|  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Roll No |  |  |  |  |  |  |  |  |  |  |  |  |

 ****

**Presidency University**

**Bengaluru**

 **Ph.D. Course Work End Term Examinations – JAN-FEB 2025**

**Date**: 06-02-2025

**Time**: 9.30 AM TO 12.30 PM

**Max Marks**: 100

**Weightage**: 50%

**Semester**:

**Course Code**: CSE865

**Course Name**: Bioinformatics

**School:** SOCSE

 **Instructions:**

1. *Read the all questions carefully and answer accordingly.*
2. *Do not write any matter on the question paper other than roll number.*

**PART A**

**Answer all the Questions. Each question carries 10 marks. (6Qx 10M= 60M)**

|  |  |
| --- | --- |
| **1.** | Explain the role of substitution matrices in sequence alignments. How are alignment scores and gap penalties calculated? |
| **2.** | Outline the working principles of BLAST. How does it contribute to similarity search and sequence alignment? |
| **3.** | Explain the principles of Hidden Markov Models (HMMs) and their application in sequence analysis. |
| **4.** | Describe how Gibbs Sampling is used for motif discovery. What are its advantages and limitations? |
| **5.** | Discuss the significance of protein localization in understanding cellular processes. What techniques are used to determine protein localization? |
| **6.** | Outline the different perspectives on protein function. How do these perspectives integrate to provide a comprehensive understanding of proteins? |

**PART B**

**Answer all the Questions. Each question carries 20 marks. (2Qx 20M= 40M)**

|  |  |
| --- | --- |
| **7.** | Compare various protein identification techniques used in proteomics. Discuss how protein domains and motifs relate to their physical properties, localization, and functions. Provide case studies or examples where these techniques have contributed to significant biological discoveries. |
| **8.** | Explain the principles of protein structure, focusing on primary, secondary, and tertiary structures. Discuss the role of classification databases such as the Protein Data Bank (PDB) in studying protein structures. How does structural modeling help predict protein function and its implications in disease research? Provide examples of intrinsically disordered proteins and their roles in diseases. |