

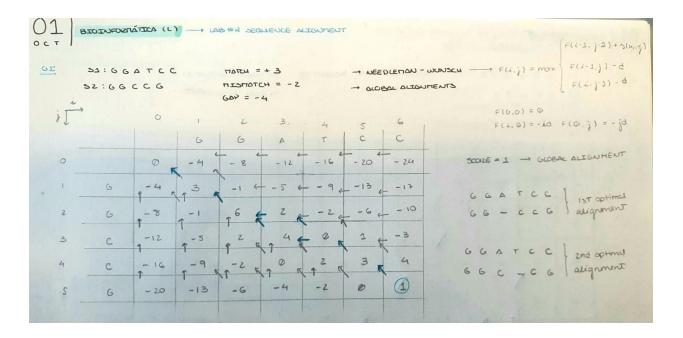
Computational Biology / Bioinformatics Lab 2 - Report

Group 22

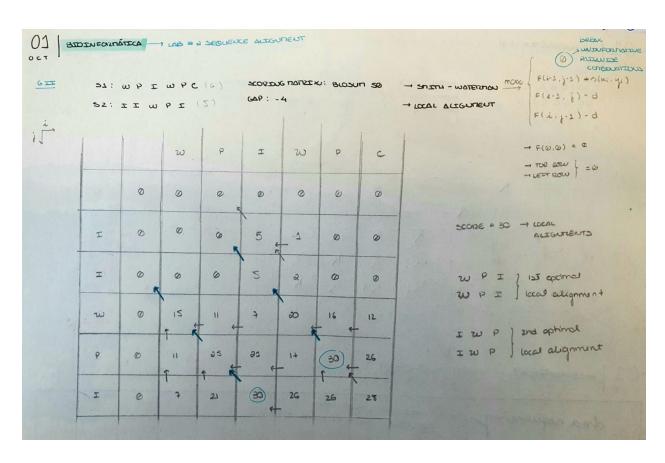
Group Members:

Alexandra Maroco 86369 André Branco 90013 Joana Alvoeiro 89469 Pedro Nunes 89525

Group I



Group II

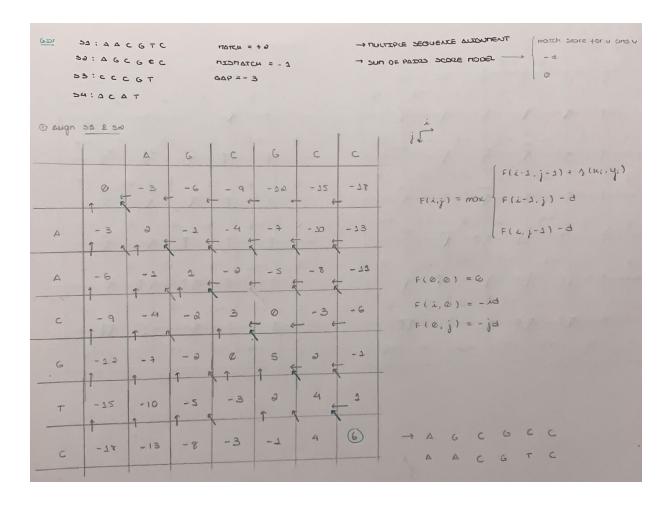


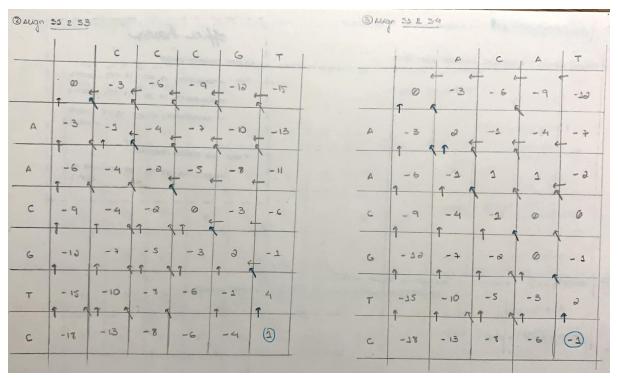
Group III

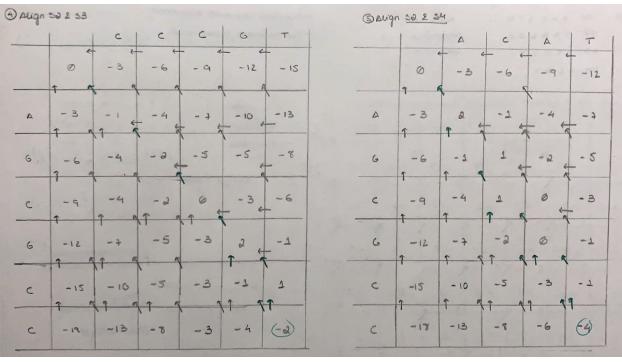
When the input provided to the program is the same as in Question II, our program outputs the following:

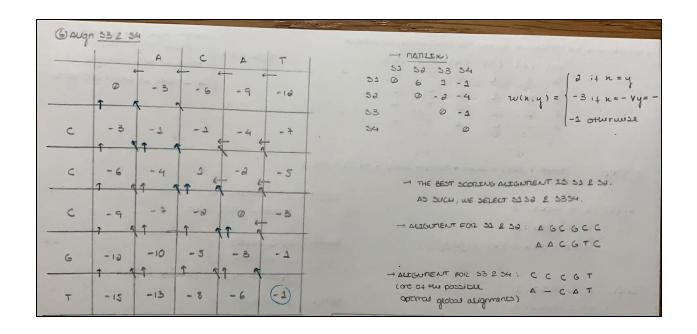
```
C:\Users\alexa\Documents\IST\5th\Bioinformática\smith_waterman>python3 smith_waterman.py
Input first sequence:
WPIWPC
Input second sequence:
IIWPI
Input gap penalty:
Score Matrix:
[[ 0 0 0 0 0 0]
[00015117]
[ 0 0 0 11 25 21]
[ 0 5 5 7 21 30]
[ 0 1 2 20 17 26]
[ 0 0 0 16 30 26]
[ 0 0 0 12 26 28]]
The best local alignment score is 30.0
Optimal partial alignments:
Alignment 0:
WPI
WPI
Alignment 1:
IWP
IWP
```

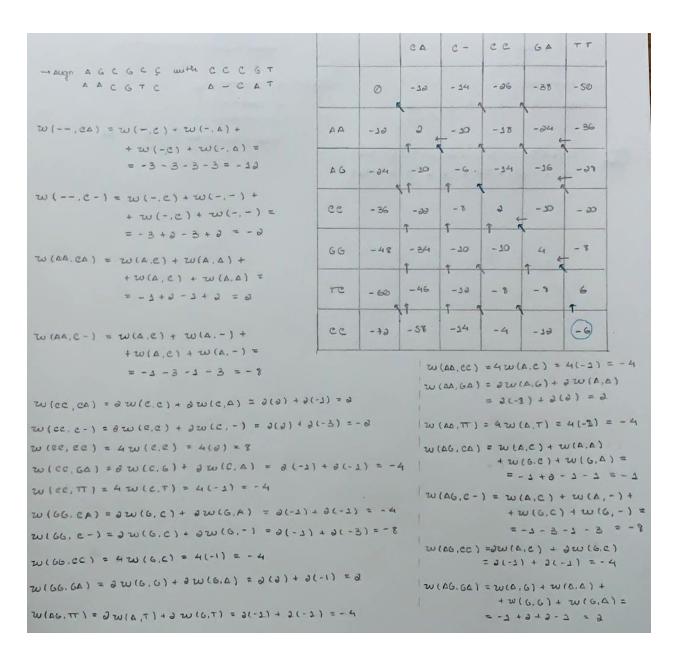
Group IV











```
- TRACING BACK THE MATRIX, WE OBTAIN THE FOLLOWING AUGUSTEUT:
                                                            ( moteh score for u and v,
                                                             it both ore residues
                                                  12(W, W) =
            (1) (8) (5) (4) (5) (6)
                                                            -dituorvisagep
            AACGTC
                                                           e is both u and v are gops
            A 6 C G C C
            c c c
                        A T -
                   C
SP-30026: 30026 = 5(3) + 5(3) + 5(3) + 5(4) + 5(5) + 5(6)
                                          5(3); C-C PADRS : 6
  5(2): A-A PADES: 3
                                           2004SE = P(9) = 79
       A - C PAIRS : 3
                                         5(4): 6-6 PADES 13
       YOUR = 3x8 + 3x(-1) = 3
                                                6- A PADES: 3
                                               SCORE = 3(2) + 3(-1) = 3
 5(8): A - G PADES: 1
                                         5(5): T - T PATES: 3
      A - C PADED : 1
                                               T - CPAIRS: 3
      A - GAP PAIRS :1
                                                acone = 3(2) + 3(-1) = 3
       6 - C PADED : 1
      6 - GAP PADES : 1
                                         5(6): C-C PATED: 1
       C - GAP PADES: 1
                                               C - GAP PADED : 4
      Score = -1 -1 -3 -1 -3 -3 = -12
                                              CAP-GAP PAIRS : 1
                                               SCORE = 1(2) +4(-3) +0 = -10
 TOTAL = 5(1) + 5(3) + 5(4) + 5(5) + 5(6)
      = 3 + (-10) + 20 + 3 + 3 + (-10)
       = -1
```