Reg No:.................. K25FY2344
Name :...................

Second Semester FYUGP Zoology and CB Examination APRIL 2025 (2024 Admission onwards) KU2DSCZCB104 (FUNDAMENTALS OF COMPUTATIONAL BIOLOGY)

(DATE OF EXAM: 28-4-2025)

Time : 90 min Maximum Marks : 50

Part A (Answer any 6 questions. Each carries 2 marks)

1. Explain the scope of bioinformatics in modern biological sciences. 2
2. Propose a method to integrate Entrez and SRS for a comprehensive biological data search. 2
3. How is the BLOSUM matrix derived? 2
4. What is homology in molecular phylogeny? 2
5. What is the role of MSA in constructing phylogenetic trees? 2
6. What are the two main types of tree-building methods used in phylogenetics? 2
7. What is the function of MEGA software in phylogenetic studies? 2
8. Explain the importance of computational tools in phylogenetic studies. 2

Part B (Answer any 4 questions. Each carries 6 marks)

9. How would you optimize computational biology tools for handling large-scale genomic data? 6
10. Evaluate the advantages of using PDB-Flat files over other protein structure file formats when working with molecular dynamics simulations. 6
11. Given an MSA result, analyze the conserved regions and explain their biological significance in protein function. 6
12. Evaluate how molecular phylogenetics can be used in forensic science for species identification. 6
13. Examine the impact of different evolutionary models on the construction of phylogenetic trees. 6
14. Compare distance-based and character-based methods in phylogenetic tree construction. 6

Part C (Answer any 1 question(s). Each carries 14 marks)

15. (a) Discuss in detail the structure of a GenBank-GBFF file. Include information about each section and how it contributes to the understanding of the biological data. Explain the role of features, annotations, and the sequence in a GenBank record. 7

    (b) Explain how the PDB-Flat file format represents protein structure data, and compare it with other formats such as mmCIF and PDBx. Highlight how these formats differ in terms of data storage, retrieval, and compatibility with molecular visualization tools. 7

16. Explain the different types of biological data used in bioinformatics, focusing on genomic DNA, cDNA, rDNA, ESTs, and GSSs. Compare their structure, function, and applications in computational biology with relevant examples. 14