



**PRESIDENCY UNIVERSITY
BENGALURU**

**SCHOOL OF ENGINEERING
END TERM EXAMINATION - JAN 2023**

Semester : Semester V - 2020

Course Code : CSE3069

Course Name : Sem V - CSE3069 - Introduction to Bioinformatics

Program : B.Tech. CAI/COM/CSE

Date : 13-JAN-2023

Time : 9.30AM - 12.30PM

Max Marks : 100

Weightage : 50%

Instructions:

- (i) Read all questions carefully and answer accordingly.
- (ii) Question paper consists of 3 parts.
- (iii) Scientific and non-programmable calculator are permitted.

PART A

ANSWER ALL THE TEN QUESTIONS

10 X 2 = 20M

1. Find the reverse compliment of the following Sequences
i. ACTGACT
ii. GCTGATCGT
(CO1) [Knowledge]
2. Enumerate the 2 commonly used substitution matrices.
(CO2) [Knowledge]
3. Find the most frequent 5-mer in GGTTCACCACTAAGCATCACTAACGGGAACCT
(CO2) [Knowledge]
4. State the importance of Dynamic Programming.
(CO3) [Knowledge]
5. Define Global Alignment.
(CO3) [Knowledge]
6. State the importance of Multiple Sequence Alignment.
(CO3) [Knowledge]
7. Enumerate any 2 Protein Sequence Databases.
(CO2) [Knowledge]
8. List the elements of Phylogenetic Tree.
(CO4) [Knowledge]
9. Describe PROSITE.
(CO4) [Knowledge]
10. What are the 2 different types of cells? Give examples for each.
(CO1) [Knowledge]

PART B

ANSWER ALL THE FIVE QUESTIONS

5 X 10 = 50M

11. i. Identify all the starting positions where Pattern appears as a substring of Text with at most 'd' mismatches.
Pattern: ATTCTGGA
Substring:CGCCCGAATCCAGAACGCATTCCCATATTTTCG
GGACCACTGGCCTCCACGGTACGGACGTCAATCAAAT
d: 3
- ii. Reconstruct the substring from the given k-mers
AAT ATG ATG ATG CAT CCA GAT GCC GGA GGG GTT TAA TGC TGG TGT
(CO2) [Comprehension]
12. Explain the following concepts in detail
i. Types of Gap Penalties
ii. Substitution Matrix and its types
(CO2) [Comprehension]
13. Illustrate the concepts of (i) Sequence Alignment and its types (ii) Clustal W
(CO3) [Comprehension]
14. Identify the optimal alignment using local alignment algorithm for the given sequences.
i) TTCATCGTCG
CTCATTCCA
ii) GCTGCATCT
CTATCTATCT
(CO3) [Comprehension]
15. a) Define Phylogenetic and Phylogenetic Tree? Explain the elements of Phylogenetic tree.
b) Trace the phylogenetic tree using the UPGMA method for the following sequences
i. ATCGATCCTA
ii. ATATACTCAT
iii. CTCGATCCAT
iv. ATATTTCACT
v. ATCCATCCTC
(CO4) [Comprehension]

PART C

ANSWER ALL THE TWO QUESTIONS

2 X 15 = 30M

16. Apply global alignment technique to find the optimal alignment for the following sequences .
The sequences are as follows:
i. CATCGATCACTA
TTCGACTACTAT
ii. CTAGGATCGAA
CTACCTCGACC
(CO3) [Application]
17. Apply Gibbs Sampling method to find the motif GACGTTA from the following sequences.
GCGATCATTA
CTGACGTACC
ACTCTAACGG
TACGAAACGT
(CO4) [Application]
