Reg. No.										

MANIPAL INSTITUTE OF TECHNOLOGY
MANIPAL
A Constituent Institution of Manipal University

II SEMESTER M.TECH (INDUSTRIAL BIOTECHNOLOGY)
END SEMESTER EXAMINATIONS, MAY 2017

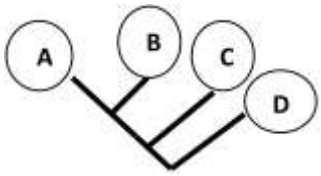
SUBJECT: ADVANCED BIOINFORMATICS [BIO 520]

Time: 3 Hours MAX. MARKS: 50

Instructions to Candidates:

- Answer **ALL** the 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.	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**
2A.	You were asked to align sequences using gap penalties. Which one would you prefer among the linear, continuous and affine gap penalties? Why?	**2**
2B.	Mr. Y would like to discover a drug against a protein target that is involved in cancer. He doesn't have any other information except the structure of the protein. Suggest him an *in silico* protocol to identify novel drugs.	**5**
2C.	Mr. Z has obtained a large number of fragments through shot-gun sequencing method. Suggest him the methods and tools for fragment assembly. Also, brief him the various problems involved during this process.	**3**
3A.	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**

3B.	What is bootstrapping? How do you evaluate a phylogenetic tree using bootstrap?	**3**
3C.	What is the terminology used to describe the relationship, if the derived characters are present in the following organisms: (i) A only, (ii) A and B, (iii) A and D  	**3**
4A.	A student wants to perform phylogenetic analysis of nucleotide sequences. Suggest the different models available for nucleotide substitution. Which ones do you think are the best and the worst? Why?	**3**
4B.	The following are the distinctive features of different organisms. Derive a character matrix and draw the corresponding cladogram that depicts their relationship. (The features that are not mentioned for the organisms should be assumed as absent) **Human Body Louse**: Three body regions, Flattened body. **Beetle**: Wings, Three body regions, Complete metamorphosis. **Ant**: Wings, Three body regions, Social, Complete metamorphosis, Mobile head. **Assassin Bug**: Wings, Three body regions. **Bee**: Wings, Three body regions, Social, Complete metamorphosis, Mobile head. **Millipede**: All the above features are absent.	**4**
4C.	What is a perfect phylogenetic tree? Discuss the problems involved in constructing this tree?	**3**
5A.	Do you think whether a drug that is being used for one disease could be used for another? How? Critically discuss if it is advantageous to the patient and pharma industry.	**7**
5B.	A pharma company has identified a novel drug through *in silico*, *in vitro* and *in vivo* experiments. It would like to market this drug before its rival companies come up with a generic drug. What steps do you suggest, with respect to bioinformatics, to shorten the lab-to-market period?	**3**