Name : ....

Roll No. : ....

Invigilator's Signature : ....

CS/M.Sc.(GE)/SEM-3/MSGEN-302/2009-10
2009
GENOMICS, PROTEOMICS AND BIOINFORMATICS

Time Allotted : 3 Hours   Full Marks : 70

The figures in the margin indicate full marks.

Candidates are required to give their answers in their own words as far as practicable.

GROUP – A
(Multiple Choice Type Questions)

1. Choose the correct alternatives for any *ten* of the following :

    $10 \times 1 = 10$

    i)   Global alignment is associated with

        a)   the Baum-Welch algorithm

        b)   Needleman Wunuch algorithm

        c)   the Viterbi algorithm

        d)   none of these.

    ii) Genbank file ends with

        a)   \ \   b)   / /

        c)   ENDML   d)   > !

    iii) Example of metabolic pathway database is

        a)   RESS   b)   BLISS

        c)   OMIM   d)   KEGG.

iv) MSDN stands for

    a)   Micro Soft Data Network

    b)   Microbes Sequence Diversity Nomenclature

    c)   Microbial Strain Data Network

    d)   none of these.

v) In ANOVA, assumption of error is

    a) $N(0, \delta^2)$ b)   *iid* $N(0, \delta^2)$

    c)   independent   d)   none of these.

vi) Relative mutability means

    a)   Count the number of times that each amino acid has occurred multiplied by 20

    b)   Count the number of times that each amino acid mutated

    c)   Count the number of times that each amino acid has changed in an interval and the number of times that it has occurred in the sequences

    d)   None of these.

vii) ANOVA turns to be equivalent to a *t*-test in case of

    a)   1 sample   b)   3 samples

    c)   4 samples   d)   2 samples.

viii) A widely used machine learing approach is

    a)   enzymes and metal dependent pathways

    b)   energy and mechanical pathways

    c)   hidden Markov models

    d)   none of these.

ix) Statistical components of a microarray experiment involves which of the following steps ?

    a)   Design only

    b)   Pre-processing only

    c)   Inference & validation

    d)   All of these.

x) Clustalw belonging to the organization

   a) NCBI

   b) EBI

   c) SWISS Institute

   d) Cambride Institute of Bioinformatics.

xi) PSI-Blast stands for

   a) particular sequene interpretation-blast

   b) personal subscribed integrated-blast

   c) position specific iterated-blast

   d) positional sequence iterated-blast.

xii) The low complexity region among the following is

   a) 'aaaaaaaaaa'   b) 'atttattaaagcgctgcat'

   c) 'aaggtcctagtagtcga'   d) 'nnnnnnna' .

GROUP – B
(Short Answer Type Questions)

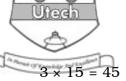Answer any *three* of the following.   3 × 5 = 15

2. How is "MALDI-TOP" used in proteomics ?

3. Write short notes on any one of the following :

   a) Chou-Fasman algorithm

   b) Needleman-Wunsch algorithm.

   c) HMM

   d) Blast.

4. Explain briefly the application of KEGG PATHWAY database.

5. Explain the term 'Functional Genomics'. Write its application in gene expression.   5

6. What are Knock out mice ?

GROUP – C

(Long Answer Type Questions)

Answer any *three* of the following.   3 × 15 = 45

7. Define E-value and Z-value of an alignment. Write down the steps. Find a nucleotide from NCBI namely cytochrome *B*. Convert it into protein. Find the homologue of the protein from the databases. Then find the similarity of the corresponding protein with other species. What are pairwise alignment and k-tupple ? Write the use of HSSP in blast.

2 + 2 + 6 + 2 + 3

8. Write down the steps for secondary structure prediction of protein. Name four publicly accessible nucleotide databases. Write down the advantages of DBMS over flat file system.

9 + 2 + 4

9. What is comparative Genomics ? How does it relate to functional genomics ? Why is model organism research important ? How mice and humans are closely related ?

4 + 4 + 4 + 3

10. You have the sequence of Indian elephant and Mamoth. How would you conclude that which one is closer descendant of African elephant ? What are the methods of aligning biological macromolecules (names only) ? Write down the significance of dot plot. Write name of the tool by which we can perform MSA and mention the application of the tool in bioinformatics field.   4 + 5 + 3 + 3

11. Why is the study of protein-protein interactions important in proteomics ? What are the different forces behind protein-protein interaction ? What are the differences between DIP and PPI servers ? How is prosite search done ? Explain the detection technique in protein array.   4 + 2 + 3 + 4 + 2