

Printed Pages : 3



BT403

(Following Paper ID and Roll No. to be filled in your Answer Book)

PAPER ID : 154403

Roll No.

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B. Tech.

(SEM. IV) THEORY EXAMINATION, 2014-15
INTRODUCTION TO BIOINFORMATICS

Time : 3 Hours]

[Total Marks : 100

Note : Attempt all questions.

1 Attempt any two parts of the following:- **10x2=20**

- (a) What are the various file formats to represent nucleotide sequences in biological databases? Explain briefly.
- (b) What do you mean by homology? How do you find it using sequence alignment tools.
- (c) Define motif and profile with examples. Explain the PROSITE database pattern.

2 Attempt any two parts of the following:- **10x2=20**

- (a) Explain the Smith-Waterman algorithm for local sequence alignment.
- (b) Define multiple sequence alignment and its applications. Describe the algorithm of CLUSTALW.
- (c) Write short note on
 - (i) Global sequence alignment
 - (ii) PielUp

3 Attempt any two parts of the following:- **10x2=20**

- (a) What are substitution matrices for protein? Explain briefly about the principles based on which these matrices are derived.
- (b) Describe the BLAST algorithm for database sequence similarity search.
- (c) Write short notes on:
 - (i) Dot matrix
 - (ii) PSI-BLAST

4 Attempt any two parts of the following:- **10x2=20**

- (a) Define Phylogeny. Explain the rooted and un-rooted tree with examples.
- (b) Explain briefly about the various phylogenetic tree analysis methods along with their merits and demerits.

- (c) Write short note on:
- (i) Distance matrix
 - (ii) Identity matrix

5 Attempt any two parts of the following:- **10x2=20**

- (a) Define the protein secondary structural elements?
Explain the GOR method.
- (b) Define the criteria of selecting methods for predicting tertiary structure of proteins. Explain the threading method in detail.
- (c) Write short note on:
 - (i) Modeller
 - (ii) Jmol.
