

VI SEMESTER B.TECH. EXTERNAL EXAMINATIONS APRIL 2019 SUBJECT: BIOINFORMATICS [BIO 3201]

Date of Exam: 23/04/2019 Time of Exam: 2.00 PM - 5.00 PM Max. Marks: 50

Instructions to Candidates:

❖ Answer ALL the questions & missing data may be suitable assumed

1A.	Assume that you have a protein of unknown function from a bacterium. You have made a knock-out mutant, but the bacteria die immediately without the corresponding gene. You have sequenced the protein. What steps would you take to guess the function of the protein? What kind of information would you look for?					
1B.	Describe the following in relation to sequence alignment: (a) GAP penalties (b) Similarity matrix (c) Distant matrix					
1C.	Do a global alignment of the sequences m (ACTGATTCA) and n (ACGCATCA) using Needleman-Wunsch algorithm and also explain the trace-back step in detail. You may use match score of +2, mismatch score of -1, and a gap score of -2					
2A.	Explain the algorithm of BLAST					
2B.	Sketch a Eukaryotic Pre-mRNA and describe the complexities of gene finding					
2C.	You are assigned to design a set of primers for the given sequence. Validate the designed primers and write down the primer sequences with orientations 5'- TTG TGG GTC ACA GTC TAT TAT GGG GTG CCT GTG TGG AAA GAA GCAACC ACC (middle part of the gene is truncated)	4				
3A.	Assume a polypeptide that is comprised of L-amino acids folds into an α-helix. What would happen if it is interrupted by inserting D-amino acids? What change do you observe in the Ramachandran's Plot? Why?	3				

3B.	What happens when a Pro26 located at the junction of beta-strand and the terminal of the following alpha helix, is replaced with Ala at 26 th position?								
3C.	Draw a flow diagram for homology modeling process with refinement steps								
4A.	How would you measure the sensitivity and specificity of a predicted gene? Give an example								
4B.	Explain "all-beta" protein topologies with examples								
4C.	Elaborate the structure-function relationship of DNA polymerase β-clamp								
5A.	Draw "by hand" the rooted tree corresponding to a given NEWICK string $((G,E),((C,((A,K,B),F)),((D,H),M)))$								
5B.	How would you explain the support structures of a butterfly wing and those of bird wings in the context of evolution?								
	Use the following	g distance matrix	and construct	a tree based on	UPGMA				
		Bovin	Pig	Rat	Mouse	Human			
	Bovin	0	0.098	0.197	0.204	0.173			
5C.	Pig	0.098	0	0.181	0.189	0.163	4		
	Rat	0.197	0.181	0	0.072	0.176			
	Mouse	0.204	0.189	0.072	0	0.204			
	Human	0.173	0.163	0.176	0.204	0			