2013

M.Sc.

3rd Semester Examination

BIOTECHNOLOGY

PAPER—BIT-304

Full Marks : 40

Time : 2 Hours

The figures in the right-hand margin indicate full marks.

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

Illustrate the answers wherever necessary.

Answer *all* questions.

Group—A

1. Answer any *five* questions from the following : 2×5

(a) What are identifiers? Mention their usage.

(b) Provide a name of a program or algorithm that performs a local multiple sequence alignment.

(c) What is the 'E' value in BLAST?

(d) What does the 62 mean for the BLOSUM62 scoring matrix?

(e) What is ORF? What is its utility?

(f) Given the two DNA sequences GCGT and GCT, and using +2 for a matchy, −2 for a mismatch, and a gap penalty of −1, give an optimum global alignment and its score.

(g) What is Clastal W? For what purpose it is used?

(h) Write down the full forms of EBI, PDB, EXPASY and NLM.

Group—B

Answer any *two* questions from the following : 5×2

2. Define gap penalty. What is an 'informative' and 'non-infomative' site? Describe some common techniques for gene prediction. 1+1+3

3. How you can differentiate 'Orthology' & 'Paralog'? How is tertiary protein structure different from its quarternary structure? Mention 2 important utility of protein 3D structure prediction. 2+2+1

4. Draw a Dot Plot for the following 2 sequences : CACG and GATCACG. Write down the full forms of EXPASY & EMBL. 4+1

5. Expand BLAST. Write short note on PSI-BLAST. Define SNP and epigenetics with one example for each. 1+2+2

Group—C

Answer any *two* questions : 10×2

6. (i) Describe NJ method. Mention its use with its advantages and disadvantages.
   (ii) Write a short note on 'human genome project'. $2\frac{1}{2}+2\frac{1}{2}+5$

7. Align the following two sequences GTACTACGA & GTACCGA by the dynamic programming algorithm. 10

8. What is GOR method? Distinguish between proteomics and genomics. What is 'accession code'? Mention the name of 2 mutation Databases. Mention one point mutation resulting a human disease. 2+3+1+2+2

9. (i) Briefly describe about post translational modifications.
   (ii) Discuss about the methods of whole genome sequence.
   (iii) Define FASTA. 4+4+2