

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

Department of Computer Science and Engineering (CSE)

MID SEMESTER EXAMINATION

WINTER SEMESTER, 2018-2019

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.

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|-------|---|----|
| 1. a) | Write short notes on genes, chromosomes and DNA. | 6 |
| b) | Describe the steps of central dogma in details. | 9 |
| c) | Explain the process of alternate splicing. | 6 |
| d) | What is mRNA degradation? How does it affect the translation process? | 4 |
| 2. a) | | |
| | Discuss on various types of translation process. | 6 |
| b) | During translation Codons are mapped to Amino Acids to form proteins. Number of different Codons and number different Amino Acids are not equal. Discuss the impact of this scenario. | 6 |
| c) | 'k-means' clustering is a method to find k number of clusters within a set of data. | |
| i. | Write down the weakness of k-means clustering method. | 3 |
| ii. | Propose at least two methods to modify k-means algorithm to overcome the weakness. | 10 |
| 3. a) | | |
| | Draw a diagram showing various forms of RNA secondary structures. | 6 |
| b) | Explain the advantages of <i>Zuker Folding Algorithm</i> over <i>Nussinov Folding Algorithm</i> to predict RNA secondary structures. | 7 |
| c) | What is sequence alignment? Discuss its importance in bioinformatics study. | 5 |
| d) | Classify sequence alignments along with short description. | 7 |
| 4. a) | | |
| | In agglomerative clustering we need to define a proximity matrix in terms of cluster similarity. Discuss various methods to define inter-cluster similarity. | 12 |
| b) | How can we evaluate clusters generated from a clustering method? Discuss them. | 4 |
| c) | What is InDel operation? Explain with example. | 4 |
| d) | Following two sequences are needed to be aligned locally and globally: | 5 |

ATGCAATCA
 TGACVGTA

Show the initialization matrix for both *smith-waterman* and *needleman-wunsch* algorithms. Consider gap, match, and mismatch penalties are -1, +2, and -2, respectively.