

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

Group—C

Answer any *two* questions :

6. Consider four species characterized by homo sequences ATCC, ATGC, TTCG and TCGG. Taking number of differences as the measure of dissimilarity between each pair of species, use UPGMA method to derive a phylogenetic tree.

7. Define Bioinformatics. What are the commonly used software tools for in-silico analysis? What are the different applicative aspects of Bioinformatics?

8. Explain the impact of genomics on medicine. How are sequences submitted in Gen Bank? What is "BLAST" in multiple sequence alignment? What is the importance of optimal sequence alignment? 4+2

9. How family is differed from super-family? Define family. Write short note on secondary structural elements. What is codon bias. Give an example of a tool for exon prediction. 2+1+4