

Name : .....

Roll No. : .....

Invigilator's Signature : .....

**CS/M.Tech(BT)/PBIR (PHMB/PHMC)/SEM-2/MBT-205/  
PHMB-205/PHMC-205/2013**

**2013**

**APPLIED 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.*

Answer Question No. 1 and any five from the rest.

1. A) Write the full forms of the following : 3 × 1

- i) PSSM
- ii) LCR
- iii) PSI-BLAST.

B) Fill in the blanks : 7 × 1

In affine gap penalty, gap extension penalty is always  
..... than gap opening penalty. ....  
and ..... are the abundantly used scoring  
matrices.

Lods ratio is the ..... of the ratio of  
..... frequency to ..... frequency.  
In BLOSUM62 the amino acid ..... has the  
maximum identity score.



2. You have been given two gene sequences and have been asked to find out which out of the two has repeats and which one has a palindrome. Which in silico study would you perform and how would you determine the difference from your expected ?

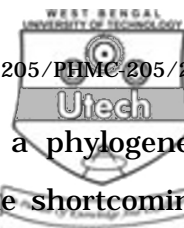
Given the primary sequence of a protein how would you predict whether it is a transmembrane protein that spans the membrane five times ?

In protein-protein docking, explain how the residues involved in complexation are determined. 1 + 3 + 4 + 4

3. Name the algorithms used for global and local alignment of sequences. Which one is used for database searches ? Justify your answer. Write how BLAST works. 2 + 1 + 3 + 6
4. What is the minimum number of sequences for multiple sequence alignment ? Explain a method of scoring such an alignment. What is the limitation of the method ? What are the applications of multiple sequence alignment ?

1 + 5 + 2 + 4

5. Given the primary sequence how can the secondary structure of a protein be predicted by Chou-Fasman method ? In what way is this method different from the GOR method ? Calculate the alpha helical propensity of amino acid  $X$  when total number of  $X$  in a database is 9520 against a total number of 21875 amino acids. Also, number of  $X$  found in alpha helices is 1425 against a total of 7500 other amino acids forming helices. Considering the propensity value judge the ability of  $X$  to form alpha helices. 5 + 2 + 4 + 1



6. Take an example and explain how to draw a phylogenetic tree using the UPGMA method. What are the shortcomings of the method ? Name a method that uses distance matrix but bypasses these shortcomings. Name two character-based methods for the construction of phylogenetic tree.

7 + 2 + 1 + 2

7. In homology modelling, when more than one structure is available, what different steps are followed to choose a single template ? Explain how a predicted model thus obtained may be refined. How does threading predict tertiary structure of proteins ?

3 + 3 + 6

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