

Total No. of Questions : 12]

SEAT No. :

P855

[4458]- 807

[Total No. of Pages : 3

B.E. (Information Technology)

BIO-INFORMATICS

(2008 Course) (Semester - II) (Elective - IV) (414451)

Time : 3 Hours]

[Max. Marks : 100

Instructions to the candidates:

- 1) *Answer Questions 1 or 2, 3 or 4, 5 or 6 from Section-I and question 7 or 8, 9 or 10, 11 or 12 from Section-II.*
- 2) *Answers to the two Sections should be written in separate answer books.*
- 3) *Neat diagrams must be drawn wherever necessary.*
- 4) *Figures to the right indicate full marks.*
- 5) *Assume suitable data, if necessary.*

SECTION - I

- Q1)** a) Explain the Central Dogma Of Molecular Biology. What is its significance in Bioinformatics? [8]
- b) Discuss applications of bioinformatics in detail. [8]

OR

- Q2)** a) The probability of a patient having a particular genetic disease is 0.6. Calculate the pretest odds? If the likelihood ratio is given as 2.75, calculate the posttest odds? Find the probability of the patient suffering from the genetic disease? [8]
- b) Explain any two limitations of Bayes' Theorem. [8]

- Q3)** a) List different computational methods of sequence alignment and discuss any two in detail. [8]
- b) What is Clustering? Explain two methods of clustering gene expression data? [8]

OR

- Q4)** a) What is the role of microarray in bioinformatics? Explain the stepwise spotting procedure of microarray in bioinformatics. [8]
- b) Discuss difference between clustering and classification. [8]

P.T.O.

- Q5)** a) Define Data mining. State and explain various data retrieval tools in Bioinformatics? [10]
b) Explain various representations of nucleotide sequence along with their particular uses and application. [8]

OR

- Q6)** a) Explain following methods of computational sequence alignment: [10]
i) Dynamic programming.
ii) Dot matrix methods.
b) What is pattern matching? Discuss different methods of pattern matching. [8]

SECTION - II

- Q7)** a) Explain Modeling and Simulation process along with the components in detail. [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 hierarchy. [10]
b) Explain the comparative modeling process of protein structure prediction. Discuss all its phases. [8]

- Q9)** a) Explain in detail FASTA algorithm and the recommended steps for a FASTA search. [8]
b) What is Hashing? How is it exploited in FASTA database algorithms?[8]

OR

- Q10)** a) Discuss Similarities and Differences of FASTA and BLAST tools for sequence alignment. [8]
b) Explain steps followed by BLAST Algorithm to find a matching sequence. [8]

Q11) a) What is Biotechnology? How Genetic engineering tools work in Biotechnology? [8]

b) Discuss the various factors responsible for degradation in the ecosystem. [8]

OR

Q12) a) Write short notes on HMM, Neural Network. [8]

b) What is Genetic Engineering? What is Genetic marker? What are the dangers of GE? [8]

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