| BICSE-008 |

B.TECH. COMPUTER SCIENCE AND ENGINEERING (BTCSVI)

00491

Term-End Examination

December, 2013

BICSE-008 : BIO-INFORMATICS

Time : 3 hours   *Maximum Marks : 70*

Note : *Attempt **any seven** questions.*
*All questions carry **equal** marks.*

1. Briefly explain about Biological databases ? Why   **10**
    is bioinformatics important and explain its
    applications in the field of biology.

2. Write short notes on :
    (a) Relationship of multiple sequence alignment   **5**
         to phylogenetic analysis.
    (b) Uses of multiple sequence alignment.   **5**

3. How can you classify sequence database ?   **10**
    Describe about nucleotide sequence data bases.

4. Who created BLAST and explain the type of   **10**
    scoring matrix used by BLAST ?

5. (a) Discuss about relationships of phylogenetic   **5**
         analysis to sequence alignment.
    (b) Write the challenges for moore's law ?   **5**

6.   What is meant by Database similarity searches ?   **10**
     Explain different ways to Database similarity
     searching ?

7.   What is a gene ? Write the fine structure of gene   **10**
     and compare the structural differences of gene
     between prokaryotes and eukaryotes ?

8.   (a)   Explain in detail about dynamic   **5**
           programming for sequence alignment.
     (b)   Write the MUSTA algorithm for geometric   **5**
           hasing.

9.   Describe the following :   **4x2.5=10**
     (a)   Structural classification of proteins
     (b)   The CATH (Class, Architecture, Topology,
           Homology) databases.
     (c)   Hidden markov models
     (d)   PDB.

10. Write short notes on :   **4x2.5=10**
     (a)   Genome aligment
     (b)   3D motifs and Final Thoughts
     (c)   Protemics
     (d)   Gen bank.

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