ST JOSEPH'S UNIVERSITY, BENGALURU -27
M.Sc. Biotechnology- III SEMESTER
SEMESTER EXAMINATION: OCTOBER 2023
(Examination conducted in November/December 2023)
BT 9123: BIOINFORMATICS AND COMPUTATIONAL BIOLOGY
(For current batch students only)

Registration Number:

Date & session:

Time: 2 hours   **Max Marks: 50**

This paper contains ONE printed page and THREE parts

PART A

Answer any SEVEN of the following: **2m x 7 = 14 marks**

1. Describe Differential Gene Expression. What is its importance in Transcriptomics?
2. What is SRA database?
3. A protein is unique with no homologous structures. Which type of protein modeling would you apply in predicting its 3D structure?
4. What is the output of Procheck tool?
5. What are COMFA and COMSIA?
6. Expand ADMET.
7. If there are five taxa, how many rooted and unrooted trees can be generated?
8. What is SCOP?
9. What are linear and affine gap scores?

PART B

Answer any FOUR of the following: **5m x 4 = 20 marks**

10. How does BLAST algorithm function? Explain with an example.
11. What is QSAR? Illustrate with an example.
12. What is Molecular Dynamics? Explain in detail.
13. Explain the concept of protein docking with an example.
14. What is an Interactome? Write a note about any interactome database.
15. Six taxa are highly divergent (low similarity) in sequence alignment. Which method of Phylogenetic analysis could be used to analyze these sequences? Describe the method in detail.

PART C

Answer any TWO of the following: **8m x 2 = 16 marks**

16. What is protein homology modeling? Illustrate the method with an example.
17. A bacterial strain's genome was sequenced by using Illumina technology. Explain the methodology for performing this experiment.
18. Perform local alignment of the following sequences using Needleman and Wunsch algorithms
    X – ATCGGATC
    Y – CGGAT