



Name :

Roll No. :

Invigilator's Signature :

CS/MBIN/SEM-1/MBIN-105/2009-10

2009

COMPUTATIONAL METHODS – I

Time Allotted : 3 Hours

Full Marks : 70

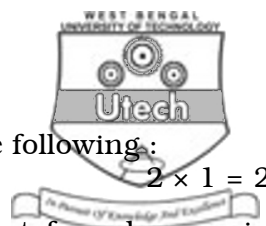
The figures in the margin indicate full marks.

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

GROUP – A

Answer *all* questions.

1. A) State whether the following statements are *True* or *False* :
5 × 1 = 5
- i) Maximum Parsimony method of phylogenetic tree construction is a distance based method.
 - ii) Gap extension penalty should be more than gap insertion penalty.
 - iii) A domain in a protein differs largely from a motif in size.
 - iv) Needleman-Wunsch algorithm uses dynamic programming to find the optimal alignment.
 - v) Protein sequence analysis provides more noise in comparison to nucleic acid sequence analysis.



B) Choose the correct alternatives for the following :

$2 \times 1 = 2$

- i) Haemoglobin from horse and that from human is an example of
- a) a paralogous pair b) an orthologous pair
- c) a xenologous pair d) an analogous pair.
- ii) A multiple sequence alignment of related sequences generates
- a) a structure file
- b) a consensus sequence
- c) a dot plot
- d) a condon bias.

C) Expand the following :

$3 \times 1 = 3$

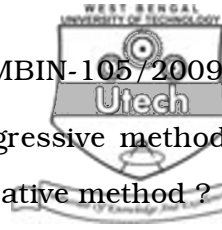
- i) MUM
- ii) UPGMA
- iii) GOR method.

GROUP – B

Answer any *five* of the following.

$5 \times 12 = 60$

2. a) 'The SP (Sum of Pairs) method tends to overweight the influence of mutations.' Explain with an example. 4
- b) Schematically explain the sequential steps of CLUSTALW. 3



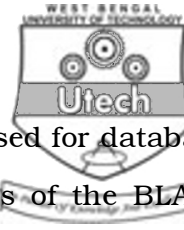
- c) How would you differentiate the progressive method of multiple sequence alignment from iterative method ? 2
- d) How is bootstrapping done to assess confidence in phylogenetic tree splits ? 3
3. a) Define the concept of propensity for the prediction of secondary structure of a protein. How would you predict helices, strands and turns from the primary sequence of a protein using the method proposed by Chou and Fasman. 2 + 6
- b) Explain how GOR method is different from it. 4
4. a) Write down and explain Karlin-Altschul equation. Where does this equation find its use and how ? 4 + 2
- b) Define the following : 3 × 2
- i) Z-score
- ii) *p*-value
- iii) *E*-value.
5. Align the below two strings for global alignment using the Needleman-Wunsch algorithm, according to the simple scoring scheme match = 0, mismatch = 20 and insertion or deletion = 25. Find the optimal score.

G A A T T C A

G G A T C G A

10 + 2

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6. Why are heuristic methods such as BLAST used for database searches ? Write down the sequential steps of the BLAST algorithm. For what purpose are SEG and DUST used in BLAST ?

2 + 6 + 4

7. Write short notes on any *four* of the following :

4 × 3

- a) Dot plot
- b) Hamming and Levenshtein distance
- c) Drawbacks of UPGMA over Neighbour-joining method
- d) Mutational probability matrix
- e) Comparison of PAM and BLOSUM
- f) Maximum Parsimony.

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