

Reg No:.....

K25FY2258

Name :.....

Second Semester FYUGP Zoology and CB Examination
APRIL 2025 (2024 Admission onwards)
KU2MDCZCB102 (MOLECULAR PHYLOGENETICS)
(DATE OF EXAM: 26-4-2025)

Time : 90 min

Maximum Marks : 50

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

1. Define the term "phylogeny." 2
2. What is the significance of protein sequences in bioinformatics? 2
3. List any two methods used for multiple sequence alignment. 2
4. What challenges are associated with multiple sequence alignment? 2
5. Why can Maximum Parsimony sometimes lead to multiple equally optimal trees? 2
6. What is the role of genomic sequencing in molecular phylogenetics? 2
7. How does the study of pathogen evolution using molecular phylogenetics contribute to treatment strategies? 2
8. What is GenBank, and why is it important for nucleotide and protein sequence retrieval? 2

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

9. How can phylogenetic methods help in understanding the evolutionary adaptations of different plant species? 6
10. What steps would you take to analyze mutations in a DNA sequence using public databases? 6
11. Given a set of misaligned sequences, analyze how improper alignment can affect phylogenetic tree construction. 6
12. Evaluate the accuracy of the Neighbor-Joining method when applied to real-world evolutionary data, considering factors like sequence length and number of species. 6
13. Compare and contrast the applications of molecular phylogenetics in diagnosing bacterial versus viral diseases, highlighting the unique challenges for each. 6
14. Using GenBank, retrieve a protein sequence for a specific enzyme and explain how you would use this data to predict the enzyme's structure and function. 6

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

15. Develop a comprehensive guide for retrieving both nucleotide and protein sequences from GenBank using various bioinformatics tools. Discuss the importance of sequence retrieval in sequence alignment and annotation processes. 14
16. (a) "Design an experimental approach to compare the accuracy of phenetic and cladistic methods in phylogenetic classification." 7
- (b) "Critically analyze how molecular phylogenetics has revolutionized our understanding of species evolution." 7