

M.SC. BOTANY
II SEMESTER EXAMINATION, MAY 2024

Paper Name: **Bioinformatics**

Paper Code: **MBO-OE202**

Time: **2 ½ hours**

Maximum Marks: **60**

Note: This paper has 3 sections A, B, and C.

Section A: Answer all the questions. Section B: Attempt any **FIVE** Out of Six

Section C: Attempt any **TWO** out of Three

Instructions: Draw well-labelled diagrams wherever necessary

Abbreviations used:

CLO-Course Learning Outcomes

CLO 1: understand the components, generations and characteristics of computer; concept of hardware, software and internet (understand);

CLO 2: recognize concept of bioinformatics and types of biological data bases (understand);

CLO 3: analyze and develop various tools of bioinformatics (analyze/create); and

CLO 4: develop programs related to bioinformatics (create).

BLT-Bloom's Taxonomy Levels

1- Remembering, 2-Understanding, 3-Applying, 4-Analyzing, 5-Evaluating, 6-Creating

SECTION A

Very Short Type Question (15 questions)

15 x 1 = 15 marks

Q.No.	Questions	Marks	CO	BTL
1	What is the purpose of an operating system?	1	1	2
2	List two examples of secondary storage devices.	1	1	1
3	What does HTML stand for?	1	1	1
4	Define the term "World Wide Web" (WWW).	1	1	2
5	Compare LAN and WAN.	1	1	4
6	Give one example of Gene Expression Database.	1	2	1
7	PubMed is the example of database.	1	2	1
8	Give one example metabolic pathways database.	1	2	1
9	List two software tools commonly used for MSA.	1	3	1
10	Define the term "algorithm".	1	3	2
11	What is the main difference between a BLAST search and a FASTA alignment?	1	3	2
12	What does "DP" stand for in the context of sequence alignment?	1	3	1
13	What is JAVA?	1	4	1
14	Define the concepts of programming languages "C".	1	4	1
15	Give one example of each: Compiled language and Interpreted language.	1	4	2

Please turn over

SECTION B

Short Type Question. (Attempt any five out of six)

5 x 5 = 25 marks

Q.No.	Question	Marks	CO	BTL
1	Explain the concept of generations of computers and discuss the key characteristics of each generation.	5	1	2
2	Differentiate between Needleman-Wunsch and Smith-Waterman algorithms for sequence alignment.	5	3	2
3	Define bioinformatics and its primary purpose.	5	2	1
4	Differentiate between system and application software.	5	1	2
5	Give a brief description on "Genomics of model eukaryotic organisms".	5	2	4
6	Describe the characteristics of "C" programming language.	5	4	2

SECTION C

Long type Question (Attempt any two out of three)

2 x 10 = 20 marks

Q.No.	Question	Marks	CO	BTL
1	Using the provided DNA sequences "ACTGTCGTAAC" and "ACGGTGCAC," i) List all possible alignments and calculate matches, mismatches and gaps for each alignment ii) Determine the best alignment using both the similarity and distance methods. (take gap penalty of gap length 1nt=2 and gap penalty of gap length 2nt=6)	2 4+4=8	3	2,3,4,5
2	Compare and contrast primary, secondary, and specialized databases in bioinformatics. Provide examples of each type, highlighting their unique features, data content, and relevance to biological research.	10	2	2,3,4
3	Briefly describe the purpose and importance of BioPerl in the field of bioinformatics. Explain how it facilitates sequence analysis and other bioinformatics tasks.	10	4	2

****END OF QUESTION PAPER****