

LMDQ/D-23**BASICS OF BIOINFORMATICS****Paper : MMB-304B**

Time : Three Hours]

[Maximum Marks : 80

Note : There are Nine questions in total. Students are required to attempt *five* question in all. Question No. 1 is compulsory. Attempt *four* questions (*one* from each unit) from remaining Eight questions. Each question carries equal marks.

Compulsory Question**1.** Explain :

- (a) Biological databases.
- (b) File format.
- (c) Global alignment.
- (d) Pair wise alignment.
- (e) PAM.
- (f) PSSM.
- (g) Motifs.
- (h) UPGMA.

UNIT-I

2. (a) Explain the classification and types of Biological databases.
(b) Write a note on :
 - (i) Uniprot.
 - (ii) PDB.
3. (a) Give a detailed description of Genbank file format and its features.
(b) Explain the tools and techniques of data submission on NCBI.

UNIT-II

4. (a) Explain Needleman-Wunsch algorithm for pairwise sequence alignment with example.
(b) Explain the concept of sequence alignment and its applications.
5. (a) Define BLAST and its various types.
(b) Explain the concept of log odd ratio. Write a note on BLOSUM matrices and its assumptions and advantages.

UNIT-III

6. (a) Write a note on :
 - (i) Methods of multiple sequence alignment.
 - (ii) Application of consensus sequence in sequence annotations.

- (b) Explain multiple sequence alignment and its significance? Describe its tools and their applications.
- 7. (a) Give a detailed overview on diversity and evolution of viral and prokaryotic genomes.
- (b) Explain the basic concept and applications of transcriptomics.

UNIT-IV

- 9. Explain various phylogenetic approaches and their assumptions.
 - 10. Describe the basic concept of genome annotations. Explain various methods and tools of gene identification.
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