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, 2006-07

BIOINFORMATICS

Time : 3 Hours *Total Marks : 100*

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

(ii) *All questions carry equal marks.*

(iii) *In case of numerical problems assume data wherever not provided.*

(iv) *Be precise in your answer.*

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

(a) Describe the term 'silicon-based' biology with proper example.

(b) Describe the steps to generate large scale molecular biology data.

(c) How to ensure the quality of the molecular biology data ?

(d) Define metadata with example.

(e) List the major sources of online protein data base.

(f) Discuss the role of information technologist in bio-informatics.

2. Attempt *any four* parts of the following : **(5x4=20)**

(a) Describe tree of life.

(b) List the major component of a cell and give their functions.

(c) Why the nucleic acid A is bound with nucleic acid C and nucleic acid T with nucleic acid G ?

(d) Explain the term gene and genome.

(e) Describe in brief the process of DNA replication.

(f) Describe in brief the process of protein forming from RNA.

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

(a) Describe the following in detail

  (i) Open reading frame (ORF)

  (ii) Introns and Exons.

(b) (i) Define amino acids. How many amino acids are found in living things ? Give the structure of any two.

  (ii) Discuss in brief the primary and secondary structure of protein.

(c) Discuss the protein folding problem in detail. Also discuss the various approaches which are being used to solve it.

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

(a) Discuss the various issues responsible for the complex nature of biological data and how to cope up with those issues.

(b) Describe the following :

  (i) Transcription factor binding site.

  (ii) Expressed sequence tags. (EST)

(c) Define the following :

    (i) Controlled vocabularies

    (ii) Object oriented databases

5. Attempt *any two* parts of the following : **(10x2=20)**

(a) Describe the Smith-Waterman algorithm for sequence alignment with example.

(b) What are some situations in which a molecular biologist might wish to perform a pairwise sequence alignment ? a multiple sequence alignment ? a sequence database search and why ?

(c) Describe the data model required for :

    (i) Macromolecular structure

    (ii) Chemical compounds

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