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

M. Sc. DEGREE EXAMINATION, APRIL 2026
BIOINFORMATICS
SECOND SEMESTER

COURSE : CORE
PAPER : GENOMICS AND TRANSCRIPTOMICS
SUBJECT CODE : 23BI/PC/GT24
TIME : 90 MINUTES MAX. MARKS: 50

Q. No.	SECTION A (10 x 1=10 marks) All questions to be answered	CO	KL
1	Identify the file format for feature annotation format for genes and genomic elements a. FASTQ b. SAM/BAM c. VCF d. GFF/GTF	CO1	K1
2	Which of the following statements is TRUE about molecular clocks? a. They measure the rate of protein degradation b. They estimate the time of divergence between species based on nucleotide substitutions c. They detect only insertions and deletions in the genome d. They are used for sequencing raw DNA reads	CO1	K1
3	Alpha diversity in metagenomics measures: a. Diversity within a single sample b. Diversity between multiple samples c. Total number of sequencing reads d. GC content of reads	CO1	K1
4	Which of the following is a key focus of epigenomic analysis? a. DNA sequence variants only b. Adapter trimming in sequencing reads c. Chromatin modifications and transcription factor binding d. Generating contigs and scaffolds	CO1	K1
5	Which of the following correctly describes the function of Cas9 nuclease? a. It introduces double-strand breaks at target DNA sequences guided by sgRNA b. It synthesizes RNA from DNA c. It edits proteins directly d. It amplifies target DNA sequences	CO1	K1
6	Which genome editing tool uses engineered DNA-binding proteins fused to nucleases for precise genome modification? a. CRISPR-Cas9 b. TALENs and ZFNs c. RNA interference (RNAi) d. Illumina sequencing	CO2	K2

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7	Single-cell RNA sequencing differs from bulk RNA sequencing in that: a. It sequences DNA instead of RNA b. It captures gene expression at the level of individual cells c. It cannot detect non-coding RNAs d. It uses microarray probes	CO2	K2
8	Gene Silencing and Regulatory RNAs Which RNA molecules are primarily involved in post-transcriptional gene silencing? a. rRNA and tRNA b. snRNA and snoRNA c. mRNA only d. miRNA and siRNA	CO2	K2
9	Functional classification and interpretation of DEGs is called _____ analysis.	CO2	K2
10	To aggregate and visualize multiple QC reports, we use _____.	CO2	K2
Q. No.	**SECTION B (10 x 2= 20 marks)** **Answers in about 50 words**	**CO**	**KL**
11	Explain how a genome is assembled from fragmented reads.	CO3	K3
12	List few appropriate bioinformatics tool or database to identify duplications and indels.	CO3	K3
13	Demonstrate how epigenetic modifications regulate gene expression.	CO3	K3
14	Apply alpha and beta diversity metrics to analyze microbial diversity in a metagenomic dataset.	CO3	K3
15	Select appropriate key factors for designing sgRNA target sites.	CO3	K3
16	Specify genome editing applications.	CO4	K4
17	Examine the importance of RNA Integrity Number.	CO4	K4
18	Comment on lncRNA.	CO4	K4
19	How SAM tools function in NGS.	CO4	K4
20	Organize the key steps involved transcriptomic data analysis.	CO4	K4
Q. No.	**SECTION C (4 x 5= 20 marks)** **Answer in about 600 words**	**CO**	**KL**
21	a) Evaluate the VCF file formats. **OR** b) Justify the choice between amplicon and shotgun sequencing in metagenomics.	CO5	K5
22	a) Evaluate the CRISPR-Cas9 genome editing mechanism. **OR** b) A patient has a point mutation causing a genetic disorder. Suggest a genome editing strategy and justify the choice of tool.	CO5	K5
23	a) Compare microarray technology and RNA-seq in terms of methodology, sensitivity, and applications. **OR** b) Enumerate the importance of miRNA and siRNA in gene silencing.	CO5	K6
24	a) Explain how FASTQC and MultiQC are used in RNA-seq data preprocessing. **OR** b) Elaborate the steps involved in predicting Differentially Expressed Genes (DEGs) and performing ontology analysis.	CO5	K6

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