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3rd year 2nd Semester B.Sc. (Engg.) Final Examination, 2023
Course Title: Bio-Informatics Course Code: ICT-3211
Time: 3 hours Full Marks: 70

[Answer Any Five Questions]

1.	(a)	Explain the Chemical structure of DNA.	4
	(b)	Explain the Process of transcription.	6
	(c)	"Roles of Ribosome in Translation"-Explain.	4
2.	(a)	Explain the role of **genome annotation** in bioinformatics. What tools are commonly used for this purpose?	4
	(b)	Compare **2D gel electrophoresis** and **liquid chromatography** for protein separation. Which method is more suitable for large-scale proteomics studies?	4
	(c)	Explain the process of Sanger sequencing.	6
3.	(a)	Align the following two sequences using the **Needleman-Wunsch algorithm** with the given scoring scheme: **Sequence 1:** AGTACGCA **Sequence 2:** TATGC **Scoring Scheme:** • **Match** = +1 • **Mismatch** = -1 • **Gap penalty** = -2 Perform the alignment and find the optimal alignment score.	10
	(b)	Compare PAM and BLOSUM.	4
4.	(a)	Align the following two sequences using the **Smith-Waterman algorithm** with the given scoring scheme: **Sequence 1:** AGTACGCA **Sequence 2:** TATGC **Scoring Scheme:** • **Match** = +2 • **Mismatch** = -1 • **Gap penalty** = -2 Perform the alignment and find the optimal local alignment score.	10
	(b)	Given the alignment of the following sequences **"MKT"** and **"MQT"**, calculate the scores from BLOSUM62:	4
5.	(a)	What is PubMed, and how can bioinformatics researchers use it to perform literature mining for identifying trends, key discoveries, or relationships between genes, proteins, and diseases?	4
	(b)	A DNA sequence consists of **exons (E)** (coding regions) and **introns (I)** (non-coding regions). Given the following **HMM parameters**,	10

i. Given DNA Sequence (Observations): A G C A T

ii. **Hidden States: E (Exon) and I (Intron)**

iii. Transition Probabilities (A)

From/To	Exon(E)	Intron(I)
Exon(E)	0.9	0.1
Intron(I)	0.2	0.8

iv. Emission Probabilities (B):

Nucleotide	Exon(E)	Intron(I)
A	0.3	0.4
G	0.2	0.1
C	0.3	0.4
T	0.2	0.1

v. Initial Probabilities (π):

State	Probability
Exon(E)	0.6
Intron(I)	0.4

Use the **Viterbi Algorithm** to:
I. Compute initial probabilities.
II. Compute the most probable path.
III. Retrieve the best state sequence.

6. (a) What is a Hidden Markov Model (HMM), and how is it used in bioinformatics for sequence analysis, such as gene prediction or protein domain identification? 5

(b) Discuss the usage of Support Vector Machines in the context of secondary structure prediction, and what are their advantages? 5

(c) If a disease is associated with mutations in 10 known genes according to OMIM, and the probability of a random mutation occurring in any gene is 0.001, calculate the likelihood of observing mutations in at least 2 of these genes in a sample of 100 individuals. 4

7. (a) Derive the equations governing the inverse kinematics of a bionic arm to compute joint angles from target positions. 5

(b) How can machine learning models be used to optimize the cost-performance ratio of bionic devices for mass production? 4

(c) Explain how advanced sensor arrays in bionic devices integrate with neural networks for real-time adaptability. 5

8. (a) Explain the Working principle of the bionic arm. 5

(b) Compare myoelectric and brain-controlled bionic arms. 4

10 (c) Describe how machine learning improves movement prediction in bionic arms. 5