## B.TECH. IN ELECTRONICS AND COMMUNICATION ENGINEERING (BTECVI)

## Term-End Examination June, 2013

**BIELE-017: BIO INFORMATICS** 

Tim	e: 3 hours Maximum Marks	Maximum Marks : 70	
Note: Attempt any seven questions. Each question carries equipmarks.		иа	
1.	What is Bio informatics? Why it is important? What are the key challenges in bio informatics? Write the name of some important software used in bio informatics.	10	
2.	Differentiate local and global similarity search methods. Write the name of tools using three methods. Write the working principle of FASTA.	10	
3.	What is RNA? Write the possible representation of secondary structure of RNA. Write RNA structure prediction method with explanation	10	
4.	What is Microarray? How Microarray is prepared? Write in brief the steps involved in Microarray experiment.	10	

5.	What do you mean by sequence alignment? Write 6 types of sequence alignment? Explain briefly. Write the use of sequence alignment in bioinformatics.	10
6.	Write the overview of MUSTA with proper flowchart. Write the area where MUSTA is used	10

- with brief description.
- Explain Hidden Markov Model. Explain its 7. 10 application in sequence alignment.
- 8. What is folding problem? Classify the protein on 10 the basis of their structure. Write about secondary structure prediction techniques.
- 9. What is Phylogenetic tree? What is the use of 10 Phylogenetic analysis? Write the method of join Phylogenetic alignment.
- Write short notes on any two: 5x2=1010.
  - (a) Genome Sequencing
  - (b) 3d Motifs
  - (c) NLP
  - (d) **NMR**