No. of Printed Pages : **2**

BIELE-017

01891

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

Term-End Examination

December, 2013

BIELE-017 : BIO INFORMATICS

Time : 3 hours *Maximum Marks : 70*

Note : *Attempt **any seven** questions. Each question carries **equal marks**.*

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1. What is computational Genomics. "Computational Genomics is a subset of BioInformatics" ? Justify this statement with proper justification. Write the contribution of computational Genomics in Biology. **10**

2. Describe the working methodology of BLAST. How is Blat different from BLAST ? **10**

3. What is Clustering ? What are the different distance measures used in clustering ? What is role of clustering in Micsanoy analysis ? **10**

4. What is vector machine ? Explain its principal. Write the application of vector machine in Bio-Informatics. **10**

5. What is Multiple Sequence Alignment ? Why do we need it ? Write an algorithm for Multiple Sequence Alignment. **10**

6. What is MOTIF ? Can MUSTA used to detect common MOTIF ? Write the overview of MUSTA with proper flowchart. 10

7. Define and explain HMM. How to use HMM in sequence alignment ? 10

8. What is protein ? Write prediction method for protein structure. Write about any 5 protein database. 10

9. What is Genome sequencing ? Write shot gun approach for genome sequencing. 10

10. Write short notes on **any three :** 10

(a) Pretomics
(b) Folding
(c) Genetic Network
(d) K-Mean Clustering