Roll. No:

NOIDA INSTITUTE OF ENGINEERING AND TECHNOLOGY, GREATER NOIDA
(An Autonomous Institute Affiliated to AKTU, Lucknow)
M.Tech
SEM: II - THEORY EXAMINATION (2022-2023 .)
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.　　　The human genome contains approximately_____ (CO1)　　　1

　　　　　(a) 6 billion base pairs

　　　　　(b) 5 billion base pairs

　　　　　(c) 4 billion base pairs

　　　　　(d) 3 billion base pairs

1-b.　　　Which of the following is a nucleotide sequence data base? (CO2)　　　1

　　　　　(a) EMBL

　　　　　(b) SWISS PROT

　　　　　(c) PROSITE

　　　　　(d) TREMBL

1-c.　　　Molecular data is used to reconstruct evolutionary history requires making a number of reasonable assumptions. Which of the following is incorrect about it? (CO3)　　　1

　　　　　(a) The molecular sequences used in phylogenetic construction are homologous

(b) The molecular sequences used in phylogenetic construction share a common origin

(c) Phylogenetic divergence cannot be bifurcating

(d) Parent branch splits into two daughter branches at any given point

1-d. Which of the following is incorrect regarding the advantages of Molecular data for phylogenetics study? (CO4) 1

(a) Sampling bias is involved

(b) They are more numerous than fossil records

(c) They are easier to obtain as compared to fossil records

(d) FSGDHD

1-e. The process of finding relative location of genes on a chromosome is called as (CO5) 1

(a) Gene mapping

(b) Gene training

(c) Gene walking

(d) Chromosome Walking

2. Attempt all parts:-

2.a. What are the two characteristics of PDB? (CO1) 2

2.b. What is the size of word for protein as well as nucleotide sequence in BLAST? (CO2) 2

2.c. What are Restriction enzymes? (CO3) 2

2.d. What are homo-oligomers? (CO4) 2

2.e. Name some tools for genomic data analysis? (CO5) 2

SECTION B 20

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

3-a. What are the data retrieval and data submission tools at NCBI? (CO1) 4

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

3-c. What do you understand by iterative alignment? (CO2) 4

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

3.e. What are the applications of restriction mapping? (CO3) 4

3.f. Write short note on Hydroxylation? (CO4) 4

3.g. What is Solexa/ Illumina sequencing? (CO5) 4

SECTION C 35

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

4-a.   Describe in detail various biological databases? (CO1)   7

4-b.   Suppose you are working on Hemoglobin protein and want to retrieve its amino-acid sequence. Which databases you can retrieve data from? (CO1)   7

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

5-a.   What is sequence alignment? Describe Global and Local sequence alignment with example? (CO2)   7

5-b.   What are the main algorithms for database searching? (CO2)   7

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

6-a.   Why multiple sequence alignment is required for phylogenetic analysis? (CO3)   7

6-b.   What are two similar genes that are found in the same species called? These genes arise from duplication and carry out different functions within a cell. (CO3)   7

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

7-a.   How post translation modification affects the function of a protein? (CO4)   7

7-b.   Suppose you want to study all the off-target effects of a drug. What type of interactions and approach you will adopt? (CO4)   7

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

8-a.   Differentiate between Sanger method and automated method of sequencing? (CO5)   7

8-b.   Explain why are normal and diseased samples are labeled with different dye in microarray technique? (CO5)   7