**Total No. of Questions :12]**

**SEAT No. :** ☐

**P3422**

**[Total No. of Pages :3**

# [4959]-197

# B.E. (Information Technology)

# a - BIOINFORMATICS

# (2008 Course) (Elective - IV) (Semester - II)

***Time : 3 Hours]*** ***[Max. Marks :100***

***Instructions to the candidates:***

1) ***Answer Q1 or Q2, Q3 or Q4, and Q5 or Q6 from section I and Q7 or Q8, Q9 or Q10 and Q11 or Q12 from section II.***
2) ***Answer 3 questions from section - I and 3 questions from section II.***
3) ***Answer to the two sections should be written in separate answer books.***
4) ***Neat diagrams must be drawn wherever necessary.***
5) ***Figures to the right indicate full marks.***
6) ***Assume suitable data, if necessary.***

## SECTION-I

***Q1)*** a) What is the scope of bioinformatics? Why is it treated as multidisciplinary field? **[8]**

b) List the various Bioinformatics databases. Explain any one Protein database in detail. Also explain its importance in analysis and developing the BI applications. **[10]**

OR

***Q2)*** a) Explain with neat diagram the central dogma of molecular biology. Explain the different molecules participating in Information flow and its importance in various Functional Sites. **[10]**

b) Explain Bioinformatics applications with respect to the following areas:**[8]**

i) Micro arrays

ii) Drug Discovery

***P.T.O.***

*Q3)* a) Explain the role and importance of clustering in Microarray data? Discuss any two methods of clustering applied on gene expression data. **[8]**

b) Discuss any two statistical methods and tools used in data analysis of BI. **[8]**

OR

*Q4)* a) List various statistical analysis tools. Define Sensitivity and Specificity of a tool. Define in brief False Negative, True Negative, True Positive and False positive. **[8]**

b) How Dynamic programming method is applicable in Sequence alignment? Write in detail about Needleman-Wunch algorithm (Global Alignment) and Smith Waterman Algorithm (Local Alignment). **[8]**

*Q5)* a) Explain the importance of pattern matching techniques in Bioinformatics. List the various techniques of pattern matching. Elaborate any one technique in detail. **[8]**

b) Write short notes on: **[8]**

i) Pairwise Sequence Alignment (PSA)

ii) Multiple Sequence Alignment (MSA)

OR

*Q6)* a) Explain the text mining with NLP Process. **[8]**

b) How the machine learning techniques are used in Bioinformatics? Discuss any two machine learning methods used in BI applications. **[8]**

## SECTION-II

*Q7)* a) Explain the process of Drug discovery. What high-throughput screening methods are employed in screening drugs? **[10]**

b) Differentiate between Ab-Initio and Heuristic methods of Protein structure prediction process. **[8]**

OR

***Q8)*** a) Draw and explain Collaboration-Communication model with appropriate examples and its hierarchy. **[8]**

b) Describe in brief the Metropolis algorithm with Monte Carlo method by considering with its major issues like consistency and performance. **[10]**

***Q9)*** a) Explain steps followed by BLAST Algorithm to find a matching sequence. **[8]**

b) Discuss Similarities and Differences of FASTA and BLAST tools for sequence alignment. **[8]**

OR

***Q10)*** a) What are the several ways of implementing the FASTA algorithm? Write the steps in FASTA algorithm. **[8]**

b) What is Hashing? How is it exploited in FASTA database algorithms? **[8]**

***Q11)*** a) Define the importance of ecosystem. Describe in detail the factors affecting the ecosystem. **[8]**

b) What is Biotechnology? Discuss the relationship between Genetic Engineering and Biotechnnology with suitable example. **[8]**

OR

***Q12)*** a) What is meant by pollutant? List different pollutants. How it affects atmosphere and hydrosphere? **[8]**

b) Discuss in brief Genetic Engineering. Explain how it helps in identifying the diseases. **[8]**

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