Total No. of Questions :12]

SEAT No. :

P1795

[Total No. of Pages :3

[4859]-197
B.E (Information Technology)
a:BIOINFORMATICS
(2008 Course) (Elective - IV) (Semester - II)

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 answer books.***
3) ***Neat diagrams must be drawn with labelled wherever necessary.***
4) ***Assume suitable data if necessary.***

SECTION - I

Q1) a) Explain with neat diagram the central dogma of molecular biology. Explain the molecules participating in information flow and the various functional sites. **[10]**

b) Discuss on Bioinformatics application indetail. **[6]**

OR

Q2) a) What is Baye's rule? Explain Baye's theorem applicable in biological system.
Explain any two limitations of Baye's theorem. **[10]**

b) Discuss any two public bioinformatics database with appropriate examples. **[6]**

Q3) a) What is Microarray? Define it. Explain the sources of variability in microarray preparation and reading. Explain how statistical analysis can be used to reduce variability. **[8]**

b) Enlist and discuss any two different computational methods of sequence alignment. **[8]**

OR

P.T.O.

Q4) a) Differentiate between classification & clustering. Discuss in brief the Kmean clustering with an example. **[8]**

b) Explain any two machine learning processes. **[8]**

Q5) a) Define data mining. State and explain various data retrieval tools in Bioinformatics. **[10]**

b) Explain various representation of nucleotide sequence along with their particular uses and application. **[8]**

OR

Q6) a) Explain methods of computational sequence alignment: **[10]**

i) Dynamic programming

ii) Dot matrix method

b) What is pattern matching? Discuss different methods for pattern matching. **[8]**

SECTION - II

Q7) a) Explain syncronous and Asynchronous collaboration with an appropriate examples. **[10]**

b) Explain the process of Drug discovery. What high-throughput screening methods are employed in screening drugs. **[8]**

OR

Q8) Explain the methods of protein structure prediction and determination: **[18]**

a) Experimental

b) Ab- initio

c) Heuristic

Q9) a) Explain the difference in the approach of BLAST and FASTA. **[8]**

b) Explain FASTA algorithm. What FASTA programs are available for sequences. **[8]**

OR

Q10)a) Explain BLAST algorithm in detail with neat diagram. **[8]**

b) Explain FASTA and the recommened steps for a FASTA search. **[8]**

Q11)a) Write short notes on: **[8]**

i) HMM

ii) Neural network

b) Explain various applications of Genetic Engineering. **[8]**

OR

Q12)a) What are the natural causes of degradation of ecosystem? **[8]**

b) Define Biotechnology. What is significance of environmental Biotechnology. **[8]**

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