Homework Week2

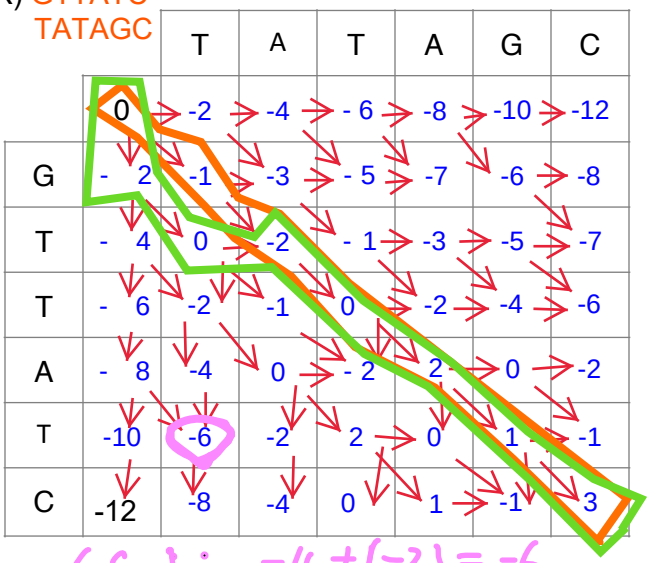
Sequence Alignment Fundamentals

http://thegrantlab.org
Dr. Barry Grant

This unit's homework consists of both (1) an online knowledge assessment quiz (see online) and (2) a Needleman-Wunsch dynamic programming assessment exercise (this document). Both components contribute 50% to this unit's grade. For the later we have two sample sequences, and we'd like to use the Needleman-Wunsch algorithm discussed in class to align them.

alignment:
GT-TATC (OR) GTTATC
-TATAGC TATAGC

optimal score is 3.



Sequence 1: **TATAGC**
Sequence 2: **GTTATC**

Using a **match score of +2**, a **mismatch score of -1**, and a **gap score of -2**. Fill in the table and translate it into a alignment.

Please submit your completed answer via **gradescope** . This should be titled "*02. Global Alignment HW Week2*". You can submit this document as a PDFor a photo of a separate page with your completed **alignment matrix** along with your **aligned sequences** and their **optimal score**.

-6 { ↓: -4+(-2) = -6
→: -8+2 = -6
→: -10+(-2) = -8

Step	Scoring Rubric/Assessment Criteria	Points	
1	Setup labeled alignment matrix	1	
2	Include initial column and row for GAPs	1	
3	All alignment matrix elements filled in	1	
4	Evidence for correct use of scoring scheme	1	
5	Direction arrows drawn between all cells	1	
6	Evidence of multiple arrows to a given cell if appropriate	1	D
7	Correct optimal score position in matrix used	1	C
8	Correct optimal score obtained for given scoring scheme	1	B
9	Traceback path(s) clearly highlighted	1	A
10	Correct alignment(s) yielding optimal score listed	1	A+

(10 Total points)