**Problem**

Consider the following substitution maxtrix for DNA sequences:

A C G T   
A 10 2 5 2   
C 2 10 2 5   
G 5 2 10 2   
T 2 5 2 10

**Question 1**: What is the optimal (here maximal) cost of an alignment of AATAAT and AAGG using the above substitution matrix and gap cost -5?

**Question 2**: What is the optimal (here maximal) cost of an alignment of [seq1.fasta](https://brightspace.au.dk/d2l/common/dialogs/quickLink/quickLink.d2l?ou=53951&type=coursefile&fileId=AiB_F2022_Project1%2fseq1.fasta) and [seq2.fasta](https://brightspace.au.dk/d2l/common/dialogs/quickLink/quickLink.d2l?ou=53951&type=coursefile&fileId=AiB_F2022_Project1%2fseq2.fasta) using the same substitution matrix and gap cost? (You probably want to implement the algorithm for computing the cost of an optimal alignment.)

**Question 3 (optional)**: How does an optimal alignment look like for the above two pairs of sequences using the given substitution matrix and gap cost -5? (you probably want to implement the algorithm for finding an optimal alignment by backtracking through the dynamic programming table.)

**Question 4 (optional)**: How many optimal alignments are for the above two pairs of sequences using the given substitution matrix and gap cost -5? Explain how you can compute the number of optimal alignments.

To test your programs you are welcome to use the two test examples in [project1\_examples.txt](https://brightspace.au.dk/d2l/common/dialogs/quickLink/quickLink.d2l?ou=53951&type=coursefile&fileId=AiB_F2022_Project1%2fproject1_examples.txt)