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Question Paper Code:U6C02

B.E./B.Tech. DEGREE EXAMINATION, APRIL / MAY 2025

Sixth Semester

Biotechnology

21UBT602 BIOINFORMATICS

(Regulations 2021)

Duration: Three hours

Maximum: 100 Marks

Answer ALL Questions

PART A - (10 x 2 = 20 Marks)

1. Outline the role of Telnet in Bioinformatics. CO1-U
2. Bioinformatics is a multidisciplinary field. Justify this statement. CO2-App
3. How Sum of Pair method (SOP) is used in sequence alignment? CO2-App
4. Outline Heuristic algorithms and its applications. CO2-App
5. Write a note on Fitch-Morgalisch algorithm. CO1-U
6. How will you evaluate phylogenetic tools? CO1-U
7. What are protein secondary structure and tertiary structure prediction methods? CO1-U
8. List out the criteria to select the template in homology modeling. CO1-U
9. What is Sequence-Tagged Site (STS)? CO1-U
10. What are the methodologies in gene identification/gene finding? CO1-U

PART – B (5 x 16= 80 Marks)

11. (a) Classify biological databases based on data type, maintainer status, data access, data source, database design and Organism. CO2-App (16)
Discuss the steps that have to be followed, to retrieve the fastasequence of c- Myc gene from NCBI.

Or

- (b) If you get a particular protein named 'Keratin'. How will you retrieve its (a) Nucleic acid sequence (b) Protein sequence Protein chains (c) Amino acid frequency etc? Describe briefly? CO2-App (16)
12. (a) Trace the optimal alignment for the given sequences using Smith-waterman algorithm. Seq 1=ACGTTTC and Seq 2=ACGTTT given scoring system as follows: match=+2, mismatch = +1, and gap penalty= -1 CO2-App (16)
- Or
- (b) Align the 2 sequences i=ACGAA and j=AGCGA using Needleman Wunch algorithm. The given scoring system is as follows: match=+1, mismatch = -1, and gap penalty= -2 CO2-App (16)
13. (a) List out the steps involved in phylogenetic tree construction and discuss with a distance based method? CO1-U (16)
- Or
- (b) What is a neighbour joining tree? How it is different from UPGMA? Also explain how Jukes Cantor model is different from Kimura model. CO1-U (16)
14. (a) How gene prediction methods are useful for research and also explain the process of *Ab initio* protein modeling? CO1-U (16)
- Or
- (b) What is the rationale behind homology modeling? Discuss the various steps involved in the same. CO1-U (16)
15. (a) Discuss the importance of string specific functions in PERL. Write down a Bioperl script to translate a DNA sequence CO1- U (16)
- Or
- (b) Describe in detail the applications of regular expressions in PERL and list five regular expression modifiers. Write down a Bioperl script to translate a DNA sequence. CO1- U (16)