

Homework Week2

Sequence Alignment Fundamentals

<http://thegrantlab.org>

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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.

Sequence 1: **TATAGC**

Sequence 2: **GTTATC**

		T	A	T	A	G	C
↑	0						
G		↖	↖	↖	↖	↖	↖
T		↖	↖	↖	↖	↖	↖
T		↖	↖	↖	↖	↖	↖
A		↖	↖	↖	↖	↖	↖
T		↖	↖	↖	↖	↖	↖
C	-12	↖	↖	↖	↖	↖	↖

Optimal alignment score: 3

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 PDF or a photo of a separate page with your completed **alignment matrix** along with your **aligned sequences** and their **optimal score**.

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)