USN ☐☐☐☐☐☐☐☐☐☐ **10BT56**

Fifth Semester B.E. Degree Examination, Dec.2016/Jan.2017

Bioinformatics

Time: 3 hrs. Max. Marks:100

Note: ***Answer FIVE full questions, selecting atleast TWO questions from each part.***

PART – A

1 a. What are Primary and Secondary databases? Explain with examples. **(04 Marks)**
b. Describe the Flat file structures of EMBL and PDB databases. **(08 Marks)**
c. Write notes on : i) KEGG ii) PROSITE. **(08 Marks)**

2 a. What is PAM250 matrix? Explain its construction and discuss its importance with regard to sequence alignments. **(06 Marks)**
b. Describe the algorithm of BLAST for homolog searches. Write a note on PSI BLAST and PHI – BLAST. **(08 Marks)**
c. Explain the logical aspects of Multiple sequence alignment method and its merits over pair – wise alignment method. **(06 Marks)**

3 a. Describe the various tree building methods to arrive at phylogenetic trees for a group of molecular sequences. **(08 Marks)**
b. Explain the tools CLUSTALW and PHYLIP for analysis of protein sequences. **(06 Marks)**
c. Derive an unrooted tree for the following distance matrix. **(06 Marks)**

	B	C	D	E
A	22	39	39	41
B	-	41	41	43
C	-	-	18	20
D	-	-	-	10

4 a. Highlighting the relevant tools, discuss the strategy adopted in predictive methods towards deciphering the various functional sites in Eukaryotic genomic sequences. **(08 Marks)**
b. What is Protein threading method? Discuss the popular tools for fold prediction exercises adopted towards analysis of protein sequences. **(08 Marks)**
c. Write a note on NCBI – ORF finder. **(04 Marks)**

PART – B

5 a. Highlighting the relevant insilico tool, discuss the approaches towards design of Primers via bioinformatics methods. Explain the factors that contribute to the stability of primers, with an illustrative example. **(10 Marks)**
b. What are restriction maps? Explain the need for deriving insilico maps. Comment on the on-line tools and databases useful in these approaches, with a relevant case study. **(10 Marks)**

6 a. Comparatively discuss the popular genome sequencing methods. Write a note on the various computational tools used in those exercises. **(10 Marks)**
b. Write short notes on Bioinformatics Tools and databases used in :
i) Micro array data analysis ii) Proteomics studies. **(10 Marks)**

Important Note : 1. On completing your answers, compulsorily draw diagonal cross lines on the remaining blank pages.
2. Any revealing of identification, appeal to evaluator and /or equations written eg, 42+8 = 50, will be treated as malpractice.

7 a. What is Molecular modeling? Discuss the relevance of these techniques in the context of computational drug design, with a suitable example. **(08 Marks)**

b. Explain the importance of molecular visualization tools in bioinformatics application. Write a note on Spdb viewer tool. **(06 Marks)**

c. Explain the concept of molecular superposition techniques and structural alignment methods, with a popular tool. **(06 Marks)**

8 a. What is Molecular docking? Explain the algorithm of Auto – Dock tool, highlighting its importance in ligard – receptor docking approaches. **(08 Marks)**

b. Discuss the importance of energy minimization tools and techniques in computational protein engineering application. **(06 Marks)**

c. Write a note on pharmocophore based drug design, with a suitable example. **(06 Marks)**

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