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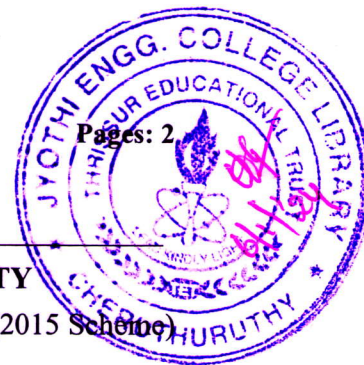
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Reg No.: _____

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APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY

Seventh Semester B.Tech Degree (S, FE) Examination December 2023 (2015 Scheme)



Course Code: CS465

Course Name: BIOINFORMATICS

Max. Marks: 100

Duration: 3 Hours

PART A

Answer all questions, each carries 4 marks.

		Marks
1	Define Bioinformatics and explain its applications	4
2	Explain the concept of base pairing. If the amount of thymine in genome is 20%, calculate the percentage of cytosine?	4
3	Explain any two protein sequence databases.	4
4	What is sequence alignment in bioinformatics? State the difference between global alignment & local alignment.	4
5	Distinguish between PAM & BLOSUM matrices.	4
6	Describe the forward algorithm in HMM.	4
7	Differentiate the genome of Prokaryotes and Eukaryotes	4
8	Define transposition with its classification	4
9	Describe the secondary structure of proteins.	4
10	With neat diagram explain the structure of amino acid.	4

PART B

Answer any two full questions, each carries 9 marks.

11	a) Show the structure of nucleic acids and discuss its components.	6
	b) A strand of DNA has the following sequence: 5'-AATTCAAATTAGG-3' What is the mRNA that will be generated from this DNA template through transcription?	3
12	a) What is the significance of data retrieval tools? Explain the features of Entrez?	3
	b) Write short note on primary biological databases.	6
13	a) Explain central dogma of molecular biology with a neat sketch	5
	b) Elaborate on composite databases	4

PART C

Answer any two full questions, each carries 9 marks.

- 14 a) Using Needleman and Wunsch dynamic programming method, construct the partial alignment score table for the following two sequences, using the following scoring parameters: match score: +1, mismatch score: -1, gap penalty: -2. 9

Sequence 1: GATTACA

Sequence 2: GTCGACGCA

- 15 a) Use UPGMA to reconstruct a phylogenetic tree using the following distance Matrix 9

SPECIES	A	B	C	D	E
B	1				
C	3	3			
D	6	6	5		
E	7	7	6	1	
F	10	10	9	7	8

- 16 a) What are scoring matrices? How PAM is derived? 3
- b) Draw the phylogenetic tree that corresponds to standard Newick format as 9((B,C)A)(D,E)). 3
- c) Explain the significance of Hidden Markov Model in bioinformatics. 3

PART D

Answer any two full questions, each carries 12 marks.

- 17 a) What is GC content? How it differ in eukaryotic and prokaryotic genomes. 6
- b) Describe different gene prediction methods. 6
- 18 a) Illustrate Nussinov Algorithm for RNA structure prediction with an example. 8
- b) Explain the Chou-Fasman and GOR method for protein secondary structure prediction 4
- 19 a) What is gene density? How it differs in prokaryotes and eukaryotes? 6
- b) Explain Zuker algorithm in detail 6
