Ph.D. ENTRANCE EXAMINATION, OCTOBER 2015

FACULTY OF APPLIED SCIENCES

COMPUTATIONAL BIOLOGY & BIOINFORMATICS

Time: 140 Minutes Maximum Marks: 160

***Note**: Answer **any twelve** questions from Section **B** and **one** question from Section **C** in the subject concerned. In Section **B, each** question carries **10** marks. Section **C** carries **40** marks. In Section **B** an answer should not exceed **100** words. In Section **C,** an answer should not exceed **500** words.*

SECTION – B

1. Explain the terms:
    a. Sequence Similarity and Sequence Identity
    b. E-value in BLAST
2. Align the following sequence using dynamic programming for Global alignment: ATTGC and AGGC
3. Compare the following sequence alignment tools:
    a. PSI-BLAST
    b. FASTA
4. What is meant by Consensus sequences in Bioinformatics? Compare Sequence logo and Consensus logo.
5. Explain the Multiple Sequence Alignment algorithm of ClustalW.
6. Describe how DNA sequence data might be used to reconstruct evolutionary (phylogenetic) trees.
7. Use UPGMA method to derive the tree and branch lengths using the following distance matrix:

	A	B	C
B	0.40		
C	0.35	0.45	
D	0.60	0.70	0.55

8. Explain the maximum likelihood method of phylogeny construction with a suitable example.
9. What are Biological databases? Explain its function and organization in detail.
10. Write notes on the following:
    a. Hidden Markov Model
    b. SVM (Support Vector Machine)
11. Explain the following:
    a. Folding Problem
    b. Motifs
12. Describe the Protein Structure Database in detail
13. Discuss the various algorithms for comparing protein structures.
14. Write notes on
    a. QSAR
    b. Docking
15. What is virtual screening in Drug discovery and design? Explain the various techniques of virtual screening.
16. What do you understand by gene regulatory network? Explain with a suitable example.

SECTION - C

1. Define the problem statement: explain the objectives and methodology to be adopted for Gene Prediction in Eukaryotic genomes using data mining method.

2. Prepare a synopsis for Computational Protein secondary structure prediction problem.

3. Prepare a detailed project proposal based on the application of a machine learning algorithm to any one problem in Bioinformatics of your choice

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