Reg. No.										

Manipal Institute of Technology, Manipal

(A Constituent Institute of Manipal University)

II SEMESTER M.TECH (INDUSTRIAL BIOTECHNOLOGY)
END SEMESTER EXAMINATIONS, MAY 2016

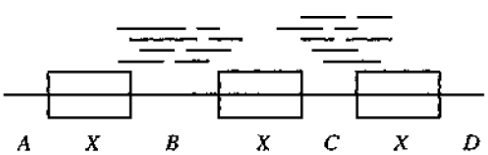
SUBJECT: PE I- ADVANCED BIOINFORMATICS [BIO 520]

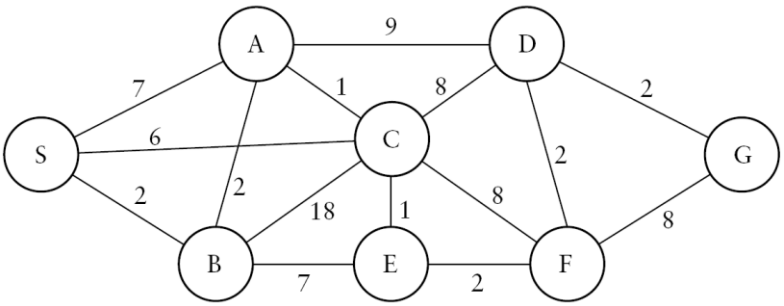
REVISED CREDIT SYSTEM

Time: 3 Hours MAX. MARKS: 50

Instructions to Candidates:

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

1A.	Assume that you are given a set of DNA sequence belonging to different species. What strategy has to be adopted to find a common pattern in such sequences?	**4**
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.	**4**
1C.	Give a schematic representation of PDB flat file. Dissect and explain its components	**2**
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: C A T A T G G C S2: C A A T A G C	**5**
2B.	Differentiate local and global alignment algorithms	**2**
2C.	In the given figure, suppose there is a fragment comprises the end of *B*, a copy of X, and the beginning of *D*. How would this fragment affect the assembly? Illustrate.  	**3**

3A.	Brief the significance of PROCHECK plots in the following order: (i) Chi1-Chi2 plots (ii) Main-chain bond lengths (iii) Main-chain bond angles (iv) Distorted geometry	**4**
3B.	Distinguish homology modeling and fold recognition methods. Which is more efficient in protein structure prediction? Why?	**3**
3C.	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**
4A.	Construct an overlap multigraph of a collection $\mathcal{F}$, where $\mathcal{F}$ = {a= TACGA; b=ACCC; c= CTAAAG; d= GACA}. Find a shortest common superstring for this collection and add a note on 'paths originating superstrings'.	**3**
4B.	Explain Sequencing by Hybridization (SBH). Also describe SBH as Hamiltonian as well as Eulerian path problems.	**3**
4C.	Differentiate Agonists from Antagonists, and Antibiotics from Disinfectants	**4**
5A.	Explain the significance of phylogenetic analysis in inferring the relationship between distantly related sequences?	**3**
5B.	Differentiate phylogram, cladogram, phenogram and ultrametric trees with illustrations	**3**
5C.	Find the shortest route between S and G. How you do you convert this problem in to a tree search? Also add a note on applications of this to phylogeny 	**4**
6A.	What are pharmacophores? Illustrate with a diagram	**3**
6B.	Differentiate Lead-likeness from Drug-likeness	**3**
6C.	Explain the outlooks and challenges for the next 20 years on the future of computer aided drug design	**4**