

Total No. of Questions : 12]

SEAT No. :

P807

[4659] - 220

[Total No. of Pages : 2

B.E. (Information Technology) (Semester - II)

BIO INFORMATICS

(2008 Pattern) (Elective - IV(a))

Time : 3 Hours]

[Max. Marks : 100

Instructions to the candidates:

- 1) *Answer 3 questions from Section I and 3 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.*

SECTION - I

- Q1)** a) Explain what is Bioinformatics. Mention its objective and definition. [8]
b) Explain central dogma of molecular biology. [10]

OR

- Q2)** a) Define Bioinformatics. Mention and explain its various applications. [10]
b) Explain the Bayes' Rule application in biological sequence analysis. [8]

- Q3)** a) Discuss and comment on resolution and accuracy of methodology and steps used to create sequence maps. [8]
b) What is clustering? Explain two methods of gene expression data. [8]

OR

- Q4)** a) Explain biology data visualization and sequence visualization. [8]
b) Differentiate clustering and classification. [4]
c) Describe advantages of clustering in molecular biology. [4]

- Q5)** a) Describe K-mean clustering method in detail with an example. [8]
b) Enlist pattern matching techniques in bioinformatics explain any one in detail. [8]

OR

- Q6)** a) Write short notes: [9]
i) Dot Matrix Analysis.
ii) Dynamic Programming
iii) Word Method
b) How bioinformatics related with machine learning techniques. Explain any one machine learning method with bioinformatic applications. [7]

P.T.O.

SECTION - II

- Q7)** a) Write a short notes on: [10]
i) Colloboration and communication model.
ii) Synchronous and usynchronous model.
b) Explain drug discovery in detail. How bioinformatics can help in novel drug discovery. [6]

OR

- Q8)** a) What are the component involved in modeling and simulation system? Explain the basic modeling and simulation process in regards to bioinformatics with neat diagram. [10]
b) Explain the comparative modeling process of protein structure prediction. [6]

- Q9)** a) Explain BLAST Algorithm in detail. [8]
b) Explain FASTA Algorithm. What FASTA programs are available for sequence alignment. [8]

OR

- Q10)**a) Enlist and explain different Bioinformatic tools. [8]
b) Compare FASTA and BLAST tools for sequence Alignment. What are the recommended steps for FASTA search. [8]

- Q11)**a) Discuss Application of Genetic engg. [10]
b) Define Bio-technology. Mention significance of biotechnology. [8]

OR

- Q12)**a) What is futurescope of bioinformatic in biotechnology. [8]
b) Explain the process of interchange and transformation of pollutants in atmosphere, hydrosphere and lithosphere. [10]

