Reg. No.										

MANIPAL INSTITUTE OF TECHNOLOGY

MANIPAL

A Constituent Institution of Manipal University

VI SEMESTER B.TECH. (BIOTECHNOLOGY)

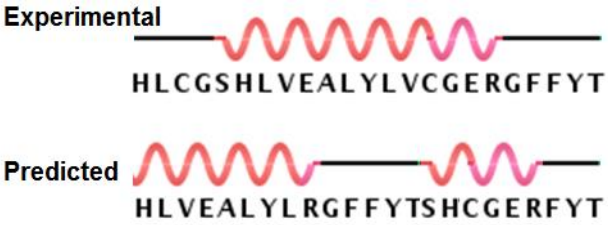
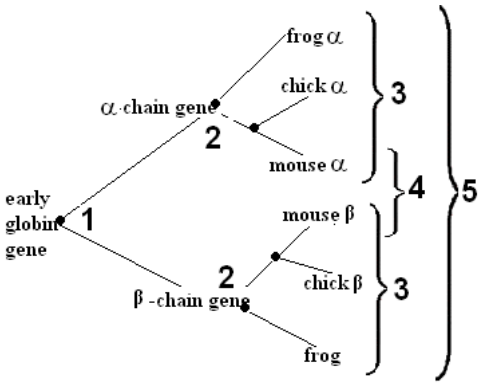
END SEMESTER EXAMINATIONS, APR/MAY 2017

SUBJECT: BIOINFORMATICS [BIO 3201]

REVISED CREDIT SYSTEM

Time: 3 Hours MAX. MARKS: 50

1A.	What is the difference between a global and a local alignment strategy?	**2**
1B.	Suppose we have the following fragments, and we know that the total length of the target molecule is about 55 base pairs. f_1 : ATCCGTTGAAGCCGCGGGC f_2 : TTAACTCGAGG f_3 : TTAAGTACTGCCCG f_4 : ATCTGTGTCGGG f_5 : CGACTCCCGACACA f_6 : CACAGATCCGTTGAAGCCGCGGG f_7 : CTCGAGTTAAGTA f_8 : CGCGGGCAGTACTT Assemble the fragments and obtain a consensus sequence. Be prepared to deal with errors. You may also have to use the reverse complement of some of the fragments.	**5**
1C.	Brief the following terms with reference to GenBank: ASN.1, PAT, STS, GSS, HTG and CON	**3**
2A.	Perform a pairwise alignment of the following sequences using dynamic programming. Calculate its score from the alignment and produce a biologically significant alignment S1: A C T G A T T C A S2: A C G C A T C A Scores: Match = 2; Mismatch = -3; Gap = -2	**4**
2B.	Compare any four structure visualization programs based on manipulation power, ease of use, GUI, documentation and OpenGL support	**2**
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*) ……. CCA TTA GGA CTA GCACCC ACC AAG GCA AAA AGA AGA GTG GTG CAG AGA GAA AAA AGA -3'	**4**
3A.	What would be the secondary structure of the following sequences? (i) polyproline (ii) polyglycine? and (iii) an alternate repeat of Gly & Pro residues	**3**

3B.	Suppose if a polypeptide chain is twisted by the same amount about each of its Cα atoms, it assumes a helical conformation. However, there are differences such as 2.2_7 ribbon, 3_{10}, 3.6_{13} and 4.4_{16} helices based on their pitch and width. Compare and contrast them.	**5**
3C.	Discuss the surface protein topologies of hemagglutinin and neuraminidase in H_1N_1 influenza virus	**2**
4A.	How would you measure the sensitivity and specificity of the following predicted protein structure? 	**3**
4B.	Elaborate the structure-function relationship of the DNA-binding protein: E.coli Polymerase I with an analogy to palm, fingers, and thumb	**5**
4C.	Proteins only have rotational symmetry, explain why inversion or mirror symmetry is not applicable to study proteins? Also add an exception to it.	**2**
5A.	Given a multiple sequence alignment to predict the informative sequence positions of the aligned columns as well as to infer the smallest number of evolutionary changes (maximum parsimony) at each aligned position to guaranty a best tree Columns: 1 2 3 4 5 6 7 Sequence 1: C T G A A T A Sequence 2: A T G T T C A Sequence 3: A T A C T G T Sequence 4: A T A C A A T	**4**
5B.	Mitochondrial DNA sequences of European, African and Asian suggests that Indian populations are genetically unique and harbour the second highest genetic diversity after Africans. Comment on the deep-rooting mtDNA lineages of India to support out-of-Africa theory. For constructing dendrogram, what mtDNA lineages of India would you choose as an out group?	**2**
5C.	Observe the following tree diagram and write your inference for the indicated numbers to reflect shared ancestral and derived characters 	**4**