

**PARUL UNIVERSITY**  
**PARUL INSTITUTE OF APPLIED SCIENCES**  
**MID SEMESTER INTERNAL EXAMINATION, SUMMER 2019-20**  
**B.Sc. Biochemistry Semester VI**

**Paper Name: Bioinformatics**

**Date: 04/03/2020**

**Paper Code: 11102252**

**Time: 1hr 30min**

**Max. Marks: 40**

**Instructions:**

1. All questions are compulsory and options are given in first and second question only.
  2. Numbers to the right of question indicate the marks of respective question.
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**Q. 1** Attempt any one question of the following. **(08)**

(i) Explain the classification of biological databases in detail. Explain Sequence databases, Structure databases, and Functional databases with examples. Explain about Primary and Secondary databases with examples.

(ii) Explain in detail Dot Matrix plots and Needleman Wunsch algorithm.

**Q. 2** Attempt any three questions of the following. **(12)**

(i) What is SwissProt database?

(ii) Short note on PlasmDB.

(iii) Short note on Smith Waterman Algorithm

(iv) Difference between global and local alignment?

(v) What is pairwise alignment and multiple sequence alignment?

**Q. 3** Do as directed. Attempt all five questions. **(05)**

(i) Give four examples of tools of Multiple Sequence Alignment.

(ii) What is sequence alignment?

(iii) What are the three main steps in dynamic programming?

(iv) The Protein Information Resource (PIR) is established in 1984 by which organization?

(v) HOVERGEN is a specialized database for which types of genes?

**Q. 4** Write correct option in your answer sheet for following 15 multiple choice questions. **(15)**

MCQ 1 GenBank, the nucleic acid sequence database is maintained by

(A) Brookhaven Laboratory

(B) DNA Database of Japan (DDBJ)

(C) European Molecular Biology

(D) National Centre for Biotechnology

Laboratory (EMBL)

Information (NCBI)

MCQ 2 The initiation of FASTA format has symbol?

(A) >

(B) <

(C) /

(D) \*

- MCQ 3 Which of the following is not a variant of BLAST?  
 (A) BLASTN (B) BLASTP  
 (C) BLASTX (D) TBLASTNX
- MCQ 4 Which of the following is the sequence alignment tool provided by NCBI?  
 (A) Chime (B) BLAST  
 (C) FASTA (D) Clustal W
- MCQ 5 The procedure of aligning two sequences by searching for patterns that is in the same order in the sequences  
 (A) sequence alignment (B) pair-wise alignment  
 (C) multiple sequence alignment (D) all of these
- MCQ 6 The alignment procedure that tries to align the entire sequence is  
 (A) multiple sequence alignment (B) pair-wise alignment  
 (C) global alignment (D) local alignment
- MCQ 7 Which is the default scoring matrix used in BLAST?  
 (A) PAM 62 (B) BLOSUM 62  
 (C) BLOSUM 45 (D) BLOSUM 80
- MCQ 8 Literature databases include  
 (A) MEDLINE and PubMed (B) MEDLINE and PDB  
 (C) PubMed and PDB (D) MEDLINE and PDS
- MCQ 9 If you want to align two sequences which are more identical in sequence, which of the following scoring matrices would be most appropriate  
 (A) BLOSSUM 35 (B) BLOSSUM 40  
 (C) BLOSSUM 62 (D) BLOSSUM 80
- MCQ 10 Among the following which one is not the approach to the local alignment?  
 (A) Smith–Waterman algorithm (B) K-tuple method  
 (C) Words method (D) Needleman-Wunsch algorithm
- MCQ 11 Which of the following statements is false when describing SWISS-PROT?  
 (A) It is a curated protein sequence database (B) Data is redundant  
 (C) Provides a high level of annotations (D) It is maintained by Swiss Institute of Bioinformatics and EBI.
- MCQ 12 Which alignment is used to predict whether two sequences are homologous or not?  
 (A) Local (B) Global  
 (C) Pair-wise (D) Multiple
- MCQ 13 The scoring matrix for protein sequences is  
 (A) PAM matrix (B) BLOSSUM matrix  
 (C) RNA sequences (D) Thure Etzold

- MCQ 14 Which of the following is not a software for dot plot analysis?  
(A) SIMMI (B) DOTLET  
(C) DOTMATCHER (D) LALIGN
- MCQ 15 For palindromic sequences, what is the structure of the dot plot?  
(A) 2 intersecting diagonal lines at the midpoint (B) One diagonal  
(C) Two parallel diagonals (D) No diagonal

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