Total No. of Questions : 12]

P807

[4659] - 220

[Total No. of Pages : 2

SEAT No. :

B.E. (Information Technology) (Semester - II) BIO INFORMATICS (2008 Pattern) (Elective - IV(a))

Time : 3 Hours]

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 it's objective a	and definition.[8]
b)	Explain central dogma of molecular biology.	[10]

OR

- **Q2)** a) Define Bioinformatics. Mention and explain it's various application.[10]
 - b) Explain the Baye's Rule application in bilogical 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:

- i) Dot Matrix Analysis.
- ii) Dynamic Programming
- iii) Word Method
- b) How bioinformatics related with machine learning techniques. Explain any one machine learning methods with bioinformatic applications. [7] P.T.O.

[Max. Marks : 100

[9]

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]

#