

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

M. Sc. DEGREE EXAMINATION, NOVEMBER 2023
BIOINFORMATICS
FIRST SEMESTER

COURSE : CORE
PAPER : ESSENTIALS OF BIOINFORMATICS
SUBJECT CODE : 23BI/PC/EB14
TIME : 1 ½ HOURS **MAX. MARKS: 50**

Q. No.	SECTION A (10 x 1=10 marks)	CO	KL
	All questions to be answered		
1	Define a biological database.	CO1	K1
2	Mention the application of OMIM.	CO1	K1
3	What is the significance of GenBank?	CO1	K1
4	What is the application of Bankit?	CO1	K1
5	Expand the abbreviation of BLAST.	CO1	K1
6	Give an example of a global sequence alignment tool.	CO2	K2
7	What is a cladogram?	CO2	K2
8	Define local alignment gaps.	CO2	K2
9	Which specialized database can be referred to for determining the pathways involved in colon cancer?	CO2	K2
10	Mention the application of SGD.	CO2	K2
Q. No.	SECTION B (10 x 2= 20 marks)	CO	KL
	Answer any TEN questions		
11	Examine the application of dynamic programming in sequence alignment.	CO3	K3
12	Report any two key features of the 1000 genomes project.	CO3	K3
13	Write the significance of Entrez.	CO3	K3
14	Explain the importance of EMBL database.	CO3	K3
15	Illustrate the usage of the PAM scoring matrix in BLAST.	CO3	K3
16	Relate any two contributions of bioinformatics to the medical field.	CO3	K3
17	Differentiate between local and global sequence alignment.	CO4	K4
18	Classify biological databases based on the type of data they contain.	CO4	K4
19	Distinguish between paralogs and orthologs.	CO4	K4
20	Correlate multiple sequence alignment with phylogenetic tree construction.	CO4	K4
21	Appraise the importance of PubMed.	CO4	K4
22	Deduce the use of PubChem in drug discovery.	CO4	K4
Q. No.	SECTION C (4 x 5= 20 marks)	CO	KL
	Answer FOUR questions with internal choice		
23	a) Evaluate the importance of the BLAST tool in performing pairwise alignments. OR b) Summarize any five significant features of the NCBI database.	CO5	K5

24	a) Recommend any five databases for retrieving gene sequences with suitable reasons. OR b) Assess the use of maximum parsimony and maximum likelihood method in phylogenetic tree construction.	CO5	K5
25	a) Speculate on the role of bioinformatics in the human genome project. OR b) Infer how Clustal tools are used for multiple sequence alignment.	CO5	K6
26	a) Bioinformatics improves our understanding of biological macromolecules and systems – Justify. OR b) Validate the importance of any two protein structure databases.	CO5	K6
