

STELLA MARIS COLLEGE (AUTONOMOUS) CHENNAI 600 086
(For candidates admitted from the academic year 2019 – 2020 & thereafter)

SUBJECT CODE: 19BI/PC/EB14

M. Sc. DEGREE EXAMINATION, NOVEMBER 2021
BIOINFORMATICS
FIRST SEMESTER

COURSE : CORE

PAPER : ESSENTIALS OF BIOINFORMATICS

TIME : 180 MINUTES

MAX. MARKS: 100

SECTION - A

ANSWER ALL THE QUESTIONS IN A LINE OR TWO (15 x 2 = 30 MARKS)

1. What is BanKit in Genbank nucleotide sequence database?
2. Write any two databases for accessing nucleotide sequences.
3. Name two sequence file formats.
4. Specify any two patterns of Dot Plots in sequence similarity analysis
5. Expand PAM and BLOSUM.
6. Write the formula to fill the matrix in Local alignment algorithm.
7. What is E-value?
8. Define BLAST
9. What is Bit score in BLAST?
10. Define MSA.
11. Mention any two uses of InterPro database
12. Name the databases embedded with MSA programs.
13. Define UPGMA
14. What is evolutionary analysis?
15. Differentiate rooted and unrooted tree.

SECTION - B

ANSWER ANY TWO QUESTIONS. EACH ANSWER SHOULD NOT EXCEED 500 WORDS. ALL QUESTIONS CARRY EQUAL MARKS. DRAW DIAGRAMS WHEREVER NECESSARY
(2 x 15 = 30 MARKS)

16. Comment on the following in brief

- a) NCBI b) SGD c) PubMed

17. Answer the following

- a) Brief out the steps of Needleman-Wunsch Algorithm
b) Differentiate Needleman-Wunsch and Smith-Waterman algorithm

18. Describe the following

- a) how to perform BLAST
b) how to interpret results in BLAST

19. Explain the Multiple Sequence Alignment and its application in PRINTS database.

SECTION – C

INTERPRET THE FOLLOWING EXERCISES AND REPORT THE RESULTS
(2 x 20 = 40 MARKS)

20. Report the highly homologous protein sequence for any of the protein mentioned in PubMed ID: 33784795 using BLAST

21. Report the number of conserved regions among the following nucleotide sequences: HM545078.1, KC522602.1, DQ305041.1, DQ195224.1, MT681740.1
