PRESIDENCY UNIVERSITY
BENGALURU

Department of Research & Development

Mid - Term Examinations - August 2024

Odd Semester: Ph.D. Course Work   **Date: 12/08/2024**

Course Code: CSE865   **Time: 02:00pm – 03:30pm**

Course Name: BIOINFORMATICS   **Max Marks**: 50

Department: CSE   **Weightage**: 25%

Instructions:
(i) Read the all questions carefully and answer accordingly.
(ii) Do not write any matter on the question paper other than roll number.

PART A (THOUGHT PROVOKING)

Answer all the Questions. Each question carries 5 marks.   **(4Qx 5M= 20M)**

1. Describe the central dogma of molecular biology and explain its significance in the field of bioinformatics.   (CO:01   BL:02)

2. Explain the difference between primary, secondary, tertiary, and quaternary structures of proteins, and describe one method used for determining each type of structure.   (CO:01   BL:02)

3. Explain the difference between global alignment and local alignment in sequence analysis. Provide an example scenario where each type would be appropriately used.   (CO:02   BL:02)

4. Describe how Hidden Markov Models (HMMs) are used in bioinformatics for sequence analysis. How does the Gibbs Sampling method contribute to motif discovery in biological sequences?   (CO:02   BL:02)

PART B (PROBLEM SOLVING)

Answer all the Questions. Each question carries 10 marks.   **(3Qx 10M= 30M)**

5. Discuss the major milestones in the development of molecular biology and bioinformatics. How have advancements in bioinformatics tools and databases enhanced our understanding of molecular biology? Provide specific examples to illustrate your points.   (CO:01   BL:03)

6. Compare and contrast two methods used for protein sequencing (e.g., Edman degradation and mass spectrometry). Additionally, discuss two techniques used for determining protein structure (e.g., X-ray crystallography and NMR spectroscopy), highlighting their principles, advantages, and limitations. How do these methods contribute to functional analysis of proteins?

(CO:02   BL:03)

7. Compare and contrast dynamic programming algorithms used for sequence alignment, specifically focusing on local alignment, global alignment, and multiple sequence alignment. Discuss the importance of motifs and patterns in biological sequences and explain how tools like PROSITE and methods such as Hidden Markov Models (HMMs) and Gibbs Sampling are used for motif discovery.

(CO:02   BL:03)