

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

M. Sc. DEGREE EXAMINATION, NOVEMBER 2024
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) ALL QUESTIONS TO BE ANSWERED (OBJECTIVE TYPE)	CO	KL
1.	Which one of the following is a secondary protein structure database? a) PubChem b) PDB c) ChemBank d) SCOP	CO1	K1
2.	Clustal W program accepts the input sequences only in the _____ format. a) Genbank b) EMBL c) PDB d) fasta	CO1	K1
3.	The family that consists of related genes in another organism is called _____. a) orthologs b) paralogs c) xenologs d) zoologs	CO1	K2
4.	EST stands for _____. a) Expressed Sequence Tag b) Expressed Site Tag c) Expressed Structure Tag d) Expressed Symbol Tag	CO1	K2
5.	When performing a database search, what is the definition of an E-value? a) The chance that a random sequence could achieve a better score than the query b) The chance that a homologous sequence could achieve a similar score to the query c) The chance that a random sequence could achieve a worse score than the query d) The chance that a homologous sequence could achieve a better score than the query	CO1	K1
6.	Dot-matrix representations denote the sequences _____. a) as the coordinates of a two-dimensional graph b) are represented in the form of trees c) as the coordinates of a 3D graph d) not represented as graph	CO1	K1
7.	Who developed PAM matrices and in which year? a) Needleman and Wunsch, 1976 b) Smith-Waterman, 1978 c) Dayhoff et al., 1978 d) Henikoff 1992	CO1	K1
8.	Which one of the following is a life science search engine? a) PubMed b) Entrez c) Mozilla d) EBI	CO1	K2
9.	Which of the following is the distance based method? a) Neural network b) Maximum parsimony c) Maximum likelihood d) Neighbor-Joining	CO1	K2

10.	Which one of the following is a command based offline tool for molecular structural visualization? a) Swiss-PDB Viewer b) RasMol c) QMol d) PyMol	CO1	K1
Q. NO.	SECTION B (10 X 2= 20 MARKS) ANSWERS IN ABOUT 50 WORDS	CO	KL
11.	Define genome sequencing.	CO2	K3
12.	Comment on Encode.	CO3	K4
13.	What is the use of Unigene?	CO2	K3
14.	List the features of SRS.	CO3	K4
15.	Define gap penalty.	CO2	K3
16.	Write on Bankit.	CO2	K3
17.	Differentiate distance and character based methods.	CO3	K4
18.	Explain Phylip.	CO3	K4
19.	Comment on chemical databases.	CO3	K4
20.	List any two pathway databases and explain.	CO3	K4
Q. NO.	SECTION C (4 X 5= 20 MARKS) ANSWER IN ABOUT 500 WORDS - INTERNAL CHOICE	CO	KL
21.	a) Explain the importance of human genome project version hg19 and hg38 and its browsers. (or) b) Brief on the types of sequence databases.	CO4	K5
22.	a) Discuss the search steps in BLAST and its scoring system. (or) b) Explain in detail about character based method of tree construction.	CO5	K6
23.	a) Enumerate the different file formats and conversion tools. (or) b) Comment on the unique features of model organism databases with examples.	CO4	K5
24.	a) Differentiate Local and Global alignment algorithms with an example. (or) b) Illustrate the MSA and its tools.	CO5	K6
