2211E786

Candidate's Seat No :_____

M.Sc Sem-3 Examination

503

Bioinformatics

Time : 2-30 Hours] **November-2024** **[Max. Marks : 70**

Q1: A. Define comparative genomics and give its applications. (7)
B. What is meant by EST? explain the applications of EST and its related databases. (7)

OR

A. Explain VISTA and Mummer tool. (7)
B. Explain comparison of gene order. (7)

Q2: A. Explain Homology Modelling and steps involved in it. (7)
B. What are motifs, folds and domains? Explain their significance. (7)

OR

A. Give importance of protein-protein interactions & computational tools utilized to predict them. (7)
B. Write a brief note on Ramachandran plot and explain the concept of outliers. (7)

Q3: A. Describe the principle of Ion Torrent sequencing technology. How does it differ from sequencing by synthesis (SBS) methods used in other platforms like Illumina? (7)
B. Explain sanger sequencing in detail. (7)

OR

A. What is meant by sequence assembly and sequence annotation? Which are the computational tools utilized for the same? (7)
B. Explain the basic principles of Illumina sequencing. How does the process of sequencing by synthesis (SBS) work, and what are its key features ? (7)

Q 4: A. Explain any one Character based method for phylogenetic tree.. (7)
B. Solve following sum by using Fitch Margolish method. (7)

A	B	C	D	E
-	22	39	39	41
	-	40	37	36
		-	20	18
			-	8
				-

OR

A. Applications of phylogenetic trees in Evolutionary biology. (7)
B. Explain Ultrametricity and Additivity in phylogenetic trees. (7)
Question 5: Answer the following: (any 7 out of 12) (14)

1. What is the purpose of genome alignment in comparative genomics?
2. How does MUMmer assist in comparing large genomes?
3. Write a difference between EST and GSS sequence.
4. Explain the key forces and interactions that drive protein folding & stabilize the final conformation.
5. Describe two potential consequences of protein misfolding within a cell, providing specific examples.
6. What is a Ramachandran plot? Explain its purpose.
7. What is the difference between sequencing depth and coverage in NGS?
8. Why is sequencing depth important for certain applications like variant detection?
9. Define BAM and SAM file format
10. What is ultrametricity and additivity in Phylo trees?
11. What are Homoplacious trees?
12. Explain Kimura K2P model.