Reg No.:_____ Name:_____

APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY

B.Tech Degree S8 (R,S) Exam April 2025 (2019 Scheme)

Course Code: CST468

Course Name: BIOINFORMATICS

Max. Marks: 100 **Duration: 3 Hours**

PART A

Answer all questions, each carries 3 marks. Marks

1		What are the differences between DNA and RNA?	(3)
2		Write down the sequence of complementary strand of following DNA strand. 5'-TAGCATGCATGCATGCATGCATGCATGC-3'	(3)
3		List any three major DNA nucleotide sequence databases.	(3)
4		Write FASTA file format of a sequence.	(3)
5		Explain the sequence alignment tool Clustal.	(3)
6		Compare pairwise alignment and multiple sequence alignment.	(3)
7		Define beta pleated sheet.	(3)
8		Write short notes on STRING database	(3)
9		What are the importances of modularity in system biology?	(3)
10		Identify three criteria for process classifications for modelling.	(3)

PART B

Answer any one full question from each module, each carries 14 marks.

Module I

11	a)	Explain in detail about the need of bioinformatics technologies. Also write various applications.	(7)
	b)	Explain the structural features of Watson and Crick model of DNA.	(7)

OR

12	a)	Explain the process of DNA replication.	(5)
	b)	What are the different steps of central dogma molecular biology? with the help of a neat diagram explain it.	(9)

Module II

13	a)	What is Primary Database sequence? Explain any three primary databases.	(9)
	b)	Compare PAM and BLOSUM scoring matrices.	(5)

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OR

14 a) What are the purposes of BLASTX, BLASTP and BLASTN? (9)

b) How the dot-plots are used for similarity analysis in bioinformatics. (5)

Module III

15 a) Explain Multiple Sequence Alignment with example. (4)

b) Explain the different steps of Smith-Waterman Algorithm and perform the local alignment on the sequences given below using Smith-Waterman algorithm. (Gap penalty -2, match score 1, Mismatch score -1) (10)
S1- ATGCT
S2- AGCT

OR

16 a) List out any four differences between prokaryotic and eukaryote gene. (4)

b) Explain the different steps of Needleman-Wunsch algorithm and perform the global alignment on the sequences given below using Needleman-Wunsch algorithm. (Gap penalty -2, match score 1, Mismatch score -1) (10)
S1- TATGA
S2- TACGA

Module IV

17 a) Explain any two methods for determining protein three-dimensional structure. (7)

b) Explain the process of predicting interactions among proteins. (7)

OR

18 a) Explain the hierarchies of protein structure. (7)

b) What do you understand by Ramachandran plot? Give its applications? (7)

Module V

19 a) Explain on Variables, Parameters, and Constants in modelling biological systems. (6)

b) Describe the importance of model development in System Biology. (8)

OR

20 a) Explain why data integration is an important part of systems biology. (6)

b) Explain the advantages of computational modelling. (8)

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