Reg.No.:

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

Question Paper Code: 90013

B.E. / B.Tech. DEGREE END-SEMESTER EXAMINATIONS – NOV. / DEC. 2025
Fifth Semester
Biotechnology
U23BT517 – COMPUTATIONAL BIOLOGY
(Regulation 2023)

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.	List the 3 methods of pairwise sequence alignment.	2	K1	CO1
2.	Name any two databases used for alignment of nucleotides.	2	K1	CO1
3.	What are the tools used for predicting gene sequences?	2	K1	CO2
4.	List the major advantages of DNA computing.	2	K1	CO2
5.	Sketch an unrooted tree for 4 taxa.	2	K2	CO3
6.	How will you determine the distance between the species of the same genus?	2	K2	CO3
7.	What are structural databases? Give an example.	2	K1	CO4
8.	What is peptide mass fingerprinting?	2	K2	CO4
9.	Write notes on clustering techniques.	2	K2	CO5
10.	Describe the application of NGS in the identification of new microorganisms.	2	K2	CO5

PART – B

(5 x 13 = 65 Marks)

Q.No.			Questions	Marks	KL	CO
11.	a)	i.	Compare BLAST and FASTA.	5	K1	CO1
		ii.	What are the BLAST programs and models available?	8	K1	

(OR)

b) Explain the primary and secondary databases in detail, highlighting their respective applications. 13 K1 CO1

12\. a) Explain the use of Hidden Markov Models in gene finding and structure predictions. 13 K2 CO2

(OR)

b) Summarize the various DNA computing techniques used in systems biology. 13 K2 CO2

13\. a) Solve the following data using UPGMA method and predict the phylogenetic tree. 13 K4 CO3

	A	B	C	D	E
A	0	-	-	-	-
B	20	0	-	-	-
C	60	50	0	-	-
D	100	90	40	0	-
E	90	80	50	30	0

(OR)

b) i. Describe the NJ algorithm to predict the phylogenetic tree. 6 K2 CO3

ii. Outline the bootstrapping technique. 7 K2

14\. a) Summarize the role and strategies of homology modeling in protein structure analysis. 13 K3 CO4

(OR)

b) Explain the basic algorithm for threading. 13 K2 CO4

15\. a) Elaborate on the working principle of microarray and clustering techniques. Write notes on its role in studying gene expression. 13 K3 CO5

(OR)

b) Outline the workflow of a typical molecular docking study to investigate interactions. Name the tools used for the same. 13 K4 CO5

PART – C

(1 x 15 = 15 Marks)

Q.No. Questions Marks KL CO

16\. a) Apply the Needleman-Wunsch algorithm to align the following short DNA strings with the provided base conditions: 15 K1 CO1

DNA 1= ATTCG

DNA 2 = ACGG

Match=+2 Mismatch+ 0 Gap= -2

(OR)

b)	i.	Write a detailed note on the importance of bioinformatics and its tools in drug discovery.	10	K1	CO1
	ii.	Analyze the impact of machine learning on bioinformatics research.	5		