

**ISLAMIC UNIVERSITY OF TECHNOLOGY (IUT)**  
**ORGANISATION OF ISLAMIC COOPERATION (OIC)**

**Department of Computer Science and Engineering (CSE)**

**MID SEMESTER EXAMINATION**

**WINTER SEMESTER, 2019-2020**

**DURATION: 1 Hour 30 Minutes**

**FULL MARKS: 75**

**CSE 4753: 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.**

1. a) What is gene expression? Discuss how gene expression can be measured. 2+4  
 b) Discuss transcription and post-transcription operations. 10  
 c) Why gene expression raw data are needed to be normalized? Explain various types of bias which are needed to be considered during normalization. 9
  
2. a) Write short notes on the followings:
  - i. GC-content 3
  - ii. Poly-A tail 3
  - iii. pseudogenes 4
  - iv. overlapping genes 5
 b) What would happen during translation process if a start codon re-appeared within mRNA? 2  
 c) What is *consensus sequence*? Four sequences are given below. Build a *consensus sequence* for them. 8  
 ACTGA  
 ACGCA  
 ATTC  
 TCCA
  
3. a) Describe various regulatory sites and transcription factor which control transcription process. 10  
 b) Write down your understanding about the content and structure of human genome. 10  
 c) Discuss how scoring matrix can be design for sequence alignment purpose. 5
  
4. a) Discuss on RNA editing in cephalopods. 10  
 b) Distance matrix D for Five sequences a, b, c, d and e are given below. You need to align them using clustalW algorithm. Step by step build the guided tree using UPGMA approach. 12

	a	b	c	d
b	5			
c	9	10		
d	9	10	8	
e	8	9	7	3

- c) What are the differences between Prokaryotic and Eukaryotic cells? 3