

MASTER OF COMPUTER SC. & ENGG. 2ND SEM. EXAMINATION - 2019

BIOINFORMATICS

Time: Three Hours

Full Marks: 100

Answer Question No. 1 and any FOUR from the rest

1. a) What are the ϕ and ψ angles in a protein backbone?
- b) What is *small world effect* in a biological network?
- c) What do mean by *hydrophobic & hydrophilic amino acids*?
- d) Write the chemical structure of a generic amino acid.
- e) What is the purpose of a *Ribosome*?
- f) What is the purpose of the PDB database?
- g) What is *Lenhoff* technique in Docking?

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

2. 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 *relative mutability*? Discuss the basic steps for construction of a PAM matrix.

10+10 = 20

3. a) What is PTM and what are the purposes of PTM? Briefly discuss the conversion of *preproinsulin* to *proinsulin* to *insulin*.
- b) Briefly discuss the n-star consensus strategy adopted in AMS3 algorithm for prediction of the PTM sites.

(4+10)+(6) = 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 = -1, gap penalty = -1
Sequence 1 = GCATGCU
Sequence 2 = GATTACA
What are the optimal global alignments between these sequences?

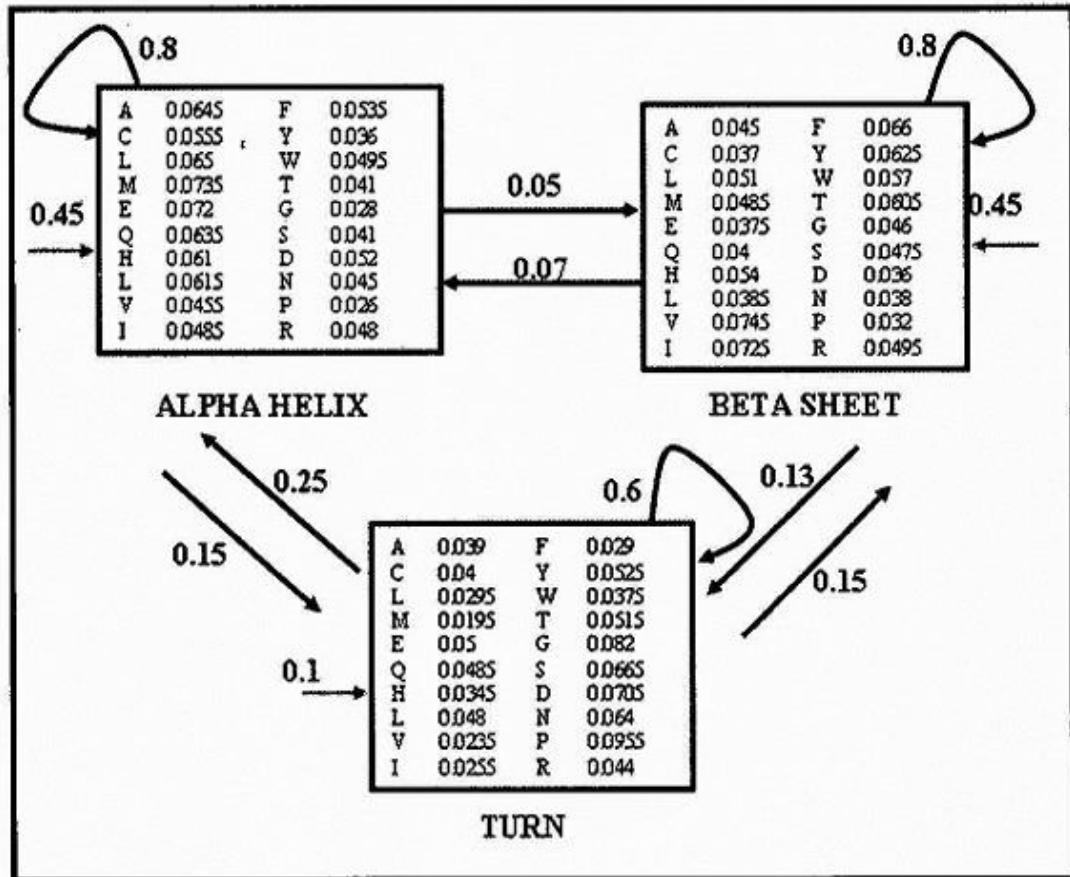
20

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

	A	B	C	D	E
A	0	8	8	5	3
B		0	3	8	8
C			0	8	8
D				0	5
E					0

20

6. What do you mean by Protein Secondary Structure Prediction (PSSP)? How to use HMM in PSSP? Given the following probability distribution, estimate the optimum secondary structure annotation for a string: TGT
Check all possible annotations of H, S and T.
T is the starting Amino Acid in the sequence.



20

7. Write short notes on the following:
- Ramachandran Plot
 - PSSM
 - DOCK
 - DALI

5x4 = 20