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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 (2024- 2025)

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. CpG islands and codon bias are tools used in eukaryotic genomics to _____. 1
CO1, K1
- (a) identify open reading frames
 - (b) differentiate between eukaryotic and prokaryotic DNA sequences
 - (c) find regulatory sequences
 - (d) look for DNA-binding domains
- 1-b. Phylogenetic relationship can be shown by. CO2, K1 1
- (a) Dendrogram
 - (b) Gene Bank
 - (c) Data retrieving tool
 - (d) Data search tool
- 1-c. If the two sequences share significant similarity, it is extremely _____ that the 1
extensive similarity between the two sequences has been acquired randomly,
meaning that the two sequences must have derived from a common evolutionary
origin. CO3, K3
- (a) unlikely
 - (b) possible
 - (c) likely
 - (d) relevant

- 1-d. Which of the following is an incorrect statement? CO4, K2 1
- (a) In a phylogram, the branch lengths represent the amount of evolutionary divergence
 - (b) Trees like cladogram are said to be scaled
 - (c) The scaled trees have the advantage of showing both the evolutionary relationships and information about the relative divergence time of the branches
 - (d) In a cladogram, the external taxa line up neatly in a row or column
- 1-e. Chain-termination is a type of _____ CO5, K2 1
- (a) Sequencing
 - (b) Vector generation
 - (c) Antibiotic production
 - (d) Gene manipulation
2. Attempt all parts:-
- 2.a. Name two protein sequence database? CO1, K1 2
- 2.b. How can we classify alignment based on number of sequences? CO2, K2 2
- 2.c. What is the first step in distance based phylogenetic tree construction method? CO3, K2 2
- 2.d. What is proteome? CO4, K1 2
- 2.e. Why washing is required, once the sample and probes are hybridized in microarray studies? CO5, K3 2

SECTION-B

20

3. Answer any five of the following:-

- 3-a. Write short note on TIGR database? CO1, K1 4
- 3-b. What do you understand by NCBI? Write about its importance in Bioinformatics? CO1, K2 4
- 3-c. What are the applications of BLAST? CO2, K2 4
- 3-d. What is the need of database searching? CO2, K3 4
- 3.e. Write about DNA strider tool? CO3, K2 4
- 3.f. Write short note on glycosylation? 4
- 3.g. Draw a flow chart of microarray data analysis? 4

SECTION-C

35

4. Answer any one of the following:-

- 4-a. What do you understand by term Bioinformatics? Why there is a need informatics tools and resources in biology? CO1, K2 7
- 4-b. Describe in details medical databases and genome databases with examples? CO1, K2 7

5. Answer any one of the following:-

- 5-a. Describe the multiple sequence alignment algorithm on which CLUSTAL program is based? CO2, K2 7

- 5-b. Why we use dynamic programming algorithm? Describe various steps involved in dynamic programming? CO3, K2 7
6. Answer any one of the following:-
- 6-a. Describe some distance matrix based phylogenetic methods? CO3, K3 7
- 6-b. Suppose you find some discrepancy in the phylogenetic tree. What will you check to minimize the error? CO3, K3 7
7. Answer any one of the following:-
- 7-a. What is the different kind of interactions you will consider while studying protein-protein interactions? CO4, K2 7
- 7-b. There is so much diversity in proteins. Describe in detail what kind of process is responsible for that? CO4, K3 7
8. Answer any one of the following:-
- 8-a. What kind of databases you will explore, if you want to identify non-synonymous SNPs associated with a disease? CO5, K2 7
- 8-b. You want to study deleterious effect of SNP's. You will focus your study on synonymous or non-synonymous SNPs. Explain? CO5, K3 7

REG:JAN_JUN-2025