

Student ID \_\_\_\_\_

Name \_\_\_\_\_

- 1) Calculate the alignment score for the following pairwise alignment.

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

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G C T G A C G A C G T
| | . |           | | . |
G C A G - - - A C C T
    
```

Ans. \_\_\_\_\_

- 2) Perform the 'Matrix Fill Step' of pairwise sequence alignment.

Fill all elements of the table below, and also answer the alignment score (bottom right value). Consider alignment between Seq1 = AGTCA, and Seq2=AGCA.

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

Leave a pointer(s) for each node, for indicating its predecessor node(s) (the node(s) which gives the maximum value to that node). (See example below.)

ex.)

		A	T	G	C
	0	0	0	0	0
A	0	2	1	0	-1
G	0	1	1	3	2
C	0	0	0	2	5

		A	G	T	C	A
	0	0	0	0	0	0
A	0					
G	0					
C	0					
A	0					

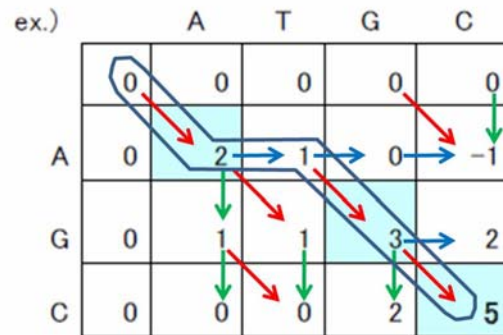
Ans. \_\_\_\_\_

- 3) Perform the 'Traceback Step' of pairwise sequence alignment.

Use score constants of exercise 2, and execute the Traceback procedure.

Show the optimal path in the table below.

(If multiple paths are found with a same optimal score, show only one of them.)



		A	G	T	C	A
		0	0	0	0	0
A	0					
G	0					
C	0					
A	0					

- 4) Show optimal pairwise alignment between Seq1= AGTCA, and Seq2=AGCA.  
 (Alignment should exactly correspond to the path chosen in exercise 3).  
 Carefully follow the format used in exercise 1. (match = '|', unmatched = '•', etc.)

Ans. \_\_\_\_\_