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 2009 BRANCH V(a) – PLANT BIOLOGY AND PLANT BIOTECHNOLOGY SIXTH SEMESTER

COURSE PAPER TIME	: INTRODUCTION TO BIOINFORMATICS : 3 HOURS MAX. MARKS: 100
ANSWER	SECTION –A $(18 \times 1 = 18)$
I.	FILL IN THE BLANKS
1.	Identifying is the simple first step in gene finding.
2.	One method of Optical mapping is
3.	The DNA sequence of BamH1 is
4.	is a structural database.
5.	BLOSUM Substitution Scoring Matrix was created by in 1992.
6.	and are the stop codons.
7. 8. 9. 10. 11.	FISH BLAST EMBL DDBJ STS
12. III. ST	ESTs 'ATE WHETHER TRUE OR FALSE:
13.	Contig maps are low –resolution physical maps.
14.	DOCK is a programme used for visualizing interacting molecules.
15.	All proteins have a motif.
16.	A number with the PAM1 matrix refers evolutionary distance of 1.
17.	Needleman – Wunsch Method is a method of Local alignment of sequences.
18.	The functional part of the protein is the small portions called as the active site.

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V. ANSWER ALL QUESTIONS. EACH ANSWER NOT TO EXCEED 50 WORDS: (6 x 3 = 18)

- 19. Differentiate primary and secondary databases.
- 20. Distinguish between Orthology and Paralogy.
- 21. Explain the following pattern $C x(2) \{GP\} [STAQ]$
- 22. What are the characteristic features of FASTA format?
- 23. Align the following two sequences –

AGTCAT

AGTCDT

24. What is Similarity and Homology?

SECTION-B

ANSWER ANY FOUR OF THE FOLLOWING. EACH ANSWER NOT TO EXCEED 200 WORDS: $(4 \times 6 = 24)$

- 25. Discuss the following databases:
 - a. PROSITE
- B. SWISS-PROT
- 26. Briefly discuss PRINTS and its significance.
- 27. With an example describe how pedigree analysis can be used to construct a genetic linkage map?
- 28. Describe in detail the Secondary structure of RNA.
- 29. Justify the statement: Genomes undergo rearrangement to give rise to new species.
- 30. What do you understand in the terms 'Chip Technology and DNA computing'?

SECTION -C

ANSWER ANY TWO OF THE FOLLOWING. EACH ANSWER NOT TO EXCEED 1200 WORDS: (2x 20 = 40)

31. Explain the two different methodologies used for nucleotide sequencing

(OR)

- a. Explain with diagrams the different levels of the protein structure.
- b. Discuss the different steps involved in designing a drug.
- 32. What is global & local alignment? Explain with examples. Add a note on MSA. (OR)

Describe in detail DNA markers. Elaborate on Physical maps.
