

STELLA MARIS COLLEGE (AUTONOMOUS) CHENNAI –600 086
(For candidates admitted from the academic year 2015 – 2016 & thereafter)

SUBJECT CODE: 15BI/PC/BI24

M. Sc. DEGREE EXAMINATION, APRIL 2017
BIOINFORMATICS
SECOND SEMESTER

COURSE : MAJOR – CORE
PAPER : BIOINFORMATICS
TIME : 3 HOURS

MAX. MARKS: 100

SECTION – A

ANSWER ALL THE QUESTIONS

(20x1=20)

1. CMBI stands for _____.
2. Which of the following is the first biological database.
a. Genbank b. DDBJ c. Atlas of protein sequence and structure d. OMIM
3. BankIt and Sequin are sequence submission tools in
a. DDBJ b. PDB c. GenBank d. EMBL
4. _____ is the search and retrieval tool of NCBI
5. BLOSUM Matrices are used for
a. Phylogenetic analysis b. Multiple sequence alignment
c. Pairwise sequence alignment d. None of these
6. BLAST X program is used for _____.
7. What is gap penalty?
8. Needleman-Wunsch algorithm was developed in the year _____.
9. Abbreviate BLAST.
10. Name few organism specific BLAST sites.
11. What is E and P value in BLAST?
12. TIGR is a _____ genome annotation.
13. What is MSA?
14. BLOCKS and PRINTS are _____.
15. InterPro is a database of _____.
16. PIR stands for _____.
17. Write any two softwares for evolutionary analysis.
18. Comment on PHYLIP.
19. Define UPGMA.
20. Mention the steps of phylogenetic construction.

SECTION – B

**Answer any Four of the following; each answers not exceeding 500 words.
Draw diagram wherever necessary. (4 X 10 =40)**

21. Explain about finding the scientific research articles using pubmed.
22. Explain in detail about the scoring matrices.
23. Give an account on dynamic programming in sequence alignment.
24. Define BLAST. What are the types of BLAST and its uses?
25. What is multiple sequence alignment? Write a note on it.
26. Explain about Neighbor-Joining method.
27. What is Maximum Parsimony and Maximum-likelihood method?

SECTION – C

**Answer any TWO of the following, each answer not exceeding 1200 words.
Draw diagram wherever necessary. (2 X 20 = 40)**

28. Write a detailed note on sequence submission and retrieval system.
29. Give a detailed account on Needleman-Wunsch and Smith-Waterman algorithm.
30. Write about the advanced BLAST searching.
31. Explain in detail about the BLOCKS and PRINTS.
