ASSIGNMENT
(Tutor Marked Assignment)

Course Code: MZO-005
Assignment Code: MZO-005/TMA/2026
Maximum Marks: 100

Note: Attempt all questions. The marks for each question are indicated against it.

1.	a).	Describe the steps of genome data analysis.	(5)
	b).	Write a note on Yeast Artificial Chromosome.	(5)
2.	a).	Distinguish between temporal and site-specific analyses of gene expression.	(5)
	b).	Outline the technique of Isotope Coded Affinity Tag.	(5)
3.	a).	Elucidate the different techniques of western blotting.	(5)
	b).	Distinguish between Matrix Assisted Laser Desorption Ionization and Electrospray Ionization.	(5)
4.	a).	Write a brief note on MALDI-TOF-TOF mass spectrometry.	(5)
	b).	How would you prepare a microarray?	(5)
5.	a).	Explain Whole Genome Shotgun Sequencing Methods with diagram.	(5)
	b).	Write a note on Multiple Sequence Alignment.	(5)
6.	a).	Explain the technique of nuclear run-on assay with diagram.	(5)
	b).	Outline the principle of cDNA-AFLP with diagram.	(5)
7.		Give a broad overview of the protein mining strategy. What is affinity chromatography?	(8+2=10)
8.		Write a note on the principle and methodology of RNA Sequencing with diagram. Explain Cot curve analysis.	(7+3=10)
9.		Discuss the genome organization of Drosophila and mammals. Mention the characteristics of microsatellites.	(7+3=10)
10.		Write notes on:	(10)
	a).	Structure of globin genes	
	b).	Pseudogenes	

1. a). Describe the steps of genome data analysis. (5)

Answer

Genome data analysis converts raw sequence reads into an interpretable description of the genome. The exact software can change with the sequencing platform, but the logical steps remain similar.

The first step is quality assessment of the raw reads. Base-call quality, read length, GC distribution, duplicated reads and possible contamination are checked. Adapter sequences and poor-quality bases are then trimmed. Reads that are too short or unreliable are removed so that errors do not propagate into later stages.

Next, the cleaned reads are either aligned to a reference genome or assembled de novo when a suitable reference is not available. In de novo assembly, overlapping reads are merged into contigs and paired-end or long-read information is used to arrange contigs into scaffolds. Assembly quality is examined through coverage, continuity, completeness and possible misassemblies.

The assembled or aligned sequence is then annotated. Repetitive DNA is identified, protein-coding genes are predicted, exon-intron boundaries are assigned, and non-coding RNAs and regulatory regions are marked where possible. Predicted genes are compared with sequence and protein databases to infer their likely functions.

The final stage is biological interpretation. Variants such as SNPs, small insertions/deletions and larger structural changes may be detected. Comparative genomics, pathway analysis and functional enrichment can then be used to relate genes and variants to phenotype, evolution or disease. Results are finally visualized and stored with adequate metadata so that the analysis can be reproduced.

b). Write a note on Yeast Artificial Chromosome. (5)

Answer

A Yeast Artificial Chromosome (YAC) is a cloning vector designed to behave like a small chromosome inside yeast. Its chief advantage is its ability to carry very large fragments of foreign DNA, commonly several hundred kilobases and in