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

PAPER ID : 154403 Roll No.

# B.Tech.

## (SEM. IV) THEORY EXAMINATION 2013-14

## INTRODUCTION TO BIOINFORMATICS

*Time : 3 Hours* *Total Marks : 100*

**Note :–** Attempt **all** questions as directed.

1. Attempt any **four** parts :- (Distinguish between following) **(5×4=20)**
   (a) Character based v/s Distance based methods
   (b) Pairwise v/s Multiple sequence alignment
   (c) Dynamic v/s Progressive sequence alignment
   (d) BLAST v/s FASTA
   (e) PAM v/s BLOSUM
   (f) Needleman Wunsch v/s Smith Waterman
2. Attempt any **two** parts of the following : **(10×2=20)**
   (a) By the use of the UPGMA (Unweighted Pair Group Method With Arithmetic Mean) find out phylogram (guided tree) from given distance matrix :

| | A | B | C | D | E | F |
|---|---|---|---|---|---|---|
| A | – | | | | | |
| B | 2 | – | | | | |
| C | 4 | 4 | – | | | |
| D | 6 | 6 | 6 | – | | |
| E | 6 | 6 | 6 | 4 | – | |
| F | 8 | 8 | 8 | 8 | 8 | – |

(b) Define the concept of file format. Write down various types of file formats that are used in Bimolecular sequences.

(c) Explain the concept of sequence patterns. Write down various pattern representations that are used in bioinformatics.

3. Attempt any **two** parts of the following : **(10×2=20)**

(a) With the help of Needleman Wunsch Algorithm, find out the optimal alignment that are existing between Seq A and Seq B

SEQ A : – ACCCTGGAT

SEQ B : – ACCGGAT

With score

Match = +5

Mismatch = –1

Gappanauty = –2

(b) Define the concept of Homology. How are Orthologues and Paralogues helpful in finding evolutionary relationship with the help of an example ?

(c) Define the concept of scoring matrix. Explain various types of scoring matrices that are used in bioinformatics.

4. Attempt any **two** parts of the following : **(10×2=20)**

(a) Define the concept of multiple sequence alignment. Write and explain various methods that are used for multiple sequence alignment.

(b) What is Database Search ? Explain various versions of Basic Blast.

(c) What is Phylogeny ? Explain various methods that are used in phylogenetics by taking an example.



5. Attempt any **two** parts of the following : **(10×2=20)**

(a) Define the term protein tertiary structure prediction. Explain various methods that are involved in it.

(b) Explain the concept of drug discovery. Write down various steps that are involved in drug designing.

(c) What is protein secondary structure prediction. Explain various methods that are used for secondary structure prediction of proteins.