Printed Page:- Subject Code:- AMTBT0201

Roll. No:

NOIDA INSTITUTE OF ENGINEERING AND TECHNOLOGY, GREATER NOIDA

(An Autonomous Institute Affiliated to AKTU, Lucknow)

M.Tech.

SEM: II - THEORY EXAMINATION (2021 - 2022)

Subject: Bioinformatics

Time: 3 Hours Max. Marks: 70

General Instructions:

1. The question paper comprises three sections, A, B, and C. You are expected to answer them as directed.
2. Section A - Question No- 1 is 1 marker & Question No- 2 carries 2 marks each.
3. Section B - Question No-3 is based on external choice carrying 4 marks each.
4. Section C - Questions No. 4-8 are within unit choice questions carrying 7 marks each.
5. No sheet should be left blank. Any written material after a blank sheet will not be evaluated/checked.

SECTION A 15

1. Attempt all parts:-

1-a. Your lab partner is using BLAST, and his best E value is 3. This means that (CO1) 1

(a) he’s found 3 proteins in the database that have the same sequence as his protein.

(b) the chance that these similarities arose due to chance is one in 10^3.

(c) there would be 3 matches that good in a database of this size by chance alon

(d) the match in amino acid sequencs is perfect, except for the amino acids at 3 positions.

1-b. BLAST programme is used in (CO2) 1

(a) DNA sequencing

(b) Amino acid sequencing

(c) DNA bar coding

(d) Bioinformatics

1-c. Proteomics is the study of (CO3) 1

(a) set of proteins

(b) set of proteins in a specific region of the cell

(c) entire set of expressed proteins in a cell

(d) none of these

1-d. Which of the following statement is not true regarding the maximum parsimony method? (CO4) 1

(a) The analysis steps are continued for every position in the sequence alignment

(b) This method is used for large numbers of sequences

(c) Those trees that produce the smallest number of changes overall for all sequence positions are identified

(d) This method is used for sequences that are quite similar

1-e DNA sequences are sometimes more biased than protein sequences because of preferential codon usage in different organisms. (CO5) 1

(a) True

(b) False

2. Attempt all parts:-

2.a. Name two nucleotide sequence database? (CO1) 2

2.b. What do understand by scoring matrices? (CO2) 2

2.c. What is phylogram? (CO3) 2

2.d. What is transcriptome? (CO4) 2

2.e. What is polymorphism? (CO5) 2

SECTION B 20

3. Answer any five of the following:-

3-a. What is the difference between primary and secondary databases? Give some examples? (CO1) 4

3-b. Write short note on RCSB?(CO1) 4

3-c. What is the difference between gap opening and gap extension penalties? (CO2) 4

3-d. What do you understand by database searching? (CO2) 4

3.e. What are the properties of a good primer? (CO3) 4

3.f. How protein-protein interactions can be divided on the basis of stability? Explain with examples. (CO4) 4

3.g. Describe the steps involved in microarray data analysis? (CO5) 4

SECTION C 35

4. Answer any one of the following:-

4-a. What is the difference between data and information? What are the different characteristics of biological databases? (CO1) 7

4-b.	Suppose you have done some experimental studies and came up with a amino-acid sequence. Describe in which database you will submit this sequence? (CO1)	7

5. Answer any one of the following:-

5-a.	Describe various methods for performing multiple sequence alignment? (CO2)	7
5-b.	What is sequence alignment and what are its applications? (CO2)	7

6. Answer any one of the following:-

6-a.	What is the difference between scoring & distance matrix. (CO3)	7
6-b.	What are the properties that a primer must have? Describe some tools for primer designing? (CO3)	7

7. Answer any one of the following:-

7-a.	What is systems biology? What are its applications? (CO4)	7
7-b.	Write detailed note on (a) Trimming (b) Protein degradation (c) Stable interactions. (CO4)	7

8. Answer any one of the following:-

8-a.	Discuss the detailed procedure to use RASMOL for visualization? (CO5)	7
8-b.	How bioinformatics may help in analysis of genetic polymorphism? (CO5)	7