M.TECH COMPUTER TECHNOLOGY 4TH SEMESTER EXAMINATION - 2018

BIO-INFORMATICS

Time: Three Hours   **Full Marks: 100**

Answer Question No. 1 and any FOUR from the rest

1. a) What is the primary function of *mRNA*?
   b) What are the *phi(ϕ) and psi (ψ)* angles in a protein backbone?
   c) What is the purpose of the PubMed database?
   d) What is *druggability index*?
   e) What is the purpose of BLASTN server?
   f) What are *parallel and anti-parallel beta sheets*?
   g) What is *closeness* property in a PPI network?

   $(2+4+2+2+2+4+4) = 20$

2. b) Use Fitch-Margoliash 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

3. a) What is Post Translational Modification (PTM)? What are the basic biological functions of PTM?
   b) Briefly discuss the classifier consensus strategy in AMS4 algorithm for prediction of the PTM sites.
   c) Write different steps of the DALI algorithm.

   $(2+6)+6+6 = 20$

4. a) Write the mathematical formulation of the Smith-Waterman algorithm.
   b) Apply the algorithm to align the following two sequences, using match score = +2 and mismatch/gap score = -1,
   Sequence 1 = ACGTATCGCGTATA
   Sequence 2 = GATGCTCTCGGAAA

   $5+15=20$

5. 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) Explain the estimation of the Clustering Coefficient in a network with an example.
   c) What are the properties of a *scale-free network*?

   10+5+5=20

6. a) Briefly discuss the PSI-Pred method for protein secondary structure prediction.
   b) What is *relative mutability*? Discuss the basic steps for construction of a PAM matrix.

   8+(2+10)=20

7. Write short notes on the following:
   a) DOCK
   b) PPI-SVM
   c) Protein Threading
   d) Dot Plot

   5x4 = 20