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Printed Pages – 3 CS – 024 / IT – 704

(Following Paper ID and Roll No. to be filled in your Answer Book)

PAPER ID : 1014   Roll No. | | | | | | | | | | | |

B.Tech.

SEVENTH SEMESTER EXAMINATION, 2004-2005

BIO-INFORMATICS

Time : 3 Hours   *Total Marks : 100*

Note :   (i)   *Attempt **ALL** questions.*

      (ii)   *All questions carry equal marks.*

      (iii)   *This paper contains five questions.*

1.   Attempt *any four* of the following : –   (5x4=20)

    (a)   What do you mean by Metadata ?

    (b)   What are the application area of Bio- informatics ?

    (c)   "Artificial Intelligence is a part of Bioinformatics". Justify your answer.

    (d)   List and explain the various uses of Metadata.

    (e)   What do you mean by Bioinformatics ?

    (f)   Explain how computer skills can be used to enrich the bioinformatics.

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2. Explain *any four* of the following : –   (5x4=20)

   (a) The diversity of life forms.

   (b) Information Storage - Nucleic acid

   (c) Information expression - Proteins

   (d) Biochemical reaction chain

   (e) Replication

   (f) Translation

3. Attempt *any two* of the following : –   (10x2=20)

   (a) What are the various levels of protein structure
        and what are the different methods of studying
        protein structure at the primary, secondary
        and tertiary levels ?

   (b) How is protein sequence related to structure
        and structure to function ?

   (c) What are the rules of protein structure ?
        Describe the agents that can denature the
        protein.

4. Attempt *any two* of the following : –   (10x2=20)

   (a) Discuss the various data retrival technique in
        Bioinformatics.

   (b) What are the molecular Biological data storage
        technique ? Compare these techniques.

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(c) Discuss the following :

    (i) Genome sequencing

    (ii) Single nucleotide polymorphism

    (iii) Gene expression

    (iv) Transcription factor binding sites

Attempt *any two* of the following : –   **(10x2=20)**

(a) What is multiple sequence alignment ? Explain domain motifs, families. What can be inferred from multiple sequence alignment ?

(b) What are the information that can be obtained from structural super position of proteins ?

(c) How will you represent the patterns ? Discuss about alignment, regular expression and graphical models.

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