ISLAMIC UNIVERSITY OF TECHNOLOGY (IUT)
ORGANISATION OF ISLAMIC COOPERATION (OIC)
Department of Computer Science and Engineering (CSE)

MID SEMESTER EXAMINATION
DURATION: 1 Hour 30 Minutes

WINTER SEMESTER, 2017-2018
FULL MARKS: 75

CSE 4741: Bioinformatics

Programmable calculators are not allowed. Do not write anything on the question paper.
There are **4 (four)** questions. Answer any **3 (three)** of them.
Figures in the right margin indicate marks.

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1. a) *"The size of the genome (base pair count) and the number of genes in the genome of a lifeform does not represent the complexity of that lifeform"* – Justify this statement. 10
   b) What is sequence alignment? Discuss the importance of sequence alignment. 10
   c) Briefly describe the transcription process of central dogma. 5

2. a) Compare DNA and a computer program. 10
   b) During translation process Codons are mapped to Amino Acids to form proteins. But, number of different Codons and number different Amino Acids in living being are not equal. Discuss the effect of this scenario on lifeforms. 10
   c) Discuss on insert, delete and align operation during pairwise sequence alignment. 5

3. a) State the constraints to form RNA secondary structures. 5
   b) Write down Nussinov folding algorithm to predict RNA secondary structures. 5
   c) Using Nussinov folding algorithm predict secondary structure of the following RNA sequence. 15

   GGGAAUUCC

4. a) Discuss on RNA editing and its impact in cephalopods. 10
   b) Following 5 sequences are needed to be aligned using ClustalW method. 5+10

   S1: AGGCTATG
   S2: TGCCTTAG
   S3: GTTGCTTA
   S4: ATGCTTAG
   S5: CTGCTCAG

   i. Build the distance matrix D for the sequences.
   ii. Step by step build the rooted guide-tree using UPGMA approach.