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Inviailator's Sianature:	

CS/B. Tech (CSE) /SEM-7/CS-704B/2011-12

2011 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.

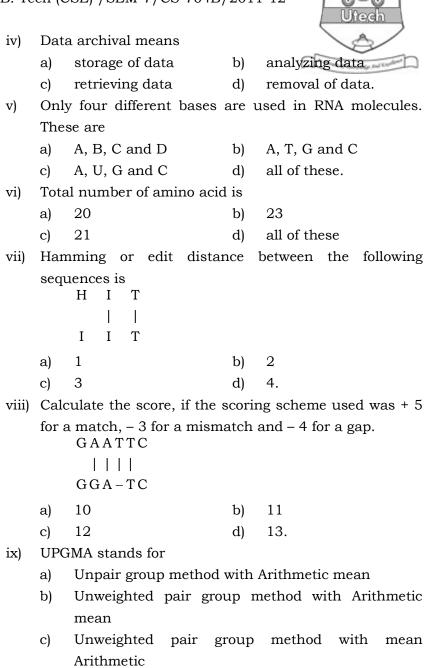
GROUP - A (Multiple Choice Type Questions)

- 1. Choose the correct alternatives for the following: $10 \times 1 = 10$
 - i) Threading refers to which of the following?
 - a) Sequence alignment
 - b) Fold recognition
 - c) Gap in structure
 - d) Sequencing method of DNA.
 - ii) Which one of the following does not match with the rest *three*?
 - a) EMBL

- b) DDBJ
- c) Gene bank
- d) MIPS.
- iii) Orthologs are defined as
 - a) homologous sequences in different species that share an ancestral gene
 - b) homologous sequences that share little amino acid identity but share great structural similarity
 - c) homologous sequences in the same species that arose through gene duplication
 - d) homologous sequences in the same species which have similar and often redundant function.

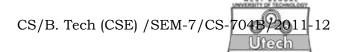
7402 [Turn over

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d)

none of these.



- x) Which of the following is not an example of neighbour algorithms?
 - a) SOPM

- b) GORIV
- c) SOPMA
- d) PREDATOR.

GROUP - B

(Short Answer Type Questions)

Write short notes on any three of the following.

 $3 \times 5 = 15$

2. Describe Central Dogma

- 5
- 3. a) Explain the differences between Bioinformatics and Computational Biology.
 - b) Writ down the complementary and reverse DNA sequences for
 - GGGATTTCGGAATCGTACGCCTTGGAATTG

3 + 2

- 4. Write down the distinction between Global Alignment and Local Alignment for two sequences.
- 5. a) What do you mean by Blosum 62 in scoring protein sequence alignment?
 - b) How disease predication is done in Bioinformatics?

2 + 3

6. What is PAM? Explain with an example

2 + 3

GROUP - C

(Long Answer Type Questions)

Answer any *three* of the following.

 $3 \times 15 = 45$

- 7. a) Write down the methods of sequence alignment.
 - b) Define EMBL.
 - c) What are the applications of multiple alignment, suboptimal alignment and parametric alignment. 5 + 5 + 5

7402 3 [Turn over

CS/B. Tech (CSE) /SEM-7/CS-704B/2011-12

- 8. a) Using a gap penalty of 2 (i.e., deduction 2 from the score for each gap), find the best alignment of AWAP and APP using a Needleman-Wunsch dynamic programming approach. Show your working (i.e., draw and fill in the S-W matrix).
 - b) Find a simple dot plot for the words CORRELATIONS and RELATIONSHIP. 10 + 5
- 9. a) What is Microarray?
 - b) Write down some features of microarray.
 - c) Explain Fold recognition in Bioinformatics. 5 + 5 + 5
- 10. a) What are the applications of Neural network in Bioinformatics? Explain with an example.
 - b) What are the modern usages of phylogenies ? (5 + 5) + 5
- 11. a) What are the parts of FASTA?
 - b) Explain Chao-Fasman algorithm with an example.

5 + 10

- 12. Write short notes on any *two* of the following : $2 \times 7\frac{1}{2}$
 - a) Metabolic pathway
 - b) HMM
 - c) Nearest Neighbour method for secondary structure prediction.

7402 4