CMPE - 59H
Assignment 1
Pairwise Sequence Alignment with Affine Gap Penalty

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Contents

1 Alignment algorithms

1.1 Global Alignment Algorithm

As requested in assignment description, I have used Needleman-Wunsh algorithm with affine gap penalties to align given 2 protein sequences. I have tested given 3 protein sequence pairs with my global alignment program. Results follow,


```
(bioinformatics)  atakan1@Atakan  ~/Desktop/Bioinformatics/assignments/Assignment-1   master   python PairwiseAlignment.py test-pair1.txt 11 1 global
Method: Global Alignment
Score: -1
Alignments
----------
PLEASANTLY
_MEAN___LY
(bioinformatics)  atakan1@Atakan  ~/Desktop/Bioinformatics/assignments/Assignment-1   master   python PairwiseAlignment.py test-pair2.txt 11 1 global
Method: Global Alignment
Score: 8
Alignments
----------
PRT___EINS
PRTWPSEIN_
(bioinformatics)  atakan1@Atakan  ~/Desktop/Bioinformatics/assignments/Assignment-1   master   python PairwiseAlignment.py test-pair3.txt 11 1 global
Method: Global Alignment
Score: 144
Alignments
----------
YHFDVPDCWAHRYWVENPQAIAQME_____QICFNWFPSMMMK_____QPHVFKV___DHHMSCRWLPIRGKKCSSCCTRMRVRTVWE
YHEDV____AHE_____DAIAQMVNTFGFVWQICLNQFPSMMMKIYWIAVLSAHVADRKTWSKHMSCRWLPI____ISATCARMRVRTVWE
(bioinformatics)  atakan1@Atakan  ~/Desktop/Bioinformatics/assignments/Assignment-1   master 
```

Figure 1: Global Alignment Results

1.2 Local Alignment Algorithm

As requested in assignment description, I have used Smith-Waterman algorithm with affine gap penalties to align given 2 protein sequences. In addition to that, for local alignment, I have only printed our best score local alignments of protein sequences. Let's see some results.

```
(bioinformatics)  atakan1@Atakan   ~/Desktop/Bioinformatics/assignments/Assignment-1   master   python PairwiseAlignment.py test-pair1.txt 11 1 local
Method: Local Alignment
Score: 12
Alignments
----------
LEAS
MEAN
(bioinformatics)  atakan1@Atakan   ~/Desktop/Bioinformatics/assignments/Assignment-1   master   python PairwiseAlignment.py test-pair2.txt 11 1 local
Method: Local Alignment
Score: 19
Alignments
----------
PRT___EIN
PRTWPSEIN
(bioinformatics)  atakan1@Atakan   ~/Desktop/Bioinformatics/assignments/Assignment-1   master   python PairwiseAlignment.py test-pair3.txt 11 1 local
Method: Local Alignment
Score: 144
Alignments
----------
YHFDVPDCWAHRYWVENPQAIAQME_____QICFNWFPSMMMK_____QPHVFKV___DHHMSCRWLPIRGKKCSSCCTRMRVRTVWE
YHEDV____AHE_____DAIAQMVNTFGFVWQICLNQFPSMMMKIYWIAVLSAHVADRKTWSKHMSCRWLPI____ISATCARMRVRTVWE
(bioinformatics)  atakan1@Atakan   ~/Desktop/Bioinformatics/assignments/Assignment-1   master
```

Figure 2: Local Alignment Results

2 Test Results

My program also saves results as ".txt" file into "results" folder that creates it in the current working directory

Here are the contents of ".txt" files:

"test-pair-1-global-result.txt"

Score: -1
PLEASANTLY
_MEAN___LY

"test-pair-1-local-result.txt"

Score: 12
LEAS
MEAN

"test-pair-2-global-result.txt"

Score: 8
PRT___EINS
PRTWPSEIN_

"test-pair-2-local-result.txt"

Score: 19
PRT___EIN
PRTWPSEIN

"test-pair-3-global-result.txt"

Score: 144

4

YHFDVPDCWAHRYWVENPQAIAQME_____QICFNWFPSMMMK_____
QPHVFKV__DHHMSCRWLPIRGKKCSSCCTRMRVRTVWE
YHEDV____AHE_____DAIAQMVNTFGFVWQICLNQFPSMMMKIYWIAV
LSAHVADRKTWSKHMSCRWLPI___ISATCARMRVRTVWE
"test-pair-3-local-result.txt"
    Score: 144
YHFDVPDCWAHRYWVENPQAIAQME_____QICFNWFPSMMMK_____
QPHVFKV__DHHMSCRWLPIRGKKCSSCCTRMRVRTVWE
YHEDV____AHE_____DAIAQMVNTFGFVWQICLNQFPSMMMKIYWIAV
LSAHVADRKTWSKHMSCRWLPI___ISATCARMRVRTVWE