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Total number of pages : 02

M.Tech
BTPC202

2nd Semester Regular/Back Examination-2015-16
Advanced Bioinformatics
Q Code : W758
Full Marks-70
Time: 3 Hours

Answer Question No. 1 which is compulsory and any Five from the rest.
The figures in the right-hand margin indicate marks.

- 1) Answer the following questions [2X10]
- a) What is Prosite?
 - b) Differentiate between Swissprot and trEMBL.
 - c) What is the significance of gap extension penalty?
 - d) What do you mean by Entrez?
 - e) What is threading?
 - f) What is PDB?
 - g) Explain Pfam.
 - h) What is gi number?
 - i) Explain Clustal W.
 - j) Name any two secondary structure prediction softwares.
- 2) a) Briefly write about data submission procedures and retrieval tools of various databases. [5]
- b) What are substitution matrixes? What are the uses of these matrixes? [5]
- 3) Explain comparative modeling approaches for protein. Describe the steps of homology modeling approach. [10]
- 4) Describe different steps of FASTA algorithm? How is it different from BLAST? [10]
- 5) a) Explain Markov models and its application in bioinformatics. [5]
b) State the significance of Boot strap analysis. [5]
- 6) a) Differentiate between Maximum parsimony methods and Maximum likely hood method. [5]
b) Explain different clustering based methods for phylogenetic analysis. [5]

7) a) Write a note on Neighbor joining method.

[5]

b) Explain SCOP.

[5]

8) Write short notes .

[2.5X4]

a) ExPasy

b) Genbank

c) Genetic algorithm

d) DDBJ sequence database
