Reg. No. : ☐☐☐☐☐☐☐☐☐☐☐☐☐

Question Paper Code: 2145030

B.E. / B.Tech. DEGREE EXAMINATIONS, NOV/ DEC 2024
Fifth Semester
Bio Technology
U20BT501 – ESSENTIALS OF BIOINFORMATICS
(Regulation 2020)

Time: Three Hours   Maximum: 100 Marks

Answer ALL Questions

PART – A   (10 x 2 = 20 Marks)

1.   Differentiate the raw and processed data of a database.

2.   Find out the role of data mining.

3.   Mention the purpose of gene sequence alignment.

4.   Write the importance of annotation.

5.   Highlight the role of protein-protein interactions.

6.   How can you locate the binding site in the protein-protein complex?

7.   Provide the necessity of protein structure comparison.

8.   Define the concept of motifs.

9.   List the composition of human genome.

10. Give the techniques actively participated for gene finding.

11. (a) Write a detailed note on biological database model and explain data mining and data storage.   (16)

(OR)

(b) i) How can the data base stored and give the retrieval of data from data base.
ii) Give the use of BLAST and FASTA.   (10+6)

12. (a) Describe the importance of Hidden Markov Models (HMM) in bioinformatics and Explain the mode of conjugated genes prediction from sequences.   (16)

(OR)

(b) Elaborate the local, global and multiple sequence alignment.   (16)

13. (a) i) Elucidate the steps involved in protein-protein interaction.
ii) Extract the essentials of phylogenitic tree analysis.   (8+8)

(OR)

(b) Propose the protein structure comparison by using protein structure database.(16)

14. (a) Reveal the comparison of distance matrices in protein structure.   (16)

(OR)

(b) Explain the evolution of protein structure and sequence by different software tools.

15. (a) Discuss the essence and need of human genome in bioinformatics studies.   (16)

(OR)

(b) Write an essay on functional genomics with suitable examples.   (16)

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