

BIMM-143: INTRODUCTION TO BIOINFORMATICS

Lecture 2, "Sequence Alignment Fundamentals" Homework

https://bioboot.github.io/bimm143_F18/lectures/#2

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. 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 Chao Shi via email: (bioshichao@gmail.com). 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 | 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)