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

M.A / M. Sc. DEGREE EXAMINATION, NOVEMBER 2024
THIRD SEMESTER

COURSE : ELECTIVE
PAPER : INTRODUCTION TO BIOINFORMATICS
SUBJECT CODE : 23BI/PE/IB23
TIME : 3 HOURS **MAX. MARKS:100**

Q. No.	SECTION A ANSWER ALL. (10X1=10)	CO	KL
1.	Which of the following pairs of amino acids are correctly matched with their single-letter codes? a) Glycine - G; Lysine – L b) Aspartic acid - D; Leucine - L c) Serine - S; Arginine – A d) Alanine - A; Tryptophan - W	CO1	K1
2.	Which of the following is a commonly used biological data format for storing sequence data? a) FASTA b) JPEG c) XML d) CSV	CO1	K1
3.	What does the acronym BLAST stand for in bioinformatics? a) Basic Local Alignment Search Tool b) Biological Local Alignment Sequence Tool c) Bioinformatics Local Alignment Search Tool d) Basic Local Alignment Sequence Test	CO1	K1
4.	What is PyMOL primarily used for in the field of bioinformatics? a) DNA sequencing b) Molecular visualization c) Protein structure prediction d) Gene expression analysis	CO1	K1
5.	Which type of phylogenetic tree includes a common ancestor at the base? a) Rooted tree b) Unrooted tree c) Circular tree d) Linear tree	CO1	K1
6.	What is the main purpose of evolutionary analysis in biology? a) To determine the environmental impact on species b) To understand the genetic basis of traits c) To infer the relationships and divergence among species d) To classify organisms based on their physical characteristics	CO1	K2
.7	Which of the following methods is commonly used for gene finding based on homology? a) Gene prediction algorithms b) Hidden Markov Models (HMMs) c) Comparative genomics d) Machine learning approaches	CO1	K2

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8.	What is the primary purpose of repeat sequence mapping in genomics? a) To identify novel genes in the genome b) To determine the locations and types of repetitive DNA elements in a genome c) To analyze gene expression levels d) To predict protein structures	CO1	K2
9.	Which component of SDS-PAGE is responsible for denaturing proteins? a) Gel matrix b) SDS (Sodium dodecyl sulfate) c) Staining dye d) Buffer solution	CO1	K2
10.	What is a common application of restriction enzymes in genetic engineering? a) DNA replication b) Sequencing DNA c) Cloning DNA fragments into plasmids d) Amplifying DNA through PCR	CO1	K2
Q. No.	**SECTION B** **ANSWER IN ABOUT 50 WORDS. (10X2=20)**	**CO**	**KL**
11.	List the symbols used to represent the nucleotides.	CO2	K2
12.	Classify the biological database.	CO2	K2
13.	Brief about MSA.	CO2	K2
14.	List the uses of Visualization tools.	CO2	K2
15.	Distinguish cladistic and phenetic methods.	CO2	K2
16.	Give a note on bootstrapping strategies.	CO3	K3
17.	Define gene and genome.	CO3	K3
18.	Mention few gene prediction tools.	CO3	K3
19.	Name the types of restriction enzyme and function.	CO3	K3
20.	What are the four levels of protein structure?	CO3	K3
Q. No.	**SECTION C** **ANSWER IN ABOUT 600 WORDS. (4X10=40)**	**CO**	**KL**
21.	a) Describe the steps and the types of BLAST to interpret the sequence similarity. **(OR)** b) How will you utilize the PDB to determine the structure and function of the protein?	CO4	K4
22.	a) Distinguish rooted and unrooted tree in phylogenetic analysis. **(OR)** b) Comment on the steps involved in Mega software to construct the phylogenetic tree.	CO4	K4

23.	a) Explain in detail about the sequence retrieval system in the NCBI database. **(OR)** b) What are Repeat sequences and its types? Explain.	CO5	K5
24.	a) Elucidate the steps and importance of SDS-PAGE in protein separation. **(OR)** b) Classify the protein structure and emphasize its function of proteins.	CO5	K5
Q. No.	**SECTION D** **ANSWER IN ABOUT 1200 WORDS. (2X15=30)**	**CO**	**KL**
25.	a) Comment on the applications of Bioinformatics in various fields. **(OR)** b) Elaborate the different methods employed in phylogenetic tree construction.	CO5	K6
26.	a) Discuss in detail about the gene prediction methods. **(OR)** b) Expand the types of restriction enzyme and its application.	CO5	K6

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