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VIVEKANANDHA COLLEGE OF ENGINEERING FOR WOMEN  
 [AUTONOMOUS INSTITUTION AFFILIATED TO ANNA UNIVERSITY, CHENNAI]  
 Elayampalayam – 637 205, Tiruchengode, Namakkal Dt., Tamil Nadu.

**Question Paper Code: 90030**

B.E. / B.Tech. DEGREE END SEMESTER EXAMINATIONS – JAN. 2025

Sixth Semester

Biomedical Engineering

U19BTOE4 – BASICS OF BIOINFORMATICS

(Regulation 2019)

Time: Three Hours

Maximum: 100 Marks

Answer ALL the questions

Knowledge Levels (KL)	K1 – Remembering	K3 – Applying	K5 - Evaluating
	K2 – Understanding	K4 – Analyzing	K6 - Creating

PART – A

(10 x 2 = 20 Marks)

Q.No.	Questions	Marks	KL	CO
1.	What is a DNA sequence?	2	K1	CO1
2.	List the different types of data that are stored in biological databases.	2	K1	CO1
3.	Expand EMBL.	2	K2	CO2
4.	Write a short note on types of common sequence file formats used in biological databases.	2	K1	CO2
5.	Write a short note on PDB.	2	K2	CO3
6.	What is the implementation FASTA program available in the database?	2	K1	CO3
7.	Give a brief note Molecular Dynamics.	2	K1	CO4
8.	Brief out AB initio approaches of protein structure modeling.	2	K2	CO4
9.	List the methodologies in gene identification / gene finding.	2	K1	CO5
10.	State the significance of Structural genomics in bioinformatics.	2	K2	CO5

PART – B

(5 x 13 = 65 Marks)

Q.No.	Questions	Marks	KL	CO
11. a)	Describe biological databases with its classification, types and examples.	13	K3	CO1
	(OR)			
b)	Describe the sequence retrieval methods available for accessing biological databases.	13	K3	CO1
12. a)	Compare and contrast protein sequence databases and protein structure databases.	13	K3	CO2
	(OR)			
b)	Differentiate between nucleotide sequence databases and organism specific databases with suitable examples.	13	K3	CO2
13. a)	Explain about SRS & DBGET data retrieval tools for biological databases.	13	K2	CO3
	(OR)			
b)	Analyze the major differences between global and local alignment. Explain in detail.	13	K2	CO3
14. a)	Portray Needleman Wunsch algorithm and Smith Waterman algorithm in detail.	13	K3	CO4
	(OR)			
b)	Enumerate the various types of multiple sequence alignment. Give the programs under each category, and mention the drawbacks of progressive alignment.	13	K3	CO4
15. a)	Exemplify the secondary structure prediction of protein using artificial neural networks.	13	K4	CO5
	(OR)			
b)	Elaborate the stepwise approach to genome annotation with its types with neat sketch.	13	K4	CO5

PART – C

(1 x 15 = 15Marks)

Q.No.	Questions	Marks	KL	CO
16. a)	BLAST: An introductory tool for researcher to bioinformatics applications. Defend the above statement with proper justifications.	15	K4	CO1
	(OR)			
b)	Narrate and analyze the steps involved in phylogenetic tree construction and discuss with a distance based method.	15	K4	CO5