

**B.TECH. COMPUTER SCIENCE AND
ENGINEERING (BTCSVI)**

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Term-End Examination

December, 2012

BICSE-008 : BIO-INFORMATICS

Time : 3 hours

Maximum Marks : 70

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

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1. (a) What are the current approaches for bioinformatics and what are the problems ? 5
(b) What are the tools for bioinformatics and comparative genomics ? What is Genome browser data integration ? 5
 2. (a) What are the challenges for Moore's law ? 5
(b) What is the need to get more efficient in how the data is processed, organized and accessed ? 5
 3. Briefly describe the following terms : 2x5=10
(a) Gen bank, (b) EMBL,
(c) DDBJ, (d) SWISS-PROT,
(e) PDB
 4. (a) What are the sequence - based database searches ? 5x2=10
(b) Explain BLAST and FASTA algorithms in detail.

5. (a) What is the basic concepts on identification of disease genes ? $5 \times 2 = 10$
(b) Explain integrated genomic maps in detail.
6. (a) Explain difference between primary and secondary nucleotide sequence database. $5 \times 2 = 10$
(b) What are the different types of bioinformatics databases ?
7. (a) What are the methods for 3d structure prediction ? $5 \times 2 = 10$
(b) Explain 3-D structure of macromolecule using DSSP and STRIDE methods.
8. Explain difference between $5 + 5 = 10$
(a) Protein and amino acid,
(b) DNA and RNA,
9. Write short notes on *any two* of the following : $5 + 5 = 10$
(a) Single sequence alignments in sequence alignment.
(b) Multiple sequence alignments in sequence alignment.
(c) PSI-BLAST.
10. Explain critical assessment of structure prediction (CASP) and structures of oligomeric proteins. 10
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