Printed Page:- 04 Subject Code:- ABT0304
Roll. No:

NOIDA INSTITUTE OF ENGINEERING AND TECHNOLOGY, GREATER NOIDA
(An Autonomous Institute Affiliated to AKTU, Lucknow)
B.Tech
SEM: III - THEORY EXAMINATION (2024- 2025)
Subject: Bioinformatics

Time: 3 Hours Max. Marks: 100

General Instructions:

IMP: *Verify that you have received the question paper with the correct course, code, branch etc.*

1. This Question paper comprises of three Sections -A, B, & C. It consists of Multiple Choice Questions (MCQ's) & Subjective type questions.

2. Maximum marks for each question are indicated on right -hand side of each question.

3. Illustrate your answers with neat sketches wherever necessary.

4. Assume suitable data if necessary.

5. Preferably, write the answers in sequential order.

6. No sheet should be left blank. Any written material after a blank sheet will not be evaluated/checked.

SECTION-A 20

1. Attempt all parts:-

1-a. In which year did the SWISSPROT protein sequence database begin? (CO1, K1) 1

(a) 1985
(b) 1986
(c) 1988
(d) 1987

1-b. Name of sequence retrieval tool of EMBL? (CO1,K1) 1

(a) BankIt
(b) Sakura
(c) SRS
(d) NCBI

1-c. BLAST was developed and controlled by which organization? (CO2, K2) 1

(a) EBI
(b) DDBJ
(c) NCBI
(d) PDB

1-d. Identify the input format is used in BLAST? (CO2,K2) 1

(a) FASTA
(b) XML
(c) HTML

(d) Text

1-e. Pick the incorrect statement concerning the terminologies of phylogenetics. (CO3,K2) 1

(a) branches are the lines in the tree
(b) tips of the branches have long lost sequences or species
(c) node indicate inferred ancestor of extant taxa
(d) connecting point joining two adjacent branches is a node

1-f. Identify the software used for constructing phylogenetic tree? (CO3, K2) 1

(a) MEGA
(b) TIGR
(c) SIGNOR
(d) Primer 3.0

1-g. Choose which one is not the mechanism of Epigenetics? (CO4, K3) 1

(a) DNA Methylation
(b) Histone Modification
(c) Non-coding Associated gene
(d) Mutation

1-h. Interpret the CRISPR? (CO4, K3) 1

(a) Sequences derived from viral DNA fragments
(b) A gene-editing tool
(c) A bacterial defence mechanism
(d) All options correct

1-i. Interpret the methods we use to find the best fit line for data in Linear Regression? (CO5, K3) 1

(a) Least square error
(b) Maximum likelihood
(c) Logrithimic loss
(d) None

1-j. Choose the correct suitable option for Protein Secondary structure ? (CO5, K3) 1

(a) Vander Waals forces
(b) Covalent bonding
(c) Hydrogen bonding
(d) Ionic bonding

2. Attempt all parts:-

2.a. Why secondary biological databases are also known as derived databases? (CO1, K1) 2

2.b. Describe the optimal sequence alignment? (CO2, K2) 2

2.c. Express any two applications of Phylogenetic analysis? (CO3, K2) 2

2.d. Illustrate the role of epigenetics in Biotechnology? (CO4,K3) 2

2.e. Interpret the role of Regression in Bioinformatics. (CO5, K3) 2

<u>SECTION-B</u> 30

3. Answer any <u>five</u> of the following:-

3-a. What is the importance of patent databases in bioinformatics? (CO1,K1) 6

3-b. How primary biological databases are different from secondary databases? Discuss in detail. (CO1, K1) 6

3-c. Explain dynamic programming? Describe the various types of Algorithms used in dynamic programming? (CO2,K2) 6

3-d. Explain how Heuristic algorithm works? Explain different steps involved in Heuristic algorithm? (CO2,K2) 6

3.e. How molecular phylogeny is different from phenotypic phylogeny? Explain with the help of examples. (CO3, K2) 6

3.f. Illustrate the term genetical diseases? Interpret how these type of diseases can be identify using epigenetics? (CO4, K3) 6

3.g. Sketch the applications of Machine learning in Bioinformatics? Illustrate various terminologies used in machine learning? (CO5,K3) 6

<u>SECTION-C</u> 50

4. Answer any <u>one</u> of the following:-

4-a. Write down the names of different types of protein sequence databases and explain each of them? (CO1, K1) 10

4-b. What are various in silico tools of rDNA technology? Explain various types of in silico tools for rDNA in detail. (CO1, K1) 10

5. Answer any <u>one</u> of the following:-

5-a. Explain is the importance of entrez for NCBI databases? Discuss various integration of entrez with NCBI databses? (CO2, K2) 10

5-b. Dynamic program is the basis of sequence alignment. Discuss various algorithms used in dynamic programming in detail.(CO2, K2) 10

6. Answer any <u>one</u> of the following:-

6-a. Express the advantages and disadvantages of Unweighted Pair Group Method with Arithmetic Mean? Explain in detail. (CO3, K2) 10

6-b. Discuss in detail what is phylogenetic analysis. Enlist and explain different applications of phylogenetic analysis. (CO3, K2) 10

7. Answer any <u>one</u> of the following:-

7-a. Interpret how the cancer in patients is diagnosed with the help of Epigenetics? Illustrate epigenetics studies in detail. (CO4, K3) 10

7-b. Illustrate the various types of biomarkers? Demonstrate the importance of biomarkers in disease diagnosis with the help of examples. (CO4, K3) 10

8. Answer any <u>one</u> of the following:-

8-a. Interpret the major differences between Classification and Regression algorithms used in Machine Learning? (CO5, K3) 10

8-b. Illustrate the various available methods for validation of structure of protein. How these methods are use to validate the protein structure? (CO5, K3) 10