Total No. of Questions : 12] [Total No. of Pages : 3

P957

[3664]-352

B.E. (Information Technology)

BIOINFORMATICS sem 1

(2003 Course) (Elective I)

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. Mention and explain its various applications. **[9]**

b) Explain the major types of protein databases with most suitable example for each. **[7]**

OR

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

b) What is genomics? Explain the difference between structural & functional genomics. State the tools & techniques included in both. **[8]**

Q3) a) What is structure visualization? State & explain the various features of representative protein structure rendering programs and compare them. **[9]**

b) Explain user interface and information theory. Also explain the four basic components in user interface hierarchy with neat diagram. **[8]**

OR

Q4) a) Describe the working of microarray with spotting technique. What are the sources of variability in spotting? Compare spotting and affimetrix microarray preparation process. **[9]**

b) Explain various data mining methods with neat diagrams. **[8]**

P.T.O.

Q5) a) Explain centralized and distributed data mining infrastructure in detail. **[8]**

b) What are the types of machine learning processes? Explain any three machine learning techniques in detail. **[9]**

OR

Q6) a) What is text mining? Explain the NLP process of text mining with its various phases, in detail. **[8]**

b) List different computational methods of sequence alignment. Explain any two of them. **[9]**

SECTION - II

Q7) a) What are the different methods of protein structure prediction? Explain the Ab Initio method of protein structure prediction process with the help of neat diagrams. **[7]**

b) What are the components involved in a modelling and simulation system? Explain the basic modelling and simulation process in regards to bioinformatics with neat diagram. **[10]**

OR

Q8) a) Write short notes on:-

i) Collaboration and communication model. **[5]**

ii) Synchronous and asynchronous collaboration. **[5]**

b) Explain the comparative modelling process of protein structure prediction. Discuss all its phases in detail. **[7]**

Q9) a) Explain FASTA algorithm. What FASTA programs are available for sequence alignment? **[6]**

b) What are the recommended steps for FASTA search? **[6]**

c) Compare FASTA and BLAST tools for sequence alignment. **[5]**

OR

*Q10)*a) Explain BLAST algorithm in detail with neat diagrams. **[6]**

b) What is an E ( ) value? Explain its significance giving suitable examples. **[4]**

c) Explain gapped - BLAST, alongwith all the major refinements included. What is filtering in BLAST? **[7]**

*Q11)*a) Explain the process of interchange and transformation of pollutants in atmosphere, hydrosphere and lithosphere. **[8]**

b) Define Biotechnology. What is the significance of environmental biotechnology? Discuss various factors responsible for degradation of the ecosystem. **[8]**

OR

*Q12)*a) Write short notes on:-

i) Genetic Markers. **[5]**

ii) Polymerase Chain Reaction. **[5]**

b) Explain various applications of genetic engineering. **[6]**