



Name :

Roll No. :

Invigilator's Signature :

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.



- iv) Data archival means
- a) storage of data
 - b) analyzing data
 - c) retrieving data
 - d) removal of data.
- v) Only four different bases are used in RNA molecules. These are
- a) A, B, C and D
 - b) A, T, G and C
 - c) A, U, G and C
 - d) all of these.
- vi) Total number of amino acid is
- a) 20
 - b) 23
 - c) 21
 - d) all of these
- vii) Hamming or edit distance between the following sequences is
- | | | |
|---|---|---|
| H | I | T |
| | | |
| I | I | T |
- a) 1
 - b) 2
 - c) 3
 - d) 4.
- viii) Calculate the score, if the scoring scheme used was + 5 for a match, - 3 for a mismatch and - 4 for a gap.
- | | | | | | |
|---|---|---|---|---|---|
| G | A | A | T | T | C |
| | | | | | |
| G | G | A | - | T | C |
- a) 10
 - b) 11
 - c) 12
 - d) 13.
- ix) UPGMA stands for
- a) Unpair group method with Arithmetic mean
 - b) Unweighted pair group method with Arithmetic mean
 - c) Unweighted pair group method with mean Arithmetic
 - d) none of these.



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.