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**PRESIDENCY  
UNIVERSITY  
BENGALURU**

**School of Computer Science and Engineering  
Mid - Term Examinations - November 2024**

**Semester:** 5

**Date:** 06/11/2024

**Course Code:** CSE3069

**Time:** 02.00pm to 03.30pm

**Course Name:** Introduction to Bioinformatics

**Max Marks:** 50

**Program:** CSE

**Weightage:** 25%

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**Instructions:**

*(i) Read all questions carefully and answer accordingly.*

*(ii) Do not write anything on the question paper other than roll number.*

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**Part A**

**Answer ALL the Questions. Each question carries 2marks.**

**5QX2M=10M**

- |   |   |         |           |     |
|---|---|---------|-----------|-----|
| 1 | RNA is found in which kind of cells with expansion and describe how it is different from DNA. | 2 Marks | Knowledge | CO2 |
| 2 | Show the Reverse complement of GGCCCTAGCT with appropriate steps.                             | 2 Marks | knowledge | CO2 |
| 3 | Define the following i.Gene ii.Gene expression.   | 2 Marks | Knowledge | CO1 |
| 4 | Explain PIR file format in detail.  | 2 Marks | Knowledge | CO2 |
| 5 | Expand the following i) NCBI ii) EBI  | 2 Marks | Knowledge | CO3 |

**Part B**

**Answer ALL Questions. Each question carries 10 marks.**

**4QX10M=40M**

- |   |  |          |             |     |
|---|--|----------|-------------|-----|
| 6 | Nucleotide sequences need to be stored in a standardized plain text format for ease of data management and analysis. Discuss the commonly used sequence file formats, providing clear examples for each. | 10 Marks | Application | CO2 |
|---|--|----------|-------------|-----|

Or

**7** Find the frequent words and K MER for the DNA sequence  
"ACA ACTAAGCATCACTAACGGGAACTAACCT" 10 Marks Application CO2

**8** Explain the types of DNA sequencing methods in detail. 10 Marks Comprehension CO3

Or

**9** DNA sequence SSS: "ACAAGCATAAACATTAAGAG"  
Pattern P: "AAAA" Maximum mismatches d: 1 10 Marks Comprehension CO3

**10** What is K MER ?Explain the applications of K MER counting. 10 marks Comprehension CO3

Or

**11** What is string reconstruction problem, Explain in detail with an example. 10 Marks Comprehension CO3

**12** What is Biological Database? Explain the GENOMIC DATABASES in detail. 10 marks Comprehension CO3

Or

**13 a.** What is PAM and blosum explain. 5 marks Comprehension CO3

**b.** Calculate the alignment score for  
S1=CCTCTCACTGAGACTCAGCC and S2=CGA-ACTCTT-  
GTTC-TGCA, For the alignment rules Match=+1,  
Mismatch=-1 and Gap=0 5 marks Comprehension CO3