

Total No. of Questions : 12]

SEAT No. :

P1484

[Total No. of Pages : 3

[4164] - 737 ✓

May - June 2012

B.E. (Information Technology)

BIOINFORMATICS

(2008 Pattern) (Elective - IV) (Sem. -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) 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) Define bioinformatics. Explain bioinformatic applications related to the following areas : **[10]**

- i) Phylogenetic Analysis.
- ii) Genome Annotation.
- iii) Proteomics.
- iv) Drug Discovery.

b) Classify and explain major databases in bioinformatics giving examples of each database. **[8]**

OR

Q2) a) Explain central dogma of molecular biology with neat diagram. Explain how is it an information science. **[8]**

b) State and explain various data retrieval tools in bioinformatics. Explain the steps for data mining and knowledge discovery of biological databases. **[10]**

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- Q3)** a) What is structure visualization? Explain the various rendering tools in structure visualization. [8]
b) Explain microarray spotting process flow in detail. How is microarray result analysis done? [8]

OR

- Q4)** a) Explain in detail the various methods of data mining for extracting patterns from data. [8]
b) Differentiate between clustering and classification. Explain hierarchical and k-means clustering in brief. [8]

- Q5)** a) Explain the basic machine learning process with neat diagram. Describe following machine learning processes in brief: [8]
i) Neural networks.
ii) Decision Trees.
b) What is text mining? Explain NLP approach of text mining in detail, giving significance of each stage. [8]

OR

- Q6)** a) Explain major steps in pattern recognition and discovery process. [8]
b) Explain following methods of computational sequence alignment: [8]
i) Dot Matrix Analysis.
ii) Word - based Method.

SECTION - II

- Q7)** a) Explain modeling and simulation process alongwith the components involved in detail. [8]
b) Differentiate between Ab-Initio and Heuristic methods of protein structure prediction. Explain the general ab-initio prediction process in detail with neat diagram. [10]

OR

- Q8)** a) Draw the collaboration - communication model. Explain collaboration and communication hierarchy in detail with neat diagram and appropriate examples. [10]
b) Explain synchronous and asynchronous collaboration. [8]

- Q9)** a) Explain similarities and differences between BLAST and FASTA tools for sequence alignment. [8]
- b) Explain FASTA algorithm in detail with recommended steps for similarity searching. [8]

OR

- Q10)** a) Explain BLAST algorithm. State the major refinements included in gapped BLAST. [8]
- b) Explain the significance of E() value with example. What is filtering in BLAST? [8]

- Q11)** a) Discuss various factors responsible for degradation in the ecosystem. [8]
- b) Explain how interchange and transformation of pollutants take place in atmosphere, hydrosphere and lithosphere. [8]

OR

- Q12)** a) Define genetic engineering. Explain any two techniques of genetic engineering in detail. [8]
- b) Write short notes on : [8]
- i) Significance of Biotechnology.
- ii) Applications of genetic engineering.

