



RAN - 2103001106020002

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**B.Sc. Biotechnology (Sem - VI) Examination March - 2025**

**BT - 18 : Introduction to Bioinformatics**

**Time: 2 Hours ]**

**[ Total Marks: 50**

**સૂચના : / Instructions**

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નીચે દર્શાવેલ નિશાનીવાળી વિગતો ઉત્તરવહી પર અવશ્ય લખવી.  
**Fill up strictly the details of signs on your answer book**

Name of the Examination:

**B.Sc. Biotechnology (Sem - VI)**

Name of the Subject :

**BT - 18 : Introduction to Bioinformatics**

Subject Code No.: **2103001106020002**

Seat No.:

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Student's Signature

- (2) Figures to the right indicate full marks.  
(3) Draw neat and labeled diagrams wherever necessary.

**Q.1 Give Specific Answer (Any Four)**

**08**

- Explain the concept of Genomics in simple terms.
- List one key difference between BLAST and FASTA.
- What is the full form of CATH and KEGG?
- What is % identity in BLAST results?
- Give two examples of metabolic pathway database.
- Give two examples of secondary nucleotide sequence databases

**Q.2 Attempt Any Two:**

**14**

- Write in detail about the different branches of bioinformatics with their applications.
- Why is PDB considered a crucial resource in structural bioinformatics? Justify your answer.
- Demonstrate how to use the NCBI database for sequence alignment.

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**[ P.T.O. ]**

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- Q.3 Explain in detail Any Two: 14**
- A. Demonstrate how to compute a local alignment using the Smith-Waterman algorithm.
  - B. Explain the types of gap penalties used in sequence alignment.
  - C. What does TIGR stand for in bioinformatics? Explain the purpose of the TIGR nucleotide sequence database.

- Q.4 Write Short note (Any Two) 14**
- A. Why is the Dot Plot method preferred for visualizing sequence similarities? Justify your answer.
  - B. Demonstrate how to calculate the Sum of Pairs score for a given multiple sequence alignment.  
(Scoring system: identity 1, mismatch -2, gap -4)  
ACCTGTGAC  
AC-TGTAAC  
ACCTGT-AC
  - C. Basic Local Alignment Search Tool(BLAST)
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