2015

M.Sc.

3rd Semester Examination BIOTECHNOLOGY

PAPER-BIT-304

Full Marks: 40

Time: 2 Hours

The figures in the right-hand margin indicate full

Candidates are required to give their answers in own words as far as practicable.

Illustrate the answers wherever necessary.

Answer all questions.

Group-A

- 1. Answer any five questions from the following
 - (a) State the difference between paralog with
 - (b) What is tBLASTx?
 - (c) What is meant by 62 in BLOSUM62 matr

- (d) Define cellomics.
- (e) Expand BLAST, NCBI, FASTA, SCOP.
- (f) Name two programs which are used for homology based gene prediction approaches.
- (g) Define ORF. How many reading frame exists?
- (h) What is CATH?

Group-B

Answer any two questions from the following: 2×5

- 2. What are the advantages of "Human Genome Project"?
- Define gene. Explain feature based gene prediction approach.
- 4. Define biological database. Give an account of protein structure database, and oncogenic database. 1+2+2
- 5. State the difference between global alignment and local alignment. What is the importance of phylogenetic analysis?

Group-C

Answer any two questions:

- 6. Consider four species characterized by homo sequences ATCC, ATGC, TTCG and TCGG. Takin number of differences as the measure of dissin between each pair of species, use UPGMA methoderive a phylogenetic tree.
- 7. Define Bioinformatics. What are the commonly software tools used for in-silico analysis? What a different applicative aspect of Bioinformatics?
- 8. Explain the impact of genomics on medicine. sequences are submitted in Gen Bank? What is "Bl in multiple sequence alignment? What is the impoof optimal sequence alignment? 4+2
- 9. How family is differed from super-family? Define Write short note on secondary structural elements. codon bias. Give an example of a tool for exon pred

2+1+4