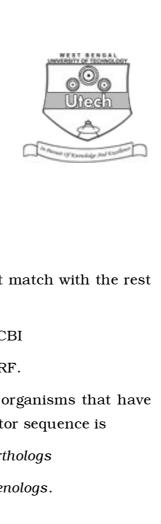
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Roll	<i>No.</i> :	• • • • •		• • • • •	••••			• • • • • •	• • • • •	A Special Of Exercising 2nd Explaint
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			C	S/	в.т	ech		E)/\$	SEM	I-7/CS-704B/2009-10
					BIO	OIN			AT	ICS
Time	e Alloi	ted	: 3 F							 Full Marks : 70
						the	mar	gin i	ndic	ate full marks.
Ca	ndida	ıtes	are r	eqı	uirec	_				swers in their own words cable.
						G	RO	UP -	Α	
			(M	Iult	iple	e Ch	oice	Ty	pe Q	uestions)
1.	Cho	ose	the c	orr	ect a	alter	nati	ves (of th	e following: $10 \times 1 = 10$
	i)	Ha:	mmi	ng (or e	dit c	lista	nce	for f	following two given word
				N	MID	DLE				
				F	RIDI	OLE				
		a)	2						b)	0
		c)	5						d)	none of these.
	ii)	Tot	otal number of useful amino acids are							
		a)	23						b)	20
		c)	19						d)	none of these.
	iii)	What is the score for following two sequences (assume match = $+2$, mismatch = -1 , indel = -2)								
			A	T	C	G	G	A	T	СТ
			Α	_	С	G	G	-	A	СТ
		a)	7						b)	6
		c)	10						d)	none of these.

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- iv) HMM stands for
 - a) Hidden Markov of Model
 - b) Hidden Material Method
 - c) Hidden Markov Model
 - d) None of these.
- v) Which one of the following does not match with the rest three?
 - a) PDB

b) NCBI

c) EMBL

- d) ORF.
- vi) Similar sequences in two different organisms that have been derived from a common ancestor sequence is
 - a) Homologs
- b) Orthologs
- c) Paralogs
- d) Xenologs.
- vii) UPGMA stands for
 - a) Unweighted Pair Group Method with Arithmetic Mean
 - b) Unpair Group Method with Arithmetic Mean
 - c) Unweighted Pair Group Method with Mean Arithmetic
 - d) None of these.
- viii) Which one of the following is the appropriate tool for a description of a sequence line with the symbol >

2

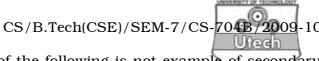
a) FASTA

b) BLAST

c) MMD

d) None of these.

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- ix) Which one of the following is not example of secondary structure prediction algorithm?
 - a) SOPM

- b) PREDATOR
- c) SOPMA
- d) All of these.
- x) Needleman Wunch algorithm is used for
 - a) single alignment pair
 - b) pairwise sequence alignment
 - c) multiple alignment
 - d) all of these.

GROUP – B (Short Answer Type Questions)

Answer any *three* of the following. $3 \times 5 = 15$

- 2. a) What is phylogenetic tree?
 - b) What are the modern usages of phylogenies.

2 + 3

- 3. a) Describe the features of DNA sequence analysis.
 - b) Explain Central Dogma of Molecular biology with neat diagram. 2 + 3
- 4. Explain Swiss Port. What is PDB?

3 + 2

- 5. a) What are the application of Neural network in Bioinformatics?
 - b) How is disease predication done in Bioinformatics?

2 + 3

- 6. a) Write down the different kinds of DNA sequences.
 - b) Are you planning to use bioinformatics tools after the course?
 - i) If yes, for what purpose / experiments?
 - ii) If no, why?

2 + 3

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GROUP - C

(Long Answer Type Questions) Answer any *three* of the following.



- 7. a) Briefly describe dynamic programming.
 - b) What is multiple sequence alignment? What is the goal of multiple sequence alignment?
 - c) Explain simultaneous methods and progressive methods for multiple alignments? 5 + 5 + 5
- 8. a) Write down the differences between PAM matrix and BLOSUM matrix with examples. Which one is better?

 Justify your answer.
 - b) Write down steps of the FASTA.

8 + 7

10 + 5

- 9. a) What is Gen Bank? Explain the structure of Gen Bank entries.
 - b) Why do we create secondary databases?
- 10. a) Why is HMM required for symbol identification? How is it used?
 - b) Describe Vetervi algorithm in HMM. (5+5)+5
- 11. a) Using the Smith Waterman algorithm, construct the partial alignment score table for the following two sequences. Assume the scoring parameters + 1 for match score, 0 for mismatch score and 1 for gap penalty.

Sequence 1: ATGCGCTACGTATT

Sequence 2: ATGCGCT

- b) Write the differences between Needleman Wunsch algorithm and Smith Waterman algorithm with an example. 10 + 5
- 12. Write short notes on any *three* of the following: $7\frac{1}{2} + 7\frac{1}{2}$
 - a) Protein folding
 - b) Chao-Fasman algorithm
 - c) Treading.

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