

## BIMM-143: INTRODUCTION TO BIOINFORMATICS

### Lecture 2, "Sequence Alignment Fundamentals" Homework

[https://bioboot.github.io/bimm143\\_S18/lectures/#2](https://bioboot.github.io/bimm143_S18/lectures/#2)

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This unit's homework consists of both (1) an online [knowledge assessment quiz](#) 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						
G							
T							
T							
A							
T							
C							

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 to Alex via email: ( [arsharp@ucsd.edu](mailto:arsharp@ucsd.edu) ). This should 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	10	
2	Include initial column and row for GAPs	10	
3	All alignment matrix elements filled in	10	
4	Evidence for correct use of scoring scheme	10	
5	Direction arrows drawn between all cells	10	
6	Evidence of multiple arrows to a given cell if appropriate	10	D
7	Correct optimal score position in matrix used	10	C
8	Correct optimal score obtained for given scoring scheme	10	B
9	Traceback path(s) clearly highlighted	10	A
10	Correct alignment(s) yielding optimal score listed	10	A+

(100 Total points)