

Branch - **BIOTECHNOLOGY**

BIOINFORMATICS

Time: Three Hours

Maximum: 75 Marks

SECTION-A (10 Marks)

Answer **ALL** questions

ALL questions carry **EQUAL** marks

(10 × 1 = 10)

Module No.	Question No.	Question	K Level	CO
1	1	What does "debugging" refer to in programming? (i) Writing code (ii) Testing code (iii) Fixing errors in code (iv) Documenting code	K1	CO1
	2	Which of the following data type is used to store decimal numbers in programming? (i) Integer (ii) String (iii) Float (iv) Boolean	K2	CO1
2	3	Which of the following is not an application of bioinformatics? (i) Drug designing (ii) Gene expression analysis (iii) In vivo cloning (iv) Phylogeny construction	K1	CO2
	4	Which database is specifically dedicated to protein sequences? (i) GenBank (ii) SWISS-PROT (iii) EMBL (iv) DDBJ	K2	CO2
3	5	What is the role of evolutionary conservation analysis in bioinformatics? (i) Studying protein interactions (ii) Analysing gene expression (iii) Identifying conserved regions in genome (iv) RNA interference	K1	CO3
	6	Which type of sequence alignment compares two sequences at a time? (i) Global alignment (ii) Pairwise alignment (iii) Multiple sequence alignment (iv) Local alignment	K2	CO3
4	7	Which of the following is incorrect about Swiss-PDB Viewer? (i) It is a structure viewer for multiple platforms (ii) It is a structure viewer for single platforms (iii) It is essentially a Swiss-Army knife for structure visualization and modelling (iv) It is capable of structure visualization, analysis, and homology modelling	K1	CO4
	8	Which of the following is untrue regarding Ab Initio-Based Methods? (i) This type of method predicts the secondary structure based on a single query sequence (ii) This type of method predicts the secondary structure based on a multiple query sequence (iii) It measures the relative propensity of each amino acid belonging to a certain secondary structure element (iv) The propensity scores are derived from known crystal structures	K2	CO4
5	9	The most favourable bonding between ligand and protein is ____. (i) Covalent bonding (ii) Metal Binding (iii) Van der Waals Bonding (iv) Hydrogen bonding	K1	CO5
	10	_____ is the common language for AI (i) Lisp (ii) Python (iii) PHP (iv) Java	K2	CO5

Cont...

SECTION - B (35 Marks)

Answer ALL questions

ALL questions carry EQUAL Marks

(5 × 7 = 35)

Module No.	Question No.	Question	K Level	CO
1	11.a.	Define the rules for declaring the variables.	K1	CO1
		(OR)		
	11.b.	What are data types? List different types of databases with their sizes?		
2	12.a.	Compare the salient features of NCBI and Pubmed.	K2	CO2
		(OR)		
	12.b.	Define Protein Data Bank (PDB) in database? Explain its role in Bioinformatics.		
3	13.a.	How are Pairwise Sequence Alignment and Multiple Sequence Alignment (MSA) useful in bioinformatics.	K3	CO3
		(OR)		
	13.b.	Identify the role of phylogenetic analysis in understanding the evolutionary relationships between species.		
4	14.a.	Examine the Common Molecular Visualization Software's used with the process and application.	K4	CO5
		(OR)		
	14.b.	Enlist the significant importance of threading in homology modelling.		
5	15.a.	Evaluate the concept of NGS? Add a note on its application and challenges.	K5	CO5
		(OR)		
	15.b.	Deduct the relationship between rigid docking (lock-and-key) and flexible docking (induced fit).		

SECTION -C (30 Marks)

Answer ANY THREE questions

ALL questions carry EQUAL Marks

(3 × 10 = 30)

Module No.	Question No.	Question	K Level	CO
1	16	Explain the characteristics of different types of programming languages with its advantages and disadvantages.	K1	CO1
2	17	Explain the salient features of Protein structure database with reference to PDB and MMDB.	K2	CO2
3	18	Elaborate the process and steps of BLAST and FASTA sequence analysis tool and its application.	K3	CO3
4	19	Compare and contrast <i>ab initio</i> and homology-based (e.g., neural network) methods for secondary structure prediction of protein.	K4	CO4
5	20	Discuss the role of bioinformatics in modern drug discovery. Add a note on the methods and steps involved in drug design.	K5	CO5

Z-Z-Z

END