

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

Paper ID : 154403

Roll No.

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B.TECH BIOTECHNOLOGY

Theory Examination (Semester-VI) 2015-16

INTRODUCTION TO BIOINFORMATICS

Time : 3 Hours

Max. Marks : 100

1. Attempt ALL parts : (10×2 = 20)

- (a) What is the difference between orthologues and paralogues?
- (b) What do you mean by motifs?
- (c) What are the basic foundations of BI?
- (d) What is "k-tuples"?
- (e) What are the different layers involved in neural networking?
- (f) What do you understand by homology modelling?
- (g) What is phylogenetic analysis?

- (h) Correlate trEMBL and EMBL.
- (i) What is the secondary database?
- (j) What does BLOSUM stands for?

2. Attempt any FIVE of the following : (5×10 = 50)

- (a) What are the different tools for protein structure prediction?
- (b) Discuss the FM algorithm of phylogenetic tree building in detail covering all the formulations behind it.
- (c) What are the major differences between PAM & BLOSUM?
- (d) What are the differences between global and local alignment with reference to alignment algorithm?
- (e) What is the role of bio-informatics in Drug Designing?
- (f) What is the concept behind UPGMA approach for phylogenetics?
- (g) What is laboratory data submission? Discuss any one of the tools.

- (h) Discuss the Nearest Neighbour method for protein identification in detail.

3. Attempt any TWO of the following : (2×15 = 30)

- (a) Construct the phylogenetic tree using UPGMA approach-

| | A | B | C | D | E |
|---|---|---|----|----|----|
| A | - | 5 | 14 | 29 | 29 |
| B | - | - | 14 | 29 | 29 |
| C | - | - | - | 29 | 29 |
| D | - | - | - | - | 7 |
| E | - | - | - | - | - |

- (b) What is the concept behind data processing in Neural Network Modelling?
- (c) Write short notes on:
- Rasmol,
 - PSI-BLAST,
 - PROSITE.