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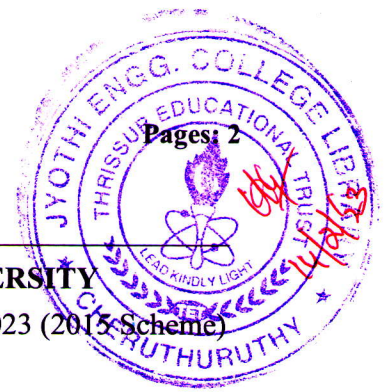
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Reg No.: _____

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APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY

Seventh Semester B.Tech Degree (S, FE) Examination January 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 | Differentiate between bioinformatics and computational biology. | (4) |
| 2 | Define genetic codes. Also explain start and stop codons. | (4) |
| 3 | Compare primary sequence database and composite sequence database. | (4) |
| 4 | Explain the various scoring matrices for nucleic acid sequence. | (4) |
| 5 | Describe the application of HMM in bioinformatics. | (4) |
| 6 | Compare various phylogenetic tree topologies. | (4) |
| 7 | Differentiate between prokaryotic and eukaryotic cell | (4) |
| 8 | Define gene expression. | (4) |
| 9 | Explain the major RNA secondary structure elements | (4) |
| 10 | Describe the structure of amino acids | (4) |

PART B

Answer any two full questions, each carries 9 marks.

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|----|---|-----|
| 11 | a) Explain central dogma of molecular biology with a neat sketch. | (6) |
| | b) Illustrate the structure of DNA | (3) |
| 12 | a) Describe any two nucleic acid sequence database. | (5) |
| | b) Describe any two protein sequence database | (4) |
| 13 | a) Compare the structural and functional difference between DNA and RNA | (6) |
| | b) Define the data retrieval tool entrez. | (3) |

PART C

Answer any two full questions, each carries 9 marks.

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|----|--|-----|
| 14 | a) Using Needleman and Wunsch dynamic programming method, construct the partial alignment score table and find the optimal alignment for the following | (9) |
|----|--|-----|

two sequences, using the following scoring parameters:

match score: +5, mismatch score: -1, gap penalty: -2.

Sequence 1: TCCTA

Sequence 2: TCATA.

- 15 a) Use UPGMA method to reconstruct a phylogenetic tree using the following distance matrix. (9)

	A	B	C	D	E	F
A						
B	1					
C	3	2				
D	7	6	4			
E	17	16	14	10		
F	19	18	16	12	2	

- 16 a) Differentiate between PAM and Blossum matrix (4)
 b) Explain Viterbi Algorithm with an example (5)

PART D

Answer any two full questions, each carries 12 marks.

- 17 a) Explain prokaryotic and eukaryotic gene structure with appropriate diagrams (9)
 b) Explain the significance of GC content in DNA (3)
- 18 a) Explain Nussinov algorithm with an example to predict the secondary structure of RNA (9)
 b) Explain different classification of Amino acid (3)
- 19 a) Explain Chou- Fasman and GOR methods of protein secondary structure prediction (6)
 b) Define Micro array. Explain the applications of Micro array. (6)
