

## **Daffodil International University**

Department of Computer Science and Engineering Faculty of Science and Information Technology Mid Term Examination, Semester: Spring, 2017

Course Title: Introduction to Bioinformatics Section: All Course Code: CSE 235

Time: 1.5 Hours Full Marks: 25

## Answer any THREE including Question No.1

	(The figure of the right margin indicates the full marks)		
1/	What bioinformatics can do?	2.5	5
	Write the chemical composition of cell.	2.5	5
2	Write the differences between DNA and RNA.	3	
	Describe various steps of Sequencing Reaction and Capillary Electrophoresis for determining DNA sequence according to Dideoxy DNA Sequencing Technique /Sanger Method.	5	
	i) ACCTATGA.  ii) ACCGTATGC  TCGTATGA.  ACCGCCGTATGC	2	
3.	a) Multiple sequence alignments (MSA) can reveal subtle similarities that pair-wise alignment does not reveal. However, MSA faces several problems and challenges while solving through global alignment. What are those challenges? Explain.	3	
/	b) Let two DNA sequences S1 and S2 are following: Sequence1= "GACTAC"	7	
	Sequence2= "ACGC"		
	Use <b>Smith-Waterman</b> (Local Alignment) algorithm to calculate all the possible optimal alignments between given sequences. Where, matching reward=+4, mismatch penalty=-1 and gap penalty=-2.		
<b>A</b> /	a) Consider four sequences for multiple sequence alignment. How you will calculate the score of any particular position S (i, j, k, l) using dynamic programming?	5	
	(b) Why sequence alignment is necessary?	3	
(	c) Write short notes on: (i) Homolog. (ii) Paralog.	2	1

Be specific! Avoid unnecessary discussions while writing the answers.

Good Day 3