Reg. No.										

MANIPAL INSTITUTE OF TECHNOLOGY

Manipal 576 104, Karnataka, INDIA

(A Constituent Institute of Manipal Academy of Higher Education, Manipal)

VI SEMESTER B.TECH (BIOTECHNOLOGY)

END SEMESTER EXAMINATIONS, APRIL 2016

SUBJECT: BIOINFORMATICS [BIO 3201]

Time: 3 Hours. MAX. MARKS: 50

Instructions to Candidates:

- Answer **ALL FULL** questions.
- Missing data may be suitably assumed.

1A.	How many reading frames exist for a double-stranded DNA sequence? Is it possible to correlate the total number of ORFs and the actual number of genes? If yes, why? If no, why not?	3
1B.	What do you mean by Low Complexity Regions (LCRs)? How would you process the sequence with LCRs?	3
1C.	Consider the following piece of DNA 5' ... CCTCACTAGCGACCAGACTATAAATTACGTGACCTGT .... 3' 3' ... GGAGTGATCGCTGGTCTGATATTTAATGCACTGGACA ... 5' Map the fragments, a=GGTCA, b=AATTAC, c=AGTCTGG, and d=CACTAG occur in the DNA piece	4
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.	Do a global alignment of the sequences ***m*** **(CCTCACTA)** and ***n*** **(TAGTGAGG)** using Needleman-Wunsch algorithm and also explain the trace-back step in detail.	5
2C.	Explain the alignment strategy to pick a conserved pattern in the small disulfide-rich proteins of different lengths	3
3A.	Differentiate conservation, semi- conservation, and conserved substitution with examples each	3
3B.	To amplify the DNA between the two stretch of sequence shown below. Choose the listed primers pairs that will allow to amplify the DNA by PCR 5'-GACCTGTGGAGC ----------CATACGGGATTGA-3' Primers: (1) 5'-GACCTGTCCAAGC-3' (2) 5'-CGAAGGTGTCCAG-3' (3) 5'-GCTTCCACAGGTC-3' (4) 5'-GTATGCCCTAACT-3' (5) 5'-CTGGACACCTTCG-3' (6) 5'-CATACGGGATTGA-3' (7) 5'-TCAATCCCGTATG-3' (8) 5'-TGTTAGGGCATAC-3'	4

3C. Illustrate Ramachandran's Plot based on dihedral angles. Also comment on the sterically favourable, partially favourable and disallowed regions. 3

4A. Which graphical representation would you use in order to emphasize the following features of protein structure? 5

(1) all-atoms (2) bonds and angles (3) atomic volumes (4) backbone (5) secondary structure (6) solvent accessibility (7) van der Waals radii (8) electrostatic potential (9) unit cell (10) ligand

4B. List out the steps involved in homology modeling process 3

4C. How do you measure the sensitivity and specificity of a software program? 2

5A. Assume you have eight taxa (A, B, C, D … H). How many rooted and unrooted trees are possible with the same eight taxa? 2

5B. Construct a cladogram based on six taxa (A to F) using the morphological features given below 3

Character	A	B	C	D	E	F
Eyes	1	1	1	1	1	1
Tail	1	1	1	0	0	1
Legs	1	1	0	0	0	0
Wings	0	1	0	0	1	1
Fur	0	0	0	0	1	1

5C. It is common knowledge among biologists that mammals and reptiles all shared a common ancestor. The debate is whether (a) birds are part of the mammal clade or (b) whether they are part of the reptilia clade? Justify your argument. 5