

Total No. of Questions : 12]

SEAT No. :

[Total No. of Pages :3

P1445

[4759] - 200

B.E. (I.T.)

BIOINFORMATICS

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

Time : 3 Hours]

[Max. Marks : 100

Instructions to the candidates:

- 1) Answer three questions from section I and three questions from Section II.*
- 2) Answers to the two sections should be written in separate 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) Define Bioinformatics. Explain any four protein databases with most suitable example of each. [8]
- b) What is central Dogma of Molecular Biology. Explain with neat diagram. Why is Bioinformatics referred to as information science? [8]

OR

- Q2)** a) Explain Bioinformatics applications with respect to the following areas: [8]
- i) Microarrays
 - ii) Drug Discovery
 - iii) Sequence Assembly
- b) Explain the significance of DNA, RNA and protein Molecules. Explain DNA with neat diagram. [8]
- Q3)** a) Explain how microarray data analysis is applied in Bioinformatics with the help of neat diagram. [8]
- b) What is sequence alignment? List the different methods of computational sequence alignment in detail. [8]

OR

P.T.O.

Q4) a) List the various statistical analysis tools. What is meant by sensitivity and specificity of a tool? Explain any one statistical analysis tool in detail. [8]

b) What is the significance of user interface & information theory in Bioinformatics? Explain the user interface hierarchy alongwith neat diagram. [8]

Q5) a) Explain in detail the text mining process in NLP. [8]

b) What is sequence alignment? List various sequence alignment methods. Explain any two methods of sequence alignment in detail. [10]

OR

Q6) a) What are the types of machine learning processes? Explain any two processes in detail with neat diagram. [8]

b) Define sequence alignment. Explain following two sequence alignment methods in detail: [10]

i) Dynamic Programming

ii) Word method

SECTION - II

Q7) a) Explain the ab-initio and Heuristic methods of protein structure Prediction in detail with neat diagram. [8]

b) What is the need of collaboration & communication in Bioinformatics? Draw the neat diagram of collaboration & communication model with proper hierarchy. Also explain synchronous & asynchronous collaboration. [10]

OR

Q8) a) Explain the comparative modeling process of protein structure Prediction. [8]

b) What are the components involved in modeling & simulation system? Explain the basic components in this modeling and simulation system in detail with neat diagram. [10]

Q9) a) Explain FASTA algorithm in detail. List various implementations of FASTA [8]

b) Differentiate between FASTA and BLAST algorithm. Listing major differences between the two. [8]

OR

Q10)a) Explain BLAST algorithm in detail. Discuss PSI-BLAST method in brief. [8]

b) What is an E-value? Explain its significance in FASTA search. [8]

Q11)a) What is Genetic Engineering? Explain its major applications in brief. [8]

b) Explain the process of interchange and transformation of pollutants in atmosphere, hydrosphere & lithosphere. [8]

OR

Q12)a) Discuss the various factors responsible for degradation in the ecosystem. [8]

b) Explain drug discovery process. What is the importance of the cell cycle in the drug discovery process. [8]

