Printed Page:- 03 **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 (2023- 2024)

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. Shotgun cloning differs from the clone-by-clone method in which of the following ways? (CO1) 1

(a) The location of the clone being sequenced is known relative to other clones within the genomic library in shotgun cloning.

(b) Genetic markers are used to identify clones in shotgun cloning.

(c) Computer software assembles the clones in the clone-by-clone metho

(d) No genetic or physical maps of the genome are needed to begin shotgun cloning.

1-b. The first published completed gene sequence was of (CO2) 1

(a) M 13 phage

(b) T 4 phage

(c) f X174

(d) lambda phage

1-c. Which of the following is incorrect regarding sequence homology? (CO3) 1

(a) Two sequences can homologous relationship even if have do not have

common origin

(b) It is an important concept in sequence analysis

(c) When two sequences are descended from a common evolutionary origin, they are said to have a homologous relationship

(d) When two sequences are descended from a common evolutionary origin, they are said to share homology

1-d. Molecular clock is an assumption by which we can determine: (CO4) 1

(a) Time

(b) Mutation Rate

(c) DNA

(d) Evolution rate

1-e. Out of the following, which technique detect single nucleotide polymorphism? (CO5) 1

(a) RFLP

(b) AFLP

(c) SSLP

(d) SNP

2. Attempt all parts:-

2.a. Enlist any two specialized databases? (CO1) 2

2.b. Define the term global alignment. Give example in support of your answer. (CO2) 2

2.c. Enlist and explain any two distance matrix based phylogenetic tree construction method? (CO3) 2

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

2.e. Explain in detail the principle of homology modeling. Enlist various steps that are involved in homology modeling. (CO5) 2

SECTION B **20**

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

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

3-b. Write short note on secondary databases with examples? (CO1) 4

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

3-d. Write short note on features of PAM? (CO2) 4

3.e. Define the term evolutionary tree. What kind of information one can derive 4

from evolutionary tree? (CO3)

3.f. Discuss and explain the role of genomics in systems biology? (CO4) 4

3.g. What do you understand by the term genetic polymorphism? Explain with examples. (CO5) 4

SECTION C **35**

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

4-a. Explain in detail about various data retrieval and submission tools in biological databases. Give examples in support of your answer. (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 and explain in detail progressive and iterative method of alignment? (CO2) 7

5-b. Explain in detail the algorithms of PHI and PSI BLAST? (CO2) 7

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

6-a. Explain in detail various steps which is most critical in the construction of phylogenetic trees? (CO3) 7

6-b. Define the primer designing? Explain how bioinformatics tools may help in designing the primers? (CO3) 7

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

7-a. Define the term post-translation modification (PTMs)? Explain in detail various kinds of PTMs? (CO4) 7

7-b. Write detailed note on (a) Trimming (b) Protein degradation (c) Stable interactions. (CO4) 7

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

8-a. Explain why visualization tools are important in protein structure? Enlist various tools that are used for protein structure visualization? (CO5) 7

8-b. Write short notes on (a) Illumina method of sequencing (b) Pyrosequencing? (CO5) 7