Dept. Computer Science and Engineering
University of Rajshahi

Sample Question

Course ID: M 1151 Course Title: Bioinformatics
Total Time 3 Hours Total Marks 70
Answer any **six** questions taking **three** from each section

Section A

1(a) Explain the main characteristics of organism. 5
(b) What is Bioinformatics? 2
(c) What are different types of cell membrane proteins? What are their roles in a cell? Why are they targets of modern medicinal drugs? 4.66

2(a) Explain various type of mutations. 5
(b) Explain central dogma of molecular biology with neat diagram. Explain how it is an information science 6.66

3(a) What is Artificial Nucleotides? Is there any example of Artificial Nucleotides? 2
(b) The crRNA sequence of Chain B is given below: 1.66
AATTTCTACTGTTGTAGATAGATTAAAAGGTAATTCTATC
What will be its complementary base pair?
(c) A sequence is given below: 5
GATTTTAGATTCACTGGAATTCCACATTGACCCTTATGTA
Now, considering all possible reading frames (5'3' Frame 1,2,3 and 3'5' Frame 1,2,3), which Frame will encode the most sustainable protein?
(given that codon for Methionine (Met) is ATG and stops codons are TAA, TAG, TGA)
(d) Explain the Hydrogen bond. What is its role to make a spiral DNA structure? 3

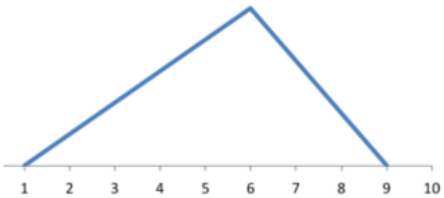
4(a) Which one is less stable between DNA and RNA? Explain your answer. 3
(b) Explain, with an example, how a Peptide bond is formed. 2
(c) A segment of Homo sapiens chromosome 3, GRCh38.p12 is given below: 4.66
GGGTTGCGGAGGGTGGGCCTGGGAGGGGTGGTGGCCATTTTTTGTCTAACCCTAACTGA
GAAGGGCGTAGGCGCCGTGCTTTTGCTCCCCGCGCGCTGT.
Derive the corresponding RNA sequence and then draw the possible secondary structure of that RNA sequence.
(c) Explain Phosphorylation. 2

Section B

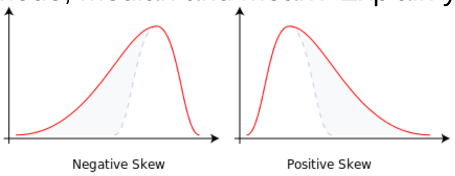
5(a) Explain FASTA algorithm in detail with recommended steps for similarity searching. 6
(b) Explain similarities and differences between FASTA and BLAST tools for sequence alignment. 5.66

6(a) Explain the following Entrez statements: 2
(i) 2500:2600[SLEN] (ii) 2:100[SLEN] (iii) 1999/07/25:1999/07/31[MDAT].
(b) What are the major header fields of a GenBank database? 4.66
(c) What are major sources for Nucleotide database? 2
(d) What are the features of RefSeq, BioSystems and Gene databases? 3

7(a) The probability distribution is given by the following figure. What is the maximum probability? 2



(b) The probability distribution is given by the following figure. What will be approximate position of mode, median and mean? Explain your answer. 2



(c) Explain, with example, level of confidence and significance level. 2

(d) Apply Median Polish Normalization algorithm on the following 2D data set. 5.66

2	6	10
5	11	3
4	6	2

8(a) What is BLOSUM 62 Substitution matrix? 2

(b) What are the difference between Smith–Waterman algorithm and Needleman–Wunsch algorithm? 3

(c) Align the following two sequence by applying Needleman-Wunsch algorithm 6.66

GCATT
ATTAG

The gap penalty is -1 and the scoring matrix is given below:

	A	G	C	T
A	1	-1	-1	-1
G	-1	1	-1	-1
C	-1	-1	1	-1
T	-1	-1	-1	1