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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: 9011

B.E. / B.Tech. DEGREE END-SEMESTER EXAMINATIONS – MAY / JUNE 2024

Sixth Semester

Biomedical Engineering

U19BTOE4 – BASICS OF BIOINFORMATICS

(Common to CST)

(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 does NCBI stand for, and what is its role in nucleotide sequence retrieval?	2	K1	CO1
2.	Name a commonly used genomic database for nucleotide sequence retrieval, and briefly describe its features.	2	K1	CO1
3.	In bioinformatics, what is the purpose of the FASTA format for nucleotide sequences?	2	K2	CO2
4.	What does PDB stand for, and what kind of information is stored in the Protein Data Bank?	2	K1	CO2
5.	What does DBGET stand for in bioinformatics?	2	K1	CO3
6.	Why is sequence similarity analysis important in bioinformatics and molecular biology?	2	K2	CO3
7.	Define BLAST, and how does it facilitate nucleotide sequence retrieval?	2	K2	CO4
8.	What does BLOSUM stand for in the context of scoring matrices?	2	K1	CO4
9.	Write a short note on orthologous genes.	2	K1	CO5
10.	List the main components of genome annotation.	2	K1	CO5

PART – B

(5 x 13 = 65 Marks)

Q.No.	Questions	Marks	KL	CO
11.	a) Describe the hierarchical levels of protein structure, including primary, secondary, tertiary, and quaternary structures. Provide examples and explain the significance of each level. (OR)	13	K2	CO1
	b) Elaborate on how the three-dimensional structure of a protein is crucial for its function. Provide examples of specific protein structures and explain how their shapes relate to their functions.	13	K2	CO1
12.	a) Describe the UniProt database and its significance in providing comprehensive information about proteins. Discuss the different sections of a UniProt entry and how it aids researchers in protein-related studies. (OR)	13	K3	CO2
	b) Discuss the Human Protein Atlas (HPA) as an organism-specific database focused on human proteins. Explain how HPA provides information on protein expression, localization, and its applications in understanding human biology and disease.	13	K3	CO2
13.	a) Explain the fundamental principles behind scoring matrices in the context of sequence alignment. How do scoring matrices assign scores to aligned residues, and what information do they encapsulate about amino acid or nucleotide substitutions? (OR)	13	K3	CO3
	b) Compare and contrast global and local sequence alignment algorithms. Provide examples of situations where each type of alignment is more suitable and explain the implications for biological interpretation.	13	K4	CO3
14.	a) Explain the significance of the BLAST tool in biological research. Discuss how BLAST is used for sequence comparison, identification of homologous sequences, and its applications in functional annotation. (OR)	13	K3	CO4
	b) Describe different methods used for sequence similarity analysis, including pairwise sequence alignment, multiple sequence alignment, and profile-based methods. Discuss the advantages and limitations of each approach.	13	K2	CO4

15. a) Discuss the role of comparative genomics in understanding human evolution and genomic diversity. 13 K3 CO5
 (OR)
 b) Discuss the role of computational methods in predicting protein secondary structure. Highlight the challenges associated with protein secondary structure prediction 13 K4 CO5

PART – C

(1 x 15 = 15 Marks)

Q.No.	Questions	Marks	KL	CO
16. a)	Explore the applications of bioinformatics in genomics research with suitable examples.	15	K5	CO5
	(OR)			
b)	Analyze the diverse applications of sequence analysis in genomics and genetics with examples each.	15	K5	CO3

