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NOIDA INSTITUTE OF ENGINEERING AND TECHNOLOGY, GREATER NOIDA
(An Autonomous Institute Affiliated to AKTU, Lucknow)

M.Tech

SEM: II - THEORY EXAMINATION (2025 - 2026)

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:-

- (1.1) As the complexity of an organism increases, all of the following characteristics emerge except _____.(CO1,K1) 1
- (a) the gene density decreases
- (b) the number of introns increases
- (c) the gene size increases
- (d) an increase in the number of chromosomes
- (1.2) A data base of current sequence map of the human genome is called (CO2,K1) 1
- (a) OMIM
- (b) HGMD
- (c) Golden path
- (d) GeneCards
- (1.3) Which of the following are not the application of bioinformatics? (CO3,K1) 1
- (a) Drug designing
- (b) Data storage and management
- (c) Understand the relationships between organisms
- (d) None of the above
- (1.4) Which of the following is untrue regarding the distance methods?(CO4,K1) 1
- (a) The sequence pairs that have the largest number of sequence changes between them are termed 'neighbors'
- (b) On a tree, these sequences share a node or common ancestor position and are each joined to that node by a branch
- (c) It produces a phylogenetic tree of the group

- (d) It employs the number of changes between each pair in a group of sequences
- (1.5) Which of the following does not describe BLAST? (CO5,K1) 1
- (a) It stands for Basic Local Alignment Search Tool
- (b) It uses word matching like FASTA
- (c) It is one of the tools of the NCBI
- (d) Even if no words are similar, there is an alignment to be considered

2. Attempt all parts:-

- (2.1) What do you understand by ExPASy? (CO1,K1) 2
- (2.2) Explain the significance of gap penalty? (CO2,K2) 2
- (2.3) Explain the two different classes of phylogenetic tree construction method? (CO3,K2) 2
- (2.4) Elaborate different forms of DNA?(CO4,K2) 2
- (2.5) Explain two applications of ESTs? (CO5,K2) 2

SECTION-B

20

Answer any one of the following:-

- (3.1) Differentiate between DDBJ and EMBL?(CO1,K2) 4
- (3.2) How bioinformatics help in managing biological databases?(CO1,K2) 4

Answer any one of the following:-

- (3.3) Explain the steps followed in progressive alignment.(CO2,K2) 4
- (3.4) What do you understand by scoring matrices? Explain with examples?(CO2,K2) 4

Answer any one of the following:-

- (3.5) Explain the advantages of the UPGMA method.(CO3,K2) 4
- (3.6) Write a note on the Primer3Plus tool.? (CO3,K2) 4

Answer any one of the following:-

- (3.7) How protein-protein interactions can be divided on the basis of their composition? (CO4,K2) 4
- (3.8) Explain the main applications of systems biology? (CO4,K2) 4

Answer any one of the following:-

- (3.9) Explain the working process of Pyrosequencing. (CO5,K3) 4
- (3.10) Explain the process of Sanger sequencing with a suitable example.(CO5,K3) 4

SECTION-C

35

4. Answer any one of the following:-

- (4.1) Define Biological Databases. Describe specialized databases with examples? (CO1,K2) 7
- (4.2) What are medical databases? Describe with example? (CO1,K2) 7

5. Answer any one of the following:-

- (5.1) Explain Dynamic Programing. What are the steps involved in Smith Waterman Algorithm? (CO2,K2) 7
- (5.2) Why do we require database searching programs? what are the main database 7

searching programs? (CO2,K2)

6. Answer any one of the following:-

(6.1) Explain phylogenetic analysis in detail with its significance in bioinformatics.(CO3,K2) 7

(6.2) Explain the Neighbor Joining and UPGMA methods for phylogenetic tree construction. (CO3,K3) 7

7. Answer any one of the following:-

(7.1) How post translational modifications effect the proteins? Explain with examples? (CO4,K2) 7

(7.2) Explain protein-protein interactions and discuss methods used for their analysis. (CO4,K2) 7

8. Answer any one of the following:-

(8.1) Describe various steps involved in microarray data analysis? (CO5,K2) 7

(8.2) Explain the concept of automated genome sequencing with suitable examples.(CO5,K2) 7

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