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**PRESIDENCY
UNIVERSITY
BENGALURU**

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

Semester: 7

Date: 05/11/2024

Course Code: CSE3069

Time: 02.00pm to 03.30pm

Course Name: Introduction to Bioinformatics

Max Marks: 50

Program: CSE

Weightage: 25%

Instructions:

- (i) Read all questions carefully and answer accordingly.
- (ii) Do not write anything on the question paper other than roll number.

Part A

Answer ALL the Questions. Each question carries 2marks.

5Qx2M=10M

- | | | | | |
|----------|---|----------------|----------------------|------------|
| 1 | Translate reverse complement of:
GATTGATACGAATCTAGCT? | 2 Marks | comprehension | CO2 |
| 2 | Analyze what is wrong about FASTA Sequence Format and describe the correct sequence format.
1.The FASTA sequence format includes a comment line identified by a ">" character in the first column followed by the name and origin of the sequence
2.The FASTA sequence format includes the sequence in standard one-letter symbols
3.This format provides a very convenient way to copy just the sequence part from one window to another because there are no numbers or other nonsequence characters within the sequence
4.The presence of '*' is not quite essential for reading the sequence correctly by some sequence analysis programs | 2 Marks | comprehension | CO2 |
| 3 | Reproduce the Composition3(GGGTATCAA) in lexicographic order is? | 2 Marks | Knowledge | CO1 |
| 4 | State any 2 database which is used as the search and retrieval tool of NCBI with explanation. | 2 Marks | Knowledge | CO2 |
| 5 | Omics refers to the collective technologies used to explore the roles, relationships describe how and explain the types of omics. | 2 Marks | Knowledge | CO3 |

Part B

Answer ALL Questions. Each question carries 10 marks.

4QX10M=40M

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|-----------|---|----------------------------------|--|--------------------------|
| 6 | Reconstruct the substring and graph for the following sequence: 'TACG', 'CAGC', 'CAAG', 'TCAG', 'AGGT', 'CGAT', 'GATC', 'TTCC', 'AAGG', 'ACGA', 'CGAT', 'GTAC', 'ATCG', 'ATCG', 'TCGA', 'GATC', 'TCGG', 'CGGA', 'CATC', 'GGTA', 'GATC', 'ATCA', 'TCCA', 'GGAT', 'CCAA', 'AGCA', 'GCAT', 'TCCA', 'ATCC'. | 10 Marks | Application | CO2 |
| Or | | | | |
| 7 | Biological macromolecules is correctly paired with one of its functions which is very necessary for all organisms for life recognize any 4 types and describe with example. | 10 Marks | Application | CO2 |
| 8 | Gap penalties are used to adjust alignment scores based on the number and length of gaps two sequences need to be aligned with each other. Explain the role of gap penalty in this and its types. | 10 Marks | Comprehension | CO3 |
| Or | | | | |
| 9 | What is a cell and explain its organelles with a neat diagram? | 10 Marks | Comprehension | CO3 |
| 10 | Difference between DNA and RNA with neat diagram | 10 Marks | Comprehension | CO3 |
| Or | | | | |
| 11 | What is a gene expression and explain the process of 3d folding of a protein structure. | 10 Marks | Comprehension | CO3 |
| 12 | i. Define : i)Chromosomes ii) Nucleotide iii) Cytoplasm
ii. Explain 3 components of bioinformatics | 5 marks
5 marks | Comprehension
Comprehension | CO3
CO3 |
| Or | | | | |
| 13 | Explain the fields of bioinformatics and application of bioinformatics in detail | 10 marks | Comprehension | CO3 |