



COMSATS University, Islamabad Campus
Department of Computer Sciences

Midterm Examination – Fall 2025

Student Name:		Registration#:	
Course code/title:	BIO310 Introduction to Bioinformatics	Course Instructor:	Dr. Maryam Mehmood
Class & Sec.	BCS-II A/B	Date:	
Total marks:	25	Obtained marks:	
Time allowed	80 minutes		

Instructions:

- Do as directed
- No extra time or re-take of this exam will be granted after the given date and time
- No over-writing/cutting is allowed
- No electronic gadgets like cell phones, watches or handouts are allowed to be kept during the exam

Question 1: MCQs. (CLO 2: Understanding) (1+1+1+1+1= 5 marks)

- i. The Bioinformatics databases which provide easy access to all global information at genome and chromosomal levels are called:
- a) Repository type DBs
 - b) Gene-centric type DBs
 - c) Genome-centric type DBs
 - d) Database management systems (DBMS)
- ii. The fundament unit of “inheritance” is called _____.
- a) Cell
 - b) Genes
 - c) RNA
 - d) Protein

iii. According to Margaret Dayhoff's hypothesis, the protein sequences reflect the evolutionary history of species and introduced a mathematical framework (probabilistic model) for amino acid substitutions to calculate evolutionary distance of closely related proteins is called:

- a) PAM
- b) BLOSUM
- c) Atlas of proteins
- d) ~~COMPROTEIN~~ *i think so.*

iv. Which type of amino acids form the "Core" region" of a 3-D protein structure?

- a) Hypdrophillic
- b) Hydrophoic
- c) Amphithatic
- d) Both (a) & (b)

v. ATP & GTP are the examples of molecules.

- a) Nucleotides
- b) Nucleosides
- c) Proteins
- d) Amino acids

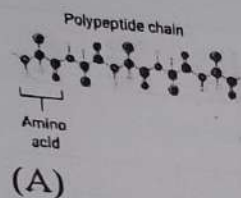
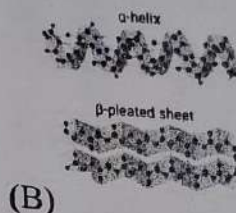
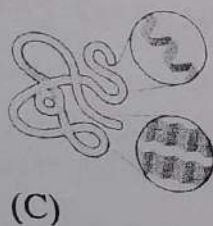
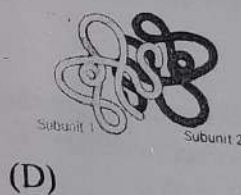
Question 2: True/False statements – If the statement is "False", re-write the "True" statement. (CLO 2; Understanding) (1+1+1+1+1= 5 marks)

- i. Nucleotide sequences are not universal and the structure of the genes (gene architecture) they encode is quite similar between *prokaryotic* organisms and *eukaryotic* organisms. (True/False)

- ii. One could predict the 3-D structure of any protein produced by an organism by 'reading its DNA'. (True/False)

- iii. Polypeptide is a simple chain of nucleotides translated from mRNA in cells. (True/False)
- iv. The biological system is represented by three fundamental characteristics of life: Metabolism, Self-replicating genome & Reproduction. (True/False)
- v. Amino acids are the building blocks (monomer units) of proteins. (True/False)

Question 3: Apply your basic knowledge on proteins structure and identify the levels of protein structure organization as shown in Figure below: (CLO 3: Apply) (2 marks)



Question 4: List the three important features (coordinates) a DB entry describing a coding prokaryotic sequence should include: (CLO 1: Remembering) (3 marks)

Question 5: Compare the given attributes to distinguish between a prokaryotic and eukaryotic gene. (CLO 4: Analyze) (5 marks)

	Attributes	Prokaryotic gene	Eukaryotic gene
1.	Genome: Single circular DNA		
2.	Genome size: 10-670 million bp		
3.	Gene density: 1 gene per 1000 bp		
4.	Non-coding region (%): ~95%		
5.	Coding region (%): ~70%		
6.	Genes isoform & splice variants		
7.	Promoter sequence elements located far away from the gene sequence controlling gene expression		
8.	A long ORF spanning the gene-transcript sequence		
9.	Colinear relationship between gene-mRNA transcript-final protein		
10.	Introns		

Question 6: Be precise and answer the following questions (CLO 2: Understanding) (2+2+1= 5 marks)

- I. State the reasons for which sequencing method (DNA sequencing or Protein sequencing) is preferred more than the other to extract useful biological information for the successive Bioinformatics analysis. (2 marks)
- II. Why is protein sequence analysis generally preferred over DNA sequence analysis in Bioinformatics? (2 marks)
- III. When treated with alkaline solution, which biomolecule (DNA, RNA & Protein) is susceptible to degradation and why? (1 mark)