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 - CARRY OVER THEORY EXAMINATION-AUGUST (2023)

Subject: Bioinformatics

Time: 3 Hours **Max. Marks: 70**

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 **15**

1. Attempt all parts:-

1-a. Which is the sequence retrieval tool of NCBI? (CO1) 1

(a) SRS

(b) EMBL

(c) ENTREZ

(d) Webin

1-b. Which bioinformatics tool compares protein query sequence against translated nucleotide sequence database?(CO2) 1

(a) Blastx

(b) tblastn

(c) blastn

(d) blastp

1-c. If cladistics were used to build a phylogenetic tree of cats, this would be the most appropriate outgroup (CO3) 1

(a) Tiger

(b) leopard

(c) domestic cat

(d) wolf

1-d. Computational and mathematical analysis and modeling of complex biological systems is known as_____. (CO4) 1

(a) Bioinformatics

(b) System Biology

(c) Biotechnology

(d) None

1-e. Find out the incorrect statement among the following? (CO5) 1

(a) WebMol is a web-based program built based on a modified RasMol code and thus shares many similarities with RasMol

(b) WebMol is a web-based program that is totally different from RasMol

(c) Chime is a plug-in for web browsers

(d) Chime is not a standalone program and has to be invoked in a web browser

2. Attempt all parts:-

2.a. Write any two characteristics of OMIM? (CO1) 2

2.b. What do you understand by substitution score? (CO2) 2

2.c. Draw a labelled diagram of a rooted tree? (CO3) 2

2.d. Which are the most common amino acids that undergo phosphorylation? (CO4) 2

2.e. What is southern blot? (CO5) 2

SECTION B **20**

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

3-a. What is KEGG database? (CO1) 4

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

3-c. What do you understand by match and mismatch in sequence alignment? (CO2) 4

3-d. What are the applications of sequence alignment? (CO2) 4

3.e. Describe in detail database for restriction enzyme? (CO3) 4

3.f. Discuss about any protein-protein interaction database? (CO4) 4

3.g. Describe the principle involved in microarray technique? (CO5) 4

SECTION C **35**

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

4-a.	Describe various protein sequence databases in detail? (CO1)	7
4-b.	Write in detail about these databases: a. PIR b. PDB (CO1)	7

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

5-a.	Describe in detail what is PSI-BLAST? (CO2)	7
5-b.	Describe in detail which alignment (LOCAL or GLOBAL) you will choose for estimating the overall similarity in the sequence? (CO2)	7

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

6-a.	Draw the basic tree for construction for phylogenetic analysis. (CO3)	7
6-b.	Why we consider genes as molecular clocks? (CO3)	7

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

7-a.	What do you understand by protein-protein interactions? Describe with examples? (CO4)	7
7-b.	You want to study different kind of conformations of a protein. How you will study different conformations of a protein? (CO4)	7

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

8-a.	What do you understand by EST? Mention some databases for EST? (CO5)	7
8-b.	What kind of study you will perform if you are interested in knowing the differential gene expression between normal and diseased samples? (CO5)	7