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Q1: A. Write a note on the milestone of Human Genome Project. (7 marks)

B. What are genome databases, and why are they important? Explain the types of information they store and how researchers use them in genomics. (7 marks)

OR

A. Define single nucleotide polymorphism and SNP related databases. (7 marks)

B. Elaborate on the comparison of gene order and its role in understanding genomes. (7 marks)

Q2: A. Describe any two-protein secondary structure prediction algorithms. (7 marks)

B. What is a Ramachandran plot? Explain in detail. (7 marks)

OR

A. Describe various types of molecular interactions and explain any three with examples. (7 marks)

B. Provide an overview of protein-protein interactions and their biological significance. (7 marks)

Q3: A. Explain the workflow of next-generation sequencing (NGS), highlighting the main steps from raw data to biological interpretation. (7 marks)

B. Describe the Sanger sequencing method in detail, including its underlying principle, key reagents, and the steps involved in generating and analyzing DNA sequences. (7 marks)

OR

A. What are the file formats commonly used in genomics. Explain (7 marks)

B. Compare and contrast the Illumina, Ion Torrent, and Oxford Nanopore sequencing platforms with respect to their underlying principles and major applications. (7 marks)

Q 4: A. Applications of phylogenetic trees in Evolutionary biology. (7 marks)

B. Solve following sum by using UPGMA method. (7 marks)

A	B	C	D	E
-	20	38	38	40
	-	40	40	42
		-	18	20
			-	8
				-

OR

A. Explain various tree models in phylogenetic trees. (7 marks)

B. Explain any one Character based method for phylogenetic tree. (7 marks)

Question 5: Answer the following: (any 7 out of 12) (14 marks)

1. What is the purpose of the VISTA tool in genome analysis?

2. Define the term synteny and explain its relevance in gene order analysis.

3. What is the purpose of genome alignment in comparative genomics?

4. What are aptamers explain briefly?

5. Describe two potential consequences of protein misfolding within a cell, providing examples.

6. Explain structure and function of leuzine-zipper interaction in DNA-Protein interaction.

7. What is OMIM explain in brief.

8. What kind of information does a VCF (Variant Call Format) file contain?

9. Define the term 'annotation file' in bioinformatics. Give one example.

10. What is ultrametricity and additivity in Phylo trees?

11. Define Taxon in Phylo tree.

12. Explain jukes cantor model.