EXAMINATION, APRIL 2007
BRANCH V (a) – PLANT BIOLOGY AND PLANT BIOTECHNOLOGY
SIXTH SEMESTER

COURSE : MAJOR – OPTIONAL
PAPER : INTRODUCTION TO BIOINFORMATICS
TIME : 3 HOURS **MAX. MARKS: 100**

SECTION – A

I FILL IN THE BLANKS: (6X1=6)

1. The full form of KEGG is _____
2. The default e-value in BLAST is _____
3. GO stands for _____
4. The terminal nodes in a phylogenetic tree are called _____
5. Chou Fasman Method is used in the prediction of _____
6. Cytogenetic maps are _____ maps.

II TRUE OR FALSE: (6X1=6)

7. Clustering techniques are used in microarray analysis.
8. The Multiple sequence alignment program ClustalW uses local alignment.
9. PAM matrices were developed by Henikoff.
10. BLOSUM 80 is derived from highly divergent sequences.
11. A BLAST hit with a good score and an e-value of 0.0 is significant.
12. Tryptophan is coded by a single codon.

III MULTIPLE CHOICE: (6X1=6)

13. Which of these is not a distance based method of phylogenetic tree construction
a) Neighbour Joining b) Fitch Margolish c) Maximum Parsimony
d) UPGMA
14. CDD (Conserved Domain Database) is derived from
a) PRINTS b) InterPro c) Pfam and SMART d) BLOCKS
15. k- tuple method is used in this
a) FastA b) BLAST c) CLUSTAL d) PHYLIP
16. Twilight zone is a zone where sequence similarity is between
a) 0-20% b) 0-35% c) 0-40% d) 0-45%
17. A hybrid approach incorporating elements of both pairwise & multiple sequence alignment methods is
a) PAUP b) PSI-BLAST c) CDD d) T-BLASTX
18. A secondary resource which provides a bridge between single-motif search methods & domain – alignment profile methods is
a) BLOCKS b) BLOSUM c) PRINTS d) PROSITE

IV SHORT ANSWERS NOT EXCEEDING 50 WORDS: (6x3=18)

19. What are contigs?
20. What are structural motifs in proteins? Give an example.
21. What is Alternative Splicing?
22. What are ORFs? How many frames of translation are conceptually possible for a nucleotide sequence.
23. What are composite databases? Give an example.
24. What are sequence motifs? In the motif VG {AL} GG what does {} signify?

SECTION – B**ANSWER ANY FOUR NOT EXCEEDING 300 WORDS (4X6=24)**

25. Discuss Maxam Gilbert method of DNA sequencing.
26. What are Genetic linkage maps? What are the map units used?
27. What is string alignment and how do you score it? Name two gap penalty schemes used in scoring.
28. What is functional annotation? When a new genome is sequenced discuss how BLAST can be used for functional annotation.
29. Discuss briefly RNA secondary structure prediction.
30. Why is prokaryotic gene finding relatively easier than eukaryotic gene finding?
31. Write a short note on COGs database.

SECTION – C**ANSWER ANY TWO NOT EXCEEDING 1200 WORDS: (2X20=40)**

32. Discuss
 - a) Any one method of phylogenetic tree construction.
 - b) Application of DNA chips in comparative genomics.
33. Discuss the steps involved in *silico* drug discovery process.
34. Describe the steps in BLAST algorithm. What is e-value, raw score and bit score? Why is a local alignment of protein sequences considered significant?
35. Discuss Needleman and Wunsch algorithm for global alignment. When is it more appropriate to go for a global alignment?
