U.S.N.										

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

Autonomous Institute Affiliated to VTU

August 2024 Supplementary Examinations

Programme: B.E. **Semester: VI**
Branch: Biotechnology **Duration: 3 hrs.**
Course Code: 19BT6DCBIN **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.

UNIT - I

1 a) With a suitable illustration, discuss the features of Genbank flatfile format. **07**

b) Give an account on tools and resources available at NCBI. **06**

c) Explicate the features of protein structure databases. **07**

UNIT - II

2 a) Perform the global alignment using Needlman wunch algorithm and determine the optimal alignment for the following sequences (Scores: Gap: and mismatch=-1 and for match=2) **10**

Seq A:CGAATCCGTCAA
Seq B: GATATCCTCATT

b) Dot-plots provide a visual representation of sequence similarity. Substantiate the statement with an example. **10**

OR

3 a) The replacement of a single amino acid in the primary structure of a protein with another single amino acid, which is accepted by the processes of natural selection. Substantiate the statement and construct the matrix. **10**

b) Perform the local alignment using Smith an Waterman algorithm and determine the optimal alignment for the following sequences (scores: Gap: -4, mismatch: -2 and for match: 4) **10**

Seq A: AGATGCTGA
Seq B: GAATGGCTA

UNIT - III

4 a) Construct a phylogenetic tree for the following distances between four taxa and determine the branch lengths using UPGMA method. **05**

	A	B	C	D
A	-	0.15	0.45	0.60
B	-	-	0.55	0.65
C	-	-	-	0.63
D	-	-	-	-

b) Discuss the architecture of a hidden Markov model representing a multiple sequence alignment. **05**

c) Construct a phylogenetic tree for the following distances between five taxa and determine the branch lengths using Neighbourhood joining method. **10**

	A	B	C	D	E
A	-	22	39	39	41
B	-	-	41	41	43
C	-	-	-	18	20
D	-	-	-	-	10
E	-	-	-	-	-

OR

5 a) Construct a Position specific scoring matrix for the following multiple alignment of nucleotide sequences. Determine the probability of a new sequence AACTCG fitting into the matrix. **10**

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

b) Discuss the principle and construction of phylogenetic tree by Maximum Parsimony method with a suitable example. **10**

UNIT - IV

6 a) A 13.4 kb circular plasmid is digested with three restriction enzymes *BamHI*, *HindIII* and *PstI* individually and in combination. The resulting fragment sizes are determined by means of electrophoresis. The results are as follows: **10**

Sl No	Restriction enzymes	Fragment sizes (kb)
1	*BamHI*	5.1, 4.5, 3.8
2	*HindIII*	8.1, 5.3
3	*PstI*	13.4
4	*BamHI and HindIII*	5.1, 3.3, 2.5, 2.0, 0.5
5	*BamHI and PstI*	5.1, 4.5, 2.5, 1.3
6	*HindIII and PstI*	8.1, 3.3, 2.0

Draw a restriction map based on these results

b) 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. **10**

UNIT - V

7 a) Explicate the structure activity relationship (SAR) and QSAR with reference to drug discovery. **05**

b) Discuss the molecular dynamics simulation model with a neat flowchart. **07**

c) With a flowchart, Discuss the steps involved in drug discovery. **08**

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