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

**2 0 2 2**

( Nov/Dec )

**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 :  $1 \times 3 = 3$

(i) The term 'bioinformatics' was coined by Hogeweg and Hesper/Margaret Dayhoff/Christian D. Wunsch/Temple F. Smith.

( 2 )

(ii) DNA Data Bank of Japan is a biological database that collects DNA / RNA / Protein / mRNA sequences.

(iii) Which of the following is an example of Homology and similarity tool?

BLAST/PAM/RasMol/ PROSPECT

(b) Fill in the blanks : 1×2=2

(i) BLOSUM stands for \_\_\_\_\_.

(ii) The SWISS-PROT protein sequence database began in the year \_\_\_\_\_.

2. Write short notes on any *three* of the following : 4×3=12

(a) ENTREZ

(b) Scope of bioinformatics

(c) Pairwise sequence alignment

(d) Application of bioinformatics in crop improvement

3. Write the difference between the following : 3×4=12

- (a) NCBI and EMBL
- (b) BLAST and FASTA
- (c) Primary and Secondary databases
- (d) Pairwise sequence alignment and Multiple sequence alignment

Or

Explain the scope and dimension of bioinformatics. How do you interpret bioinformatics and computational biology differently? 8+4=12

4. Consider the DNA strings AGATGGCCCCATCG 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 -1. Compute the best local alignment, and the best global alignment. 9+3=12

Or

Answer the following in short : 6×2=12

- (a) Write the steps used to find values for a BLOSUM amino acid similarity matrix.
- (b) Write a note on the role of bioinformatics in drug design.

( 4 )

5. Describe the various resources and databases of Protein Information Resource.

6+6=12

*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+4=12

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