حقوق النشر محفوظة
2022 ©

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Ankara University
Computer Engineering Department
Special Topics Final Exam

Duration: 100mins.
Notes: 1. Write your answers in the blanks below the questions.
2. Questions will be answered by only using the techniques explained in the classes.

QUESTIONS

1. (20 points) Find the DNA template sequence and the coding strand sequence for the given t-RNA sequence.

t-RNA	U	G	C	A	A	C	C	G	U	A
Template DNA strand	T	G	C	A	A	C	C	G	T	A
Coding DNA strand	A	C	G	T	T	G	G	C	A	T

2. (10 points) How many alternative alignments can be achieved for sequences of length 9 and 11 using gaps?

$$\sum_{k=0}^{9} 2^k \binom{9}{k}\binom{11}{k} \rightarrow 2^0\binom{9}{0}\binom{11}{0} + \dots + 2^9\binom{9}{9}\binom{11}{9}$$

$$= 7059735$$

$$\binom{N}{k} = \frac{N!}{k!(N-k)!}$$

3. (20 points) Fill in the matrix using the Smith-Waterman local alignment algorithm. Use the following scores: match=1, mismatch=-1 and gap penalty=-2. Show the traceback on the table using arrows.

		G	T	G	A	A
	0	0	0	0	0	0
G	0	1	0	1	0	0
A	0	0	0	0	2	1
C	0	0	0	0	0	1
T	0	0	1	0	0	0
T	0	0	1	0	0	0

G A
G A

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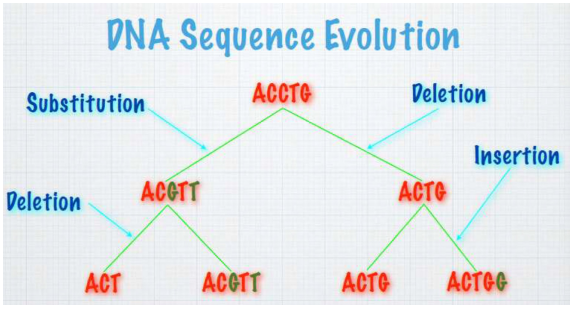
4. (10 points) What are some possible evolutionary changes that may occur in DNA sequences, explain with examples.

Mutation and selection may happen, also insertions and deletions (indels) may happen



5. (10 points) Describe the two methods that are used to identify similarity between species when creating phylogenetic trees.

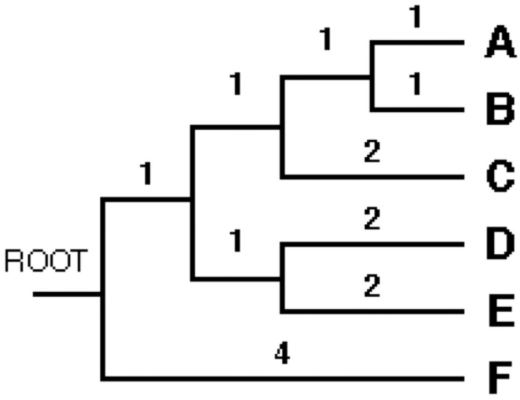
1- Clustering methods gradually build up the tree, starting from a small number of sequences and adding one sequence at each step. The output from these methods is a single tree that attempts to recover the evolutionary relationships between the sequences.

2- many different tree topologies are generated and each is tested against the data in a search for those that are optimal or close to optimal according to particular criteria.

6. (30 points) Use the UPGMA to construct the ultrametrik tree step by step for the given distance matrix..

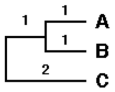
	A	B	C	D	E
B	2				
C	4	4			
D	6	6	6		
E	6	6	6	4	
F	8	8	8	8	8

Answer:

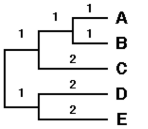


	A,B	C	D	E
C	4			
D	6	6		
E	6	6	4	
F	8	8	8	8

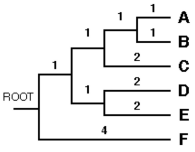
	A,B	C	D,E
C	4		
D,E	6	6	
F	8	8	8



	AB,C	D,E
D,E	6	
F	8	8



	ABC,DE
F	8



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