Name : …………………………………………………………

Roll No. : …………………………………………………

Invigilator's Signature : ……………………………………

CS/M.TECH (BT)/SEM-2/MBT-201/2013

2013

ADVANCED 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 the following :

$10 \times 1 = 10$

   i)   Which of the following is the fastest program to search for similar sequences in databases ?

   a)   BLAST   b)   FASTA

   c)   Needleman-Wunsch   d)   Smith-Waterman.

   ii) If you are aligning similar protein from diverged species, which one of the following is a better option ?

   a)   Global alignment

   b)   Local alignment

   c)   Both global and local alignment

   d)   Aligning is not possible.

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iii) Which of the following database is maintained by NCBI ?

    a) EMBL   b) PIR-PSD

    c) Genbank   d) Swiss-prot.

iv) Which of the following tool is effective to search homologous sequences in distantly related species ?

    a) Multiple alignment   b) Profile

    c) Pairwise alignment   d) None of these.

v) Genbank files can be identified uniquely searching using

    a) Text search   b) Advanced search

    c) Specific organism   d) Gi number.

vi) Which of the following is a protein family Database ?

    a) NCBI   b) Pfam

    c) PROSITE   d) Both (b) and (c).

vii) Perl stands for

    a) Pathologically Eclectic Rubbish Lister

    b) Practical Extraction and Report Language

    c) Practical Extension and Research Language

    d) Promoter Extraction and Report Language.

viii) Which of the following loop structure is special to Perl Script ?

    a) While loop   b) Do while loop

    c) For loop   d) Foreach loop.

ix) Biologically significant similar sequences have

    a) higher E-value   b) lower E-value

    c) lower Raw score   d) lower Bit score.

x) Lower k-tuple increases ………… of an algorithm.

    a) specificity   b) sensitivity

    c) both (a) and (b)   d) none of these.

GROUP – B

(Short Answer Type Questions)

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

2. What is multiple sequence alignment ? Discuss the use of multiple alignments. Explain how multiple alignment can be used to remote searching.   2 + 3

3. Discuss the significance of similar sequence searching. What are the different tools available for this type of search ? Mention with examples.   3 + 2

4. How can you find out promoter region in a genomic DNA ? Discuss few programs that predict promoter.   2 + 3

5. Discuss Chou Fasman method to predict protein secondary structure.

6. Explain Clustal W. method to align multiple protein sequences.

GROUP – C

(Long Answer Type Questions)

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

7. a) What is Dynamic programming ? Explain NW algorithm to align a pair of sequences.   2 + 8

   b) What is scoring matrix ? Write a brief note on BLOSUM series.   2 + 3
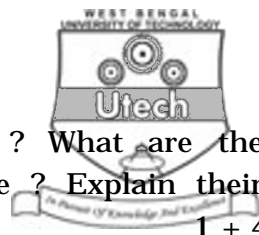
8. a) What do you mean by alignment ? What are the different types of alignment possible ? Explain their significance with examples. 1 + 4

   b) Use the following scoring matrix : 10

   And Gap penalty = – 8

   Obtain global alignment of the following *two* sequences :

   Sequence 1 : H E A G A W G H E E

   Sequence 2 : P A W H E A E

9. a) Discuss and explain the basis of the SCOP classification. 5

   b) What is Profile ? Explain significance of profile with respect to similar sequence searching. 5 + 5

10. a) What is Homology Modeling ? 3

    b) Discuss the steps in Homology Modeling to predict tertiary structure of protein. 10

    c) Write the limitations of Homology modeling. 2

11. a) What do you mean by a model ? Explain Markov processes. 2 + 4

    b) State Hidden Markov Model to solve Biological problem. 6

    c) Enlist advantages and limitations of using HMM. 3

12. Write notes on any *three* of the following : 3 × 5

    a) CATH

    b) GROMACS

    c) QSAR in Drug Design

    d) PSSM

    e) Phylip.

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