5 SEM TDC DSE BOT (CBCS) 2 (H)

2024

(November)

BOTANY

(Discipline Specific Elective)

(For Honours)

Paper : DSE–2

(Bioinformatics)

Full Marks : 53

Pass Marks : 21

Time : 3 hours

*The figures in the margin indicate full marks
for the questions*

1. *(a)* Choose the correct answer of the following : 1×3=3

   (i) PIR stands for

   (1) Primary Information Report

   (2) Protein Information Resource

   (3) Protein Index Report

   (4) Protein Index Refractive

(Turn Over)

(ii) DNA Data Bank of Japan is a biological database that collects

    (1) Nucleotide

    (2) Protein

    (3) Amino acid sequences

(iii) An example of homology and similarity tool is

    (1) BLAST

    (2) PAM

    (3) RasMol

    (4) PROSPECT

(b) Fill in the blanks $1 \times 2 = 2$

    (i) BLOSUM stands for _____.

    (ii) The SWISS–PROT protein sequence database begin in the year _____.

2. Write short notes on any *three* of the following : $5 \times 3 = 15$

    (a) Gene expression database

    (b) Scope of bioinformatics

    (c) Pairwise sequence alignment

    (d) Application of bioinformatics in crop improvement

         (*Continued*)

3. Write the difference between the following :

4×3=12

(a) GenBank and Gene databases

(b) Primary and Secondary Databases

(c) Pairwise Sequence Alignment and Multiple Sequence Alignment

4. Consider the DNA strings AGATGG-CCCCATCG and CGGTCCCCCGATGG and compute the best global alignment of the two strings and alignment score assuming match score of 1, mismatch of 0 and gap penalty of –1.

7+3=10

Or

Write short notes /answers on any *two* of the following :

5+5=10

(a) Write the steps used to find values for a BLOSUM amino acid similarity matrix.

(b) Role of bioinformatics in drug design

(c) Role of bioinformatics in crop improvement

5. Describe the various resources and databases of Protein Information Resource. 6+5=11

Or

What are scoring matrices and what are they used for? Name and differentiate between two commonly used amino acid substitution matrices. If you have more divergent sequences then which substitution matrix one should use and with high or low number?

2+2+2+2+3=11

★ ★ ★