

BIMM-143: INTRODUCTION TO BIOINFORMATICS

Lecture 2, "Sequence Alignment Fundamentals" Homework

<http://thegrantlab.org/bimm143/>

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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. 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.

		T	A	T	A	G	C
	0	-2	-4	-6	-8	-10	-12
G	-2	-1	-3	-5	-7	-6	-8
T	-4	0	-2	-1	-3	-5	-7
T	-6	-2	-1	0	-2	-4	-6
A	-8	-4	0	-2	2	0	-2
T	-10	-6	-2	2	0	1	-1
C	-12	-8	-4	0	1	-1	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 return your answer via email to both IAs. This should have the subject "[BIMM143 HW2]" and consist of an attached photo of 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)