U.S.N.										

B.M.S. College of Engineering, Bengaluru-560019

Autonomous Institute Affiliated to VTU

January / February 2025 Semester End Main Examinations

Programme: B.E. **Semester: V**

Branch: Biotechnology **Duration: 3 hrs.**

Course Code: 23BT5PCBIN / 22BT5PCBIN **Max Marks: 100**

Course: Bioinformatics

Instructions: 1. Answer any FIVE full questions, choosing one full question from each unit.
2. Missing data, if any, may be suitably assumed.

Important Note: Completing your answers, compulsorily draw diagonal cross lines on the remaining blank pages. Revealing of identification, appeal to evaluator will be treated as malpractice.

				CO	PO	Marks
			UNIT - I			
1	a)		Discuss the features of Pfam.	CO1	-	**6**
	b)		Illustrate the features of PDB format with a suitable example.	CO1	-	**6**
	c)		Elucidate the features of KEGG database of biological systems.	CO1	-	**8**
			OR			
2	a)		With a suitable illustration, discuss the features of Genbank flatfile format.	CO1	-	**6**
	b)		Give an account on tools and resources available at NCBI.	CO1	-	**8**
	c)		Explicate the features of protein structure databases.	CO1	-	**6**
			UNIT - II			
3	a)		Perform the global alignment using Needlman wunch algorithm and determine the optimal alignment for the following sequences (scores: Gap:-1,mismatch:-1 and for match:-2) Seq A: GATATCCTCATT Seq B:CGAATCCGTCAA	CO2	PO5	**10**
	b)		Dot-plots provide a visual representation of sequence similarity. Substantiate the statement with an example.	CO2	PO5	**10**
			OR			
4	a)		Elaborate the steps involved in FASTA algorithm and comment on its statistical significance.	CO1	-	**05**
	b)		Construct an alignment using Smith & Waterman algorithm. Evaluate your score to determine the optimal alignment for the following sequences. Sequence 1= **ACCTGGACACGCT** ,	CO1	-	**10**

Sequence 2 = **ACACTCCGCATCG**

Sl no.	Parameter	score
1	Identity	+4
2	Mismatch	-1
3	Gap creation	-2

	c)	Illustrate with an example, steps involved in Multiple sequence alignment using progressive alignment method.	*CO1*	-	**05**
		UNIT - III			
5	a)	Construct a phylogenetic tree for the following distances between five taxa and determine the branch lengths using Neighborhood joining method.	*CO3*	*PO2*	**10**
	b)	Discuss the principle and construction of phylogenetic tree by Maximum Parsimony method with a suitable example.	*CO1*	-	**10**
		OR			
6	a)	Apply UPGMA method to make a phylogenetic tree for the following distances between six taxa and determine the branch lengths.	*CO2*	*PO5*	**10**
	b)	Construct a Position specific scoring matrix for the following multiple alignment of nucleotide sequences. Determine the probability of a new sequence ACGAAG fit into the matrix?	*CO3*	*PO2*	**10**

	A	B	C	D	E
A	-	2	7	4	7
B	2	-	7	4	7
C	7	7	-	7	6
D	4	4	7	-	7
E	7	7	6	7	-

	A	B	C	D	E	F
A	-					
B	2	-				
C	4	4	-			
D	6	6	6	-		
E	6	6	6	4	-	
F	8	8	8	8	8	-

Position	1	2	3	4	5	6
Sequence 1	T	C	A	T	A	C
Sequence 2	A	G	G	C	G	G
Sequence 3	A	C	T	A	A	G
Sequence 4	C	T	G	A	A	C
Sequence 5	T	C	G	A	T	G

<table>
<tr><td></td><td></td><td></td><td>UNIT - IV</td><td></td><td></td><td></td></tr>
<tr><td></td><td>7</td><td>a)</td><td>Demonstrate the sequence acquisition and analysis by Illumina sequencing.</td><td>CO2</td><td>PO5</td><td>5</td></tr>
<tr><td></td><td></td><td>b)</td><td>Explicate the various tools for molecular structure visualization.</td><td>CO1</td><td>-</td><td>5</td></tr>
<tr><td></td><td></td><td>c)</td><td>A 11 kb circular plasmid pRIT455 is digested with three restriction enzymes EcoRI, BamHI and HindIII individually and in combination. The resulting fragment sizes are determined by means of electrophoresis. The results are as follows:

<table>
<tr><td>Sl No</td><td>Restriction enzymes</td><td>Fragment sizes (kb)</td></tr>
<tr><td>1</td><td>EcoRI</td><td>8.5, 2.0, 0.5</td></tr>
<tr><td>2</td><td>HindIII</td><td>5.6, 5.4</td></tr>
<tr><td>3</td><td>BamHI</td><td>6.5, 4.5</td></tr>
<tr><td>4</td><td>BamHI and EcoRI</td><td>4.5, 2.2, 2.0, 1.8, 0.5</td></tr>
<tr><td>5</td><td>EcoRI and HindIII</td><td>4.3, 4.2, 1.2, 0.8, 0.5</td></tr>
<tr><td>6</td><td>HindIII and BamHI</td><td>3.4, 3.1, 2.5, 2.0</td></tr>
</table>
Draw a restriction map based on these results</td><td>CO3</td><td>PO2</td><td>10</td></tr>
<tr><td></td><td></td><td></td><td>OR</td><td></td><td></td><td></td></tr>
<tr><td></td><td>8</td><td>a)</td><td>What is a primer? Discuss the factors to be considered for design of primers. Add a note on the computational tools for design of primers.</td><td>CO1</td><td>-</td><td>10</td></tr>
<tr><td></td><td></td><td>b)</td><td>Demonstrate the sequence acquisition and analysis by Roche 454 sequencing and applications.</td><td>CO2</td><td>PO5</td><td>10</td></tr>
<tr><td></td><td></td><td></td><td>UNIT - V</td><td></td><td></td><td></td></tr>
<tr><td></td><td>9</td><td>a)</td><td>Discuss the molecular dynamics simulation model with a neat flowchart.</td><td>CO1</td><td>-</td><td>10</td></tr>
<tr><td></td><td></td><td>b)</td><td>Demonstrate the computational method of protein structure prediction and comment on how to critically assess the quality of structure.</td><td>CO1</td><td>-</td><td>10</td></tr>
<tr><td></td><td></td><td></td><td>OR</td><td></td><td></td><td></td></tr>
<tr><td></td><td>10</td><td>a)</td><td>With a neat flowchart, discuss the steps involved in Insilco drug discovery.</td><td>CO1</td><td>-</td><td>10</td></tr>
<tr><td></td><td></td><td>b)</td><td>Explicate the structure activity relationship (SAR) and QSAR with reference to drug discovery.</td><td>CO1</td><td>-</td><td>05</td></tr>
<tr><td></td><td></td><td>c)</td><td>Explain the role of scoring functions involved in grid calculation and binding energy minimization.</td><td>CO1</td><td>-</td><td>05</td></tr>
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