Bioinformatics	(Akiyama)	Exercise #03

Student ID Name

## LOCAL ALIGNMENT

1) Execute <u>local</u> alignment between Seq1 = AGTCA, and Seq2=TTGTAG.

Fill all elements of the table below, and also answer the alignment score (<u>maximum</u> value). Use score constants of, Match = +2, Mismatch = -1, Gap = -1 (Linear Gap), and OutGap=0. Leave a pointer(s) for each node, for indicating its predecessor node(s) (the node(s) which gives the maximum value to that node).

		А	G	Т	С	А
	0	0	0	0	0	0
т	0					
т	0					
G	0					
т	0					
A	0					
G	0					

2) Show optimal <u>local</u> alignment between Seq1= AGTCA, and Seq2=TTGTAG..
(Alignment should exactly correspond to the path chosen in exercise 3).
Carefully follow the format used in exercise 1. (match = `|`, unmatch= `•`, etc.)

Ans.

## MULTIPLE ALIGNMENT

3) Fill the table below, by calculating all pairwise <u>global</u> alignment scores among three sequences : Seq1=CTAGCAG, Seq2=CATGCAG, and Seq3=CAGTTG.

Pairwise alignments are given below.

Use score constants of, Match = +2, Mismatch = -1, Gap = -1 (Linear Gap).

Seq1 : CTAGCAG	Seq1 : CTAGCAG 	Seq2 : CATGCAG
Seq2 : CATGCAG	Seq3 : C-AGTTG	Seq3 : CA-GTTG
score=	score=	score=

Ans.

$\backslash$	Seq 1	Seq 2	Seq 3	Sum
Seq 1	/			
Seq 2		$\backslash$		
Seq 3				

4) Calculate a multiple alignment of the three sequences shown in 3), by using the Star method. Choose the sequence with maximum "Sum" in the table in 3), as the Star sequence. Use the Star sequence as a pivot, and combine pairwise alignments with it to get a final multiple alignment. If you have several candidates for the Star sequence, show <u>all</u> cases.

Star sequence =

Multiple alignment : Seq1 :

Seq2 :

Seq3 :