



LOYOLA COLLEGE (AUTONOMOUS) CHENNAI – 600 034

M.Sc. DEGREE EXAMINATION – BIOTECHNOLOGY

SECOND SEMESTER – APRIL 2025



PBT2MC03 – BIOINFORMATICS AND COMPUTATIONAL BIOLOGY

Date: 29-04-2025

Dept. No.

Max. : 100 Marks

Time: 01:00 PM - 04:00 PM

SECTION A – K1 (CO1)

Answer ALL the questions

(5 x 1 = 5)

- 1 Choose the best option
- a) The GenBank database primarily contains _____.
 i) Nucleotide sequence data ii) Bibliographic data
 iii) Chemical structural data iv) Protein 3D structural data
- b) Gaps are added to the alignment because it _____.
 i) Increasing the matching of or dissimilar amino acids at subsequent portions
 ii) Reduces the overall score
 iii) Increases the matching of identical amino acids at subsequent portions
 iv) Enhances the area of the sequences.levels
- c) The word PATTERN in PROSITE denotes that the entry explains a _____.
 i) Block ii) Fuzzy regular expression iii) Profile iv) Normalization
- d) What is the primary data structure used in Biopython?
 i)Lists ii) Tuples iii) Sets iv) Dictionaries
- e) A gene whose expression helps to identify transformed cells is known as
 i) Plasmid ii) Selectable marker iii) Stuctural gene iv) Vector

SECTION A – K2 (CO1)

Answer ALL the questions

(5 x 1 = 5)

- 2 Answer in one or two sentences
- a) Expand VFF.
- b) Define Chemdraw.
- c) List any three functions available in SeqUtils.
- d) Comment on G-quadruplex.
- e) What is Hap Map?

SECTION B – K3 (CO2)

Answer any THREE of the following

(3 x 10 = 30)

- 3 Explain how SNP databases contribute to personalized medicine.
- 4 Describe how iterative alignment improves over progressive alignment.
- 5 Demonstrate Clustal Omega to align three given DNA sequences and interpret the results.
- 6 Describe how Python simplifies the automation of biological data analysis.

7	Evaluate the role of INSDC in standardizing genomic data exchange.
SECTION C – K4 (CO3)	
	Answer any TWO of the following (2 x 12.5 = 25)
8	Develop a pipeline to integrate chemical structure databases with machine learning models for drug design.
9	Evaluate the impact of hidden Markov models (HMMs) on iterative alignment.
10	Compare the computational complexity of Needleman-Wunsch and Smith-Waterman algorithms.
11	Differentiate between List, Tuple & Set with suitable examples of each.
SECTION D – K5 (CO4)	
	Answer any ONE of the following (1 x 15 = 15)
12	Examine how chemical structure databases facilitate structure-activity relationship (SAR) studies.
13	Design a Python script that reads multiple FASTA files and performs GC-content analysis.
SECTION E – K6 (CO5)	
	Answer any ONE of the following (1 x 20 = 20)
14	Design a web-based platform that integrates whole-genome and Mendelian disease databases for genetic analysis.
15	Analyze the impact of HapMap findings on drug response and pharmacogenomics.

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