STELLA MARIS COLLEGE (AUTONOMOUS) CHENNAI 600 086
(For candidates admitted from the academic year 2023 – 2024 & thereafter)

B.Sc. DEGREE EXAMINATION, APRIL 2026
BRANCH V(a) – PLANT BIOLOGY AND PLANT BIOTECHNOLOGY
FOURTH SEMESTER

COURSE : MAJOR ELECTIVE
PAPER : INTRODUCTION TO BIOINFORMATICS
SUBJECT CODE : 23BT/ME/BI45
TIME : 3 HOURS **MAX. MARKS: 100**

Q. No.	**SECTION A** **CHOOSE THE CORRECT ANSWER (5 X 1 =5)**	CO	KL
1.	Which NCBI tool is primarily used for sequence similarity searching? a) BLAST b) ClustalW c) FASTA d) BioEdit	1	1
2.	OMIM is primarily a database for a) Protein structures b) Gene expression profiles c) Human genes and genetic disorders d) Metabolic pathways	1	1
3.	Which of the following is a type of pairwise alignment? a) Global alignment b) Local alignment c) Semi-global alignment d) All of the above	1	1
4.	CLUSTAL Omega is primarily used for a) Pairwise sequence alignment b) Multiple sequence alignment c) Protein structure prediction d) Genome assembly	1	1
5.	Which software tool is commonly used to visualize 3D protein structures? a) BLAST b) PyMOL c) FASTA d) GEO2R	1	1
	FILL IN THE BLANKS. (5 X 1 =5)	**CO**	**KL**
6.	EMBL and DDBJ is a member of the ______________________ collaboration.	1	1
7.	iSakura is the sequence submission system used by ___________.	1	1
8.	The main purpose of BLAST is to identify ___________ sequences in a database.	1	1
9.	In phylogenetic trees, a node represents ________.	1	1
10.	IMPPAT stands for _______.	1	1
	STATE WHETHER TRUE OR FALSE. (5 X 1 = 5)	**CO**	**KL**
11.	Plant Cyc is a sequence submission tool.	1	1
12.	EMBL is maintained by EBI.	1	1
13.	CLUSTAL Omega is not a multiple sequence alignment program	1	1
14.	The phylogenetic tree is also known as the evolutionary tree.	1	1
15.	The Protein Data Bank is a global database of 3D structural data of biological molecule.	1	1
	MATCH THE FOLLOWING. (5 X 1 =5)	**CO**	**KL**
16.	Protein database - Genetic disorders	1	1
17.	Nucleotide database - PubMed	1	1
18.	Specialized database - DDBJ	1	1
19.	OMIM - Entrez	1	1
20.	SRS - Swissprot	1	1

Q. No.	**SECTION B** **(8 X 2 =16)** **ANSWER ANY EIGHT OF THE FOLLOWING IN 50 WORDS.**	CO	KL
21.	Define Bioinformatics	2	2
22.	List the branches of Bioinformatics	2	2
23.	Explain a domain?	2	2
24.	What is KEGG?	2	2
25.	Explain gap penalty.	2	2
26.	What is BLAST?	2	2
27.	Define clade.	2	2
28.	Outline the importance of FASTA?	2	2
29.	Define Motif finding.	2	2
30.	Specify the significance of PYMOL.	2	2
Q. No	**SECTION C** **(4 X 6 =24)** **ANSWER THE FOLLOWING IN 200 WORDS.**	**CO**	**KL**
31.	Discuss the significance of NCBI.	3	3
	(or)		
32.	Interpret the various sequence submission tools.	3	3
33.	Distinguish global alignment and local alignment.	3	3
	(or)		
34.	Identify the importance of Neighbour Joining method.	3	3
35.	Compare and contrast CLUSTAL W and CLUSTAL Omega.	4	4
	(or)		
36.	Analyse the search steps in BLAST.	4	4
37.	Differentiate the types of phylogenetic trees.	4	4
	(or)		
38.	Elucidate the tool used for drug designing.	4	4
Q. No.	**SECTION D** **(2 x 20 = 40)** **ANSWER THE FOLLOWING IN 1000 WORDS. DRAW DIAGRAMS WHEREVER NECESSARY.**	**CO**	**KL**
39.	Elucidate the various types of Biological databases.	5	5
	(or)		
40.	Explain Sequence Retrieval System and add a note on any two Specialized database	5	5
41.	Explicate the sequence alignment and the steps involved in pairwise sequence alignment.	5	5
	(or)		
42.	Summarise the methods used to construct phylogenetic trees with suitable examples.	5	5

****