

STELLA MARIS COLLEGE (AUTONOMOUS) CHENNAI 600 086
(For candidates admitted from the academic year 2004-2005 & thereafter)

SUBJECT CODE: BT/MO/IB64

B.Sc. DEGREE EXAMINATION, APRIL 2010
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. Choose the correct answer (4×1=4)

1. The term gene was coined by
a) Johansson b) Mendel c) Morgan d) Watson
2. The actual location of genes on chromosome is determined by _____ mapping.
a) Chemical b) genetic c) physical d) loop
3. Which of the following displays the result of BLAST researches that have been done for every protein sequence?
a) SMART b) BLINK c) BEAUTY d) PROW
4. In alpha helix, how many amino acid residues are present per turn?
a) 4 residues b) 3.9 residues c) 2 residues d) 3.6 residues

II. State true or false (4×1=4)

5. Computer scanning of database can be done by BLAST search.
6. When the backbone of a polypeptide chain is extended, it forms alpha helix.
7. DNA sequence of the whole genome of *Arabidopsis thaliana* is yet to be completed.
8. In Drug design, the set of features common to the series of active molecule is known as proteome.

III. Fill in the blanks (5×1=5)

9. The region of chromatin which is densely packed and stained diffusely during interphase is called _____.
10. Fredrick Sangers method is also called chain _____ method.
11. The collection of the biological data on a computer appearing as varying arrangements and subsets is regarded as a biological _____.
12. A signal molecule is also known as a _____.
13. The 3-D structure of pharmacore database is _____.

IV. Match the following**(5×1=5)**

- | | |
|--------------------------|--------------------|
| 14. AUG | a) protein |
| 15. Macrorestriction map | b) terminator |
| 16. Tertiary structure | c) gene expression |
| 17. Markers | d) initiation |
| 18. DNA microarray | e) high resolution |
| | f) SNP |

V. Answer any six the following, each within 50 words**(6× 3=18)**

19. Triplet
20. cDNA map
21. FASTA
22. The primary structure of proteins
23. Linear space optimization
24. Chip technology
25. Gene tagging
26. Heterochromatin

Section –B**Answer any four questions, each answer not exceeding 300 words****(4×6=24)**

27. Distinguish between top down mapping and bottom up mapping.
28. What are the salient features of collecting and storing data?
29. Write about protein –motif recognition.
30. Discuss about local alignment and end space alignments.
31. Write about RNA secondary prediction.
32. Write about applications of bioinformatics.

Section – C**Answer any two questions, each answer within 1200 words****(2×20=40)**

33. Give an account on Gilbert and Maxam method of DNA sequencing.
34. Write about various sequence databases. Add a note on mapping databases.
35. Discuss the various models for protein folding.
36. Give a detailed account of Multiple sequence alignment.
