



**WEST BENGAL STATE UNIVERSITY**  
B.Sc. Programme 6th Semester Examination, 2021



**BOTGDSE03T-BOTANY (DSE2)**

**BIOINFORMATICS**

Time Allotted: 2 Hours

Full Marks: 40

*The figures in the margin indicate full marks.  
Candidates should answer in their own words and adhere to the word limit as practicable.  
All symbols are of usual significance.*

1. Answer the following questions: (all the questions are compulsory) 1×16 = 16
- (a) What does NCBI stand for?
  - (b) What is the full form of MSA?
  - (c) Name a tool used to detect homology and similarity (between DNA or peptide sequences).
  - (d) Name a DNA database.
  - (e) What is PAM?
  - (f) What is transcriptomics?
  - (g) What is PIR?
  - (h) What is the purpose of using ClustalW?
  - (i) Name a software used to create Phylogenetic tree.
  - (j) Name a technique used in drug designing.
  - (k) Name a database for searching proteins.
  - (l) A software that might be used to translate DNA sequence into its amino acid sequence.
  - (m) Name a software used to predict the structure of the protein from a given amino acid sequence.
  - (n) What type of knowledge database is UniProt?
  - (o) What are the two major branches of Bioinformatics that deal with gene structure and function called?
  - (p) What is an accession number?
2. Answer any *eight* questions from the following: 3×8 = 24
- (a) What is the BLAST tool used for? What is the most popular format in which you need to submit the sequence in the search base?
  - (b) Briefly state the application of Bioinformatics.

- (c) What is Proteomics? Write a short note on its branches (Functional and Structural Proteomics).
- (d) Write a short note on Multiple Sequence Alignment and its different types.
- (e) Write a short note on Entrez.
- (f) What is FASTA? How is it represented?
- (g) Mention the importance of bioinformatics tools in drug design and discovery.
- (h) Name two methods based on which phylogenetic trees can be prepared. Name a biomarker(gene) that is most popularly used for preparation of phylogenetic tree using eukaryotic organisms.
- (i) Distinguish between a cladogram and a phenogram.
- (j) Give an example of Nucleotide Database, Protein Database, and Gene Expression Database.
- (k) Write a short note on application of Bioinformatics in crop improvement.
- (l) Write a short note on Primary and Secondary Biological Database.

**N.B. :** *Students have to complete submission of their Answer Scripts through E-mail / Whatsapp to their own respective colleges on the same day / date of examination within 1 hour after end of exam. University / College authorities will not be held responsible for wrong submission (at in proper address). Students are strongly advised not to submit multiple copies of the same answer script.*

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