

Reg. No.

प्रज्ञानं ब्रह्म



Manipal

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Manipal Institute of Technology, Manipal

(A Constituent Institute of Manipal University)



VI SEMESTER B.TECH (BIOTECHNOLOGY) END SEMESTER EXAMINATIONS, MAY 2016

SUBJECT: BIOINFORMATICS [BIO 302]

REVISED CREDIT SYSTEM

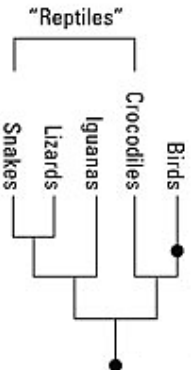
Time: 3 Hours

MAX. MARKS: 50

Instructions to Candidates:

- ❖ Answer **ANY FIVE FULL** questions.
- ❖ Missing data may be suitably assumed.

1A.	Mr. X wanted to perform a multiple sequence alignment of ten proteins that does not have structures. He searched the internet and found different software that uses exact, progressive, iterative and structure-based methods. Mr. Y suggested using progressive method. However, Mr. X disagreed and preferred to use another better method. Which method do you suggest him? Justify your answer by comparing it with other methods.	5
1B.	Calculate the molecular weight of a peptide made up of 10 glycines. What would be its probable secondary structure?	2
1C.	What do you mean by Low Complexity Regions (LCRs)? How would you process the sequence with LCRs?	3
2A.	It is well known that hemoglobin and myoglobin are evolutionarily related proteins. Correlate their similarities at sequence, structure and functional level of hemoglobin and myoglobin	2
2B.	Perform a pairwise alignment of the following sequences using dynamic programming. Calculate its score from the alignment and produce a biologically significant alignment S1: G A T A T A A T A T S2: G G A T A T A Scores: Match = 2; Mismatch = 1; Gap = 0	5
2C.	Devise a method to align small disulphide-rich proteins	3
3A.	Proteins only have rotational symmetry, explain why inversion or mirror symmetry is not applicable to study proteins? Also add an exception to it.	3
3B.	Hopfner <i>et al</i> (1998) of Max-Planck-Institut für Biochemie, Martinsried, Germany have crystallized a chimeric protein and deposited in PDB [ID: 1fxy]. The structure has passed Verify 3D but the Ramachandran plot show only 86.2% of residues in the core region. How would you improve the core percentage?	4

3C.	In the Ramachandran's Plot ϕ angles of an amino acid is constrained around -60 degrees, which amino acid? Why?	3
4A.	Assume that you have discovered a novel gene that codes for a protein. What kind of predictions you can make for the protein sequence? What are the different online tools that are available for this purpose and how would you interpret the function?	3
4B.	What are the considerations involved in designing (i) universal, (ii) species-specific and (iii) degenerate primer	3
4C.	A scientist has discovered a new organism. He has sequenced the DNA and it contains many genes that are almost similar to human. He wanted to confirm these predictions through experimental methods. Which method do you suggest for this study? Discuss in detail, the methodology that should be followed to identify the genes that are similar to human and also specific to this new organism.	4
5A.	For a labeled bifurcating tree, write the formula to calculate the total number of rooted and unrooted trees. Assume you have ten taxa, how many rooted and unrooted trees are possible? What would be its depth?	4
5B.	What do you mean by bootstrap? How do you evaluate a tree using bootstrap?	3
5C.	What are the considerations involved in multiple sequence alignment for making a phylogenetic tree?	3
6A.	Give an example each for homoplasy, plesiomorphy and synapomorphy	3
6B.	 <p>In the tree diagram, a bracket marks the groups that are considered to belong to the reptiles. Would you consider the reptile group, as labeled, to be a true clade? If yes, why? If no, why not?</p>	3
6C.	List out the challenges in constructing the universal 'tree of life'.	4