

MASTER OF COMPUTER SC. & ENGG. 2<sup>ND</sup> SEM. EXAMINATION - 2018

## BIOINFORMATICS

Time: Three Hours

Full Marks: 100

Answer Question No. 1 and any FOUR from the rest

1.
  - a) What is the function of an *RNA polymerase*?
  - b) What is *base pairing* in DNA?
  - c) What are *introns* and *exons*?
  - d) What is a protein *backbone*?
  - e) What is *Hydrophilicity* and *Hydrophobicity*?
  - f) What is the purpose of *gap penalty* in *sequence alignments*?
  - g) What is *multiple sequence alignment*?
  - h) What is the purpose of the KEGG database?

(2+2+2+2+2+3+3+4) = 20

2.
  - a) Discuss the basic differences between PAM and BLOSUM matrix.
  - b) Discuss key features of *Ramachandran Plot*
  - c) Discuss any two surface representation techniques in molecular docking?

6+6+8 = 20

3.
  - a) What is PTM? Briefly discuss the classification strategy adopted in AMS3 algorithm for prediction of the PTM sites.
  - b) Compare different properties of a *scale-free, random and hierarchical network*?

(3+7)+(10) = 20

4. Using the Needleman and Wunsch dynamic programming method, construct the partial alignment score table for the following two sequences, using the following scoring parameters: match score = +1, mismatch score = 0, gap penalty = -1  
 Sequence 1 = ACAGTCGAACG  
 Sequence 2 = ACCGTCCG  
 What is the optimal global alignment between these sequences?

20

5. Use UPGMA to reconstruct a phylogenetic tree using the following distance matrix:

	A	B	C	D
A	0	8	7	12
B		0	9	14
C			0	11
D				0

20

6. a) Briefly Describe the principle of the FASTA algorithm for sequence alignment and search. Explain with respect to the following example (word length as 1):  
Query sequence: FAMLGFIKYLPGCM  
Target sequence: TGFIKYLPGACT
- b) What is Multiple Sequence Alignment (MSA)? Name some the popular MSA algorithms.

15+(5) = 20

7. Write short notes on the following:

- a) Dot Plot
- b) PSSM
- c) PSIPRED
- d) DALI

5x4 = 20