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Reg No.:________________ Name:________________________

APJ ABDUL KALAM TECHNOLOGICAL UNIVERSITY

Eighth Semester B.Tech Degree (R,S) Examination May 2024 (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 How proteome is related to genome? (3)

2 Compare mRNA, tRNA, and rRNA. (3)

3 What are the three interpretations of dot matrix method for sequence analysis? (3)

4 Differentiate constant, Linear and Affine gap penalties. (3)

5 What are the requirements of database searching? (3)

6 What are the purpose of BLASTX, BLASTP and BLASTN? (3)

7 Compare the different methods for determining protein three dimensional structure. (3)

8 How to predict protein-protein interactions based on Domain Fusion? (3)

9 Justify the statement – Systems Biology is Modelling. (3)

10 List any two factors that determine the model behaviour of a biological system. (3)

PART B

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

Module I

11 a) What are the nature and scope of bioinformatics? (7)

b) Discuss bio-molecules involved in central dogma, its structure and types. (7)

OR

12 a) Illustrate the steps involved in the process of transcription. (7)

b) What are the applications of bioinformatics? (7)

Module II

13 a) Discuss the various classifications of biological databases in Bioinformatics with example. (10)

b) Differentiate Global and Local alignment. (4)

OR

14 a) Discuss the importance of Dynamic programming in Sequence Alignment. (7)

b) Illustrate the biological sequence format “FASTA”. (7)

Module III

15 a) Applying Smith Waterman method construct the partial alignment score table for the following two sequences, using the scoring parameters (7)

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

ACCGTGA

GTGAATA

Also write down the optimal global alignment between these sequences along with the optimal score.

b) Illustrate the structure of a gene in Prokaryotic cell with neat sketch. (7)

OR

16 a) Applying Needleman and Wunsch dynamic programming method, construct the the partial alignment score table for the following two sequences, using the scoring parameters match score : +1, mismatch score : -1, gap penalty : -2. (7)

AATC

AGC-

Also write down the optimal global alignment between these sequences along with the optimal score.

b) Illustrate the structure of a gene in Prokaryotic cell with neat sketch. (7)

Module IV

17 a) Explain the format of Protein Data Bank. (7)

b) What are the features of Protein Structural Visualization program? Mention various styles of molecular structures produced by visualization program. (7)

OR

18 a) Describe how to predict interactions among proteins. (10)

b) Explain the features of STRING database (4)

Module V

19 a) Describe the various properties of models in system biology. (10)

b) How does data integration help in understanding complex biological pathways and networks? (4)

OR

20 a) Illustrate on variables, Parameters, and constants in Biological systems? (9)

b) Differentiate the system state and steady state of biological system network. (5)

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