Reg. No.										

Manipal Institute of Technology, Manipal

(A Constituent Institute of Manipal University)

IV SEMESTER B.TECH (OPEN ELECTIVE)

END SEMESTER EXAMINATIONS, MAY/JUNE 2016

SUBJECT: INTRODUCTION TO BIOINFORMATICS [BIO 3282]

REVISED CREDIT SYSTEM

Time: 3 Hours MAX. MARKS: 50

Instructions to Candidates:

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

1A.	"By developing techniques and tools for analyzing sequence data and related structures, we can attempt to understand molecular basis of life." What is your implication about the statement?	**2**
1B.	If a data on complete set of chromosomes that determines an organism is given what is that data known as? By analyzing the data given what are the things you come across?	**2**
1C.	DNA is found in chromosomes. In eukaryotic cells, chromosomes always remain in the nucleus, but proteins are made at ribosomes in the cytoplasm. How do the instructions in DNA get to the site of protein synthesis outside the nucleus?	**2**
1D.	Name an application where you would use a method like BLAST and not a Needleman-Wunsch alignment.	**2**
1E.	"Although sequences of the ribosomal protein L36 from different species exhibit considerable diversity and only a single amino acid residue is conserved in all the sequences, they align unambiguously and are indisputable homologs". Discuss the significance of evolutionary basis of alignment.	**2**
2A.	A student asks a teacher; I'd like to know what it means when they say a protein have a modular design or such and such protein is a modular protein or has a modular nature. What is your interpretation to the student's question?	**3**
2B.	A curious question arises when comparing two sequences that are not so clearly similar but are shown to align in a promising way. In such a case what is the significance of the result statistically?	**3**
2C.	In a given protein structure map the possible structural features:	**4**

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	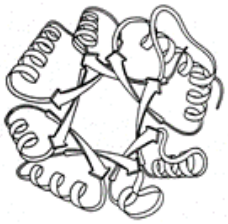	
3A.	Given is the consensus pattern of alpha-Tubulin. Describe the features of pattern represenatation. [SAG]-G-G-T-G-{SA}-G	**3**
3B.	Use the dataset below to calculate the neighbor joining trees based on alignment. CAGATCGCAGTTAGTTCCTAA CGGACCGCCGGTAGTACGCAG CAGATCGCCGGTAGTACGTAA CGGACCGCAGGTAGTTCCCAG	**4**
3C.	Discuss about the usage of UPGMA method and Neighbor-joining methods advantage one-over-other during the clustering analysis.	**3**
4A.	Briefly discuss about the process of rooting trees with an example	**4**
4B.	Elaborate on the concept of bootstrapping for evaluating the phylogenetic trees with diagram.	**4**
4C.	Classify the phylogenetic software's with examples based on their features and methods applied.	**2**
5A.	Discuss about the methods, approaches and results in Genome annotation.	**4**
5B.	Give the importance of Genome compression during execution of a genome project.	**3**
5C.	Describe the principles of comparative genome analysis in this Next generation sequencing era	**3**