

Total No. of Questions : 12]

SEAT No. :

P2025

[Total No. of Pages : 3

[5254]-197

B.E. (Information Technology)

BIO INFORMATICS

(2008 Pattern) (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) Answers 3 questions from Section - I and 3 questions from Section - II.*
- 3) Answers 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? Explain bioinformatics applications related to the following areas: **[10]**

Information Search & Retrieval.

Microarrays

Sequence Assembly

Pharmacogenomics

b) Discuss the various applications of BioInformatics and the associated technologies to those applications. **[8]**

OR

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

b) Explain major types of Protein databases with most suitable example for each. **[8]**

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

b) Explain in brief the data visualization techniques applicable to BioInformatics. Discuss any two visualization tools with example. **[8]**

OR

P.T.O.

Q4) a) Define Microarray. Explain the sources of variability in Microarray preparation and reading. Explain how statistical analysis can be used to reduce variability. [8]

b) List various statistical analysis tools. What is meant by Sensitivity and Specificity of a tool? Explain in brief False Negative, True Negative, True Positive and False positive. [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) What are the types of machine learning processes? Explain any two machine learning processes. [8]

OR

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

b) Explain computational methods of Sequence alignment [8]

i) Dynamic programming

ii) Word method

SECTION - II

Q7) a) Draw the block diagram of components of a modeling and simulation system including a model, database and engine. Also draw and explain the modeling and simulation process. [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. [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)** Define raw score, bit score and e-value in BLAST. Also explain the steps applied by BLAST Algorithm to find a matching sequence. [8]
- b) Differentiate between FASTA and BLAST algorithms. [8]

OR

- Q10)a)** Discuss the applications of PSI-BLAST program which explores protein family relationships. [8]
- b) What is Hashing? How is it exploited in FASTA database algorithms?[8]

- Q11)a)** Discuss the various factors responsible for degradation in the ecosystem.[8]
- b) What is Biotechnology? How Genetic engineering tools work in Biotechnology? [8]

OR

- Q12)a)** How does Genetic engineering work? Which models are used for identifying the diseases. [8]
- b) Discuss in brief the role of pollutants in interchange and transformation of atmosphere, hydrosphere and lithosphere. [8]

