

MASTER OF COMPUTER SC. & ENGG. 2ND SEM. EXAMINATION - 2017

BIOINFORMATICS

Time: Three Hours

Full Marks: 100

Answer Question No. 1 and any FOUR from the rest

1. a) Draw the chemical structure of a generic amino acid.
 b) What is a *Triplet Code*?
 c) What do you mean by *hub* proteins?
 d) What is *replication slippage*?
 e) What is the purpose of a *Ribosome*?
 f) What is the purpose of the MIPS database?
 g) What do mean by *hydrophobic amino acids*?
 h) What are *anti-parallel beta-sheets*?
 i) What is *closeness* property in a PPI network?
 (3+2+2+2+2+2+2+2+3) = 20
2. a) What is *relative mutability*? Discuss the basic steps for construction of a PAM matrix.
 b) Briefly discuss the *DOCK* algorithm in molecular docking?
 (2+10)+8 = 20
3. a) What are the effects of PTM? Briefly show the steps in conversion *in vivo* Preproinsulin to Proinsulin to Insulin.
 b) What is *druggability index*? What are the properties of a *scale-free network*?
 (4+8)+(2+6) = 20
4. Briefly describe Smith-Waterman algorithm. Apply the algorithm to align the following two sequences, using match score = +2 and mismatch/gap score = -1,
 Sequence 1 = CAGCRMADCGNRQ
 Sequence 2 = AGCGNRCAKGRM
 Please identify and show the trace-back corresponding to two possible local alignments.
 20
5. Use Fitch-Margoliash to reconstruct a phylogenetic tree using the following distance matrix:

Species	A	B	C	D
B	9	-	-	-
C	8	11	-	-
D	12	15	10	-
E	15	18	13	5

20

6. a) Briefly Describe the principle of the BLAST algorithm. Explain with respect to the following example (consider default word length as 4):
Input sequence: AILVPTV
Database sequence: MVQGWALYDFLKCRAILVGTVIAML
- b) What is *n-star* quality consensus? Briefly discuss the consensus strategy adopted for prediction of PTM sites in AMS4 algorithm.

8+(4+8) = 20

7. Write short notes on the following:
- Protein Threading
 - PSSM
 - PPI-SVM
 - CATH database

5x4 = 20