Register Number:……..

KUMARAGURU
college of technology
character is life

B.TECH DEGREE EXAMINATIONS: NOV/DEC 2023

(Regulation 2018)

Seventh Semester

BIOTECHNOLOGY

U18BTI7203**:** Bioinformatics

COURSE OUTCOMES

CO1: To introduce the concept of biological sequence alignment and various genome sequence protocols
CO2: To familiarize with various biological database searches, parameters and algorithm
CO3: To apply, interpret and analyze multiple sequence alignments.
CO4: To construct, interpret and access molecular phylogenetic tree prediction.
CO5: To apply, interpret and analyze protein structures prediction algorithms
CO6: To introduce the concept of computer-aided drug designing (CADD).

Time: Three Hours **Maximum Marks: 100**

Answer all the Questions:-
PART A (10 x 2 = 20 Marks)
(Answer not more than 40 words)

1.	Assume that two alignments have the same edit distance,whether the score of the alignments will be same?	CO1	[K_3]
2.	List the different types of GAPS adopted in sequence alignment.	CO1	[K_2]
3.	Differentiate PSI-BLAST and PHI-BLAST.	CO2	[K_2]
4.	"The closest BLAST hit may not often the nearest neighbors." Justify the statement	CO2	[K_3]
5.	In MSA, should an insertion be penalized as same as that of a deletion?	CO3	[K_3]
6.	Structural alignment doesn't correspond to the evolutionary history". Justify the statement by considering a multiple sequence alignment.	CO3	[K_3]
7.	How can you assess the evolutionary rate of " gene X" present in both humans and chimpanzees?	CO4	[K_4]
8.	Define a OTU	CO4	[K_2]
9.	Why alpha-helices considered as significant for membrane proteins?	CO5	[K_2]
10.	How does MODELLER program calculate the DOPE score?	CO6	[K_2]

Answer any FIVE Questions:-
PART B (5 x 16 = 80 Marks)
(Answer not more than 400 words)

11. a) Enlist the key technological advancement of Human Genome Project — CO1 [K_2]

b) What would be the deleterious effects of incorporation of low complex regions in a sequence alignment? — CO1 [K_2]

12. a) Describe a method to the identify single nucleotide polymorphism in a population of genes responsible for an infectious disease.(Hint: use only one NGS workflow) — CO2 [K_2]

b) You have been given with a NGS reads obtained from Illumina sequencing. Initial QC analysis has revealed the PHRED scores of below 20. Discuss the possible reason for the poor PHRED scores. — CO2 [K_4]

13. a) Emphasize the steps involved in the construction of a position.specific scoring matrix (PSSM) — CO3 [K_2]

b) How do you measure or ensure the quality of a multiple sequence alignment? — CO3 [K_2]

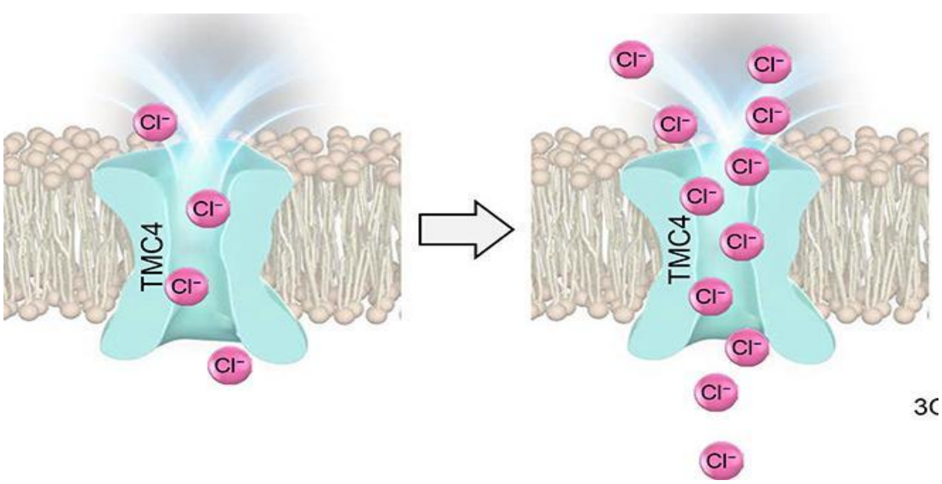
14. a) Assure that You are working with the DNA sequences of fungal samples extracted from different high-pollutant areas around the coastal regions of India and interested in generating a deeper and more divergent phylogenetic tree. What method do you adopt and justify the same. — CO4 [K_4]

b) Construct a rooted tree using the neighbor-joining method. — CO4 [K_4]

Sequence A: ATGCGA Sequence B: ATGGCA

Sequence C: CCGCCA Sequence D: ATGCCA

15. a) — CO6 [K_4]



Sodium chloride is indispensable in a variety of facets of human life. "Salty taste" sensation is evoked when sodium and chloride ions are present together in the oral cavity. Various studies have reported hTMC4 is involved in human salt

taste perception. However, an excessive sodium intake increases the risk of several physiological disorders such as vascular and renal dysfunctions. The use of potent salt taste enhancers, if available, could reduce dietary salt intake. Based on the information above, provide virtual screening protocol to identify a potent salt enhancer. Illustrate a flowchart and explain the key process.

b) Enumerate the various metrics to evaluate the protein-ligand complex in the above explained study.[vide Q. No.15(a)] CO6 [K_2]

16. a) Draw a flowchart and describe the key steps involved in the prediction of 3D structure of a protein. [Note: Initial BLAST search revealed an average of 55% sequence homology between the Protein A, B and C]. CO5 [K_3]

b) Describe the key steps in predicting the secondary structure of a protein using Hidden Markov Model. CO5 [K_2]

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