

**PARUL UNIVERSITY**  
**FACULTY OF ENGINEERING & TECHNOLOGY**  
**B.Tech. Summer 2018 - 19 Examination**

**Semester: 6**  
**Subject Code: 03111381**  
**Subject Name: Bioinformatics**

**Date: 09/05/2019**  
**Time: 10:30am to 1:00pm**  
**Total Marks: 60**

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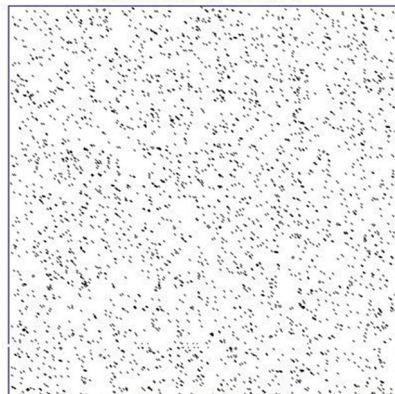
**Instructions:**

1. All questions are compulsory.
2. Figures to the right indicate full marks.
3. Make suitable assumptions wherever necessary.
4. Start new question on new page.

**Q.1 Objective Type Questions****(15)**

1. Which of the following is a sequence alignment tool:
  - a) BLAST
  - b) PRINT
  - c) PROSITE
  - d) PIR
2. The information retrieval tool of NCBI GenBank is:
  - a) Entrez
  - b) STAG
  - c) SeqIn
  - d) text search
3. DNA Data Bank of Japan was established in :
  - a.1991
  - b.1987
  - c.1986
  - d.1985
4. To be a good bioinformatician, it is necessary to have a sound knowledge of molecular biology, biochemistry, molecular biophysics, molecular modelling, computer, information technology, and biostatistics. T/F
5. MEDLINE covers the fields of medicine, nursing, dentistry, veterinary medicine, public health, and preclinical sciences. T/F
6. Which Matrix is also known as Dayhoff Matrix?
7. What is the full form of PAM and BLOSUM?
8. What is determined by backtracking step in dynamic programming method?
9. When do we get such dot matrix analysis?

DNA 1 on horizontal axis = 1348 bases  
DNA 2 on vertical axis = 2322 bases



Click on plot to get positional data

- 10. What is Expasy?
- 11. Needleman and Wunsch were the first to propose \_\_\_\_\_ method.
- 12. A genome map is a graphical representation that provides information about the location and the sequence of genes along the length of \_\_\_\_\_
- 13. \_\_\_\_\_ database is an open access, annotated collection of all publicly available nucleotide sequences and their protein translations
- 14. DNA makes RNA makes Protein, this is known as \_\_\_\_\_.
- 15. PDB refers to \_\_\_\_\_.

**Q.2** Answer the following questions. (Attempt any three) (15)

- A) Write a note on types of sequence alignment along with example.
- B) Explain about DOT matrix method.
- C) Explain about GenBank sequence Database and what is the procedure to retrieve sequence using GenBank.
- D) Explain about K-tuple Method.

**Q.3** A) Fill the matrix using dynamic programming method. Also backtrack and write the best possible sequence alignment. Write the rules which are used to fill the matrix. (07)

Values to be considered for Match = +1, Mismatch = -1, Gap penalty = -2

		A	A	T	C
A					
G					
C					

(08)

B) What are the different methods used to determine the sequence of DNA? Explain in detail about Sanger sequencing method with diagram.

**OR**

B) What are the different steps which are involved in Edman Degradation for protein sequencing? (08)

**Q.4** A) Write in details about the Shotgun Sequencing. (07)

**OR**

A) What is gel electrophoresis and how does it work? Explain with diagram. (07)

B) A sequence of human keratin protein has to be retrieved. Name and Explain in detail about the database which can be used to retrieve along with the procedure to be followed. (08)