No. of Printed Pages : 2 **BICSE-008**

B.TECH. COMPUTER SCIENCE AND ENGINEERING (BTCSVI)

Term-End Examination

June, 2013

BICSE-008 : BIO-INFORMATICS

Time : 3 hours *Maximum Marks : 70*

*Note : Attempt **any seven** questions. Parts of a question should be answered at the same place.*

1. (a) What is Gene Prediction ? **5x2=10**
   (b) Explain molecular predictions with DNA strings.

2. (a) Describe Algorithm issues in database search. **5x2=10**
   (b) What is the difference between Amino Acid substitution matrices PAM 250 and BLOSUM 62 ?

3. (a) What is Gene expression and micro arrays ? **5x2=10**
   (b) How micro array data analysis can be done ? Explain in detail.

4. (a) Why the analysis of Experimental identification of Protein - Protein interactions is necessary ? **5x2=10**
   (b) Define Protein - Protein docking algorithms.

5. Explain classical NMR spectroscopy with theoretical description. 10

6. (a) Explain Relaxation and dynamic processes of Nuclear magnetic resonance (NMR). 5x2=10
   (b) What are the experimental aspects of NMR spectroscopy ?

7. Explain regulatory RNA molecules (mi RNA, si RNA), antisense RNA and their applications in detail. 10

8. Explain computational methods for identification of polypeptides from mass spectrometry. 10

9. Explain identification / assignment of secondary structural elements from the knowledge of 3 - D structure of macromolecule using DSSP and STRI DE methods. 10

10. Write short note on **any two** of the following : 2x5=10
   (a) Multiple - threading algorithms
   (b) Homology modelling of protein - protein interactions
   (c) Protein and ligand binding
   (d) CAPRI