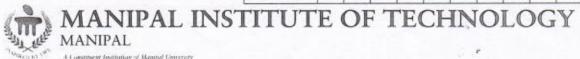## IV SEMESTER B.TECH. BIOTECHNOLOGY
END SEMESTER EXAMINATIONS, APRIL/MAY 2018
SUBJECT: INTRODUCTION TO BIOINFORMATICS [BIO 3282]
REVISED CREDIT SYSTEM

Time: 3 Hours   MAX. MARKS: 50

Instructions to Candidates:

- Answer **ALL** the questions.
- Missing data may be suitable assumed.

1A.	Next Generation Sequencing has been the basic motivation for bioinformatics and evolutionary research in the recent past. Justify the statement.	5
1B.	Describe how DNA relates to RNA relates to proteins.	3
1C.	From a digital storage point of view -- as DNA is "digital" in its format -- a base pair is equivalent to two bits of binary data and Human Genome comprise 3 billion base pairs. Calculate the size of the human genome.	2
2A.	Give a detailed procedure of searching and downloading a nucleotide sequence query using GENBANK database.	5
2B.	Discuss about the statistical significance of biological sequence analysis.	5
3A.	Given is the consensus pattern of Tubulin. Describe the features of pattern representation. **[SAG]-G-X(4)-T-G-{SA}-X**	5
3B.	Briefly discuss about the understanding and application of modular proteins in proteomics.	5
4A.	List the key elements influencing the optimal tree search.	4
4B.	Discuss the effect of applying resampling technique like bootstrapping on phylogeny data.	3
4C.	Explain the working and limitations of web based phylogenetic analysis tools with examples.	3
5A.	Explain in detail about the importance of Genome annotation in Genomics.	3
5B.	Give your inferences on the process of comparative genomics and its applications.	3
5C.	Discuss on Naïve Bit Encoding and Reference based data compression methods elaborately.	4