CMPE 484: Bioinformatics and Computational Genomics, Spring 2022
Assignment 1 - Pairwise Sequence Alignment with Affine Gap Penalty
Due: 25/04/2022, 09:00

In this assignment, you are will implement the Needleman-Wunsch *global sequence alignment* algorithm and the Smith-Waterman *local sequence alignment* algorithm. The algorithms must be implemented with linear gap penalty as well as affine gap penalty. They should take two amino acid sequences, gap penalty type (i.e. linear or affine), gap opening, and gap extension penalties as input, and should output the maximum alignment score of these sequences, as well as the alignment achieving this maximum score. If there are multiple optimal alignments, the algorithm should output one of them. For match and mismatch, please use the BLOSUM62 scoring matrix available here.

You are given a Jupyter notebook template which contains a set of function definitions, sample inputs and BioPython[1] implementation of algorithms which you can use to compare your outputs.

Note that you are allowed to modify the format as long as you provide a function that takes the following parameters and returns the maximum alignment score and the corresponding alignment:

1. two sequences

2. the alignment algorithm: local or global

3. the penalty strategy: linear or affine

4. the gap opening penalty

5. the gap extension penalty

Please produce alignments and alignment scores for the sample inputs with linear gap penalty as well as affine gap penalty with the gap opening penalty as 11 and the gap extension penalty as 1. Note that for the linear gap penalty strategy the gap opening penalty will correspond to the linear gap penalty and gap extension penalty will not be used.

Submission

You are expected to submit a single .ipynb file (i.e. Jupyter notebook) that is runnable. Name your notebook with your student id (e.g. 2019400XXX.ipynb). Note that this notebook will be your report as well, so explain your work in the related sections of the notebook.

Late Submission

The deadlines are sharp and late submissions will NOT be accepted.

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[1]https://biopython.org/