TDA507

Assignment 1: Sequence Alignment

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Output of questions 1, 2 and 3 (global_alignment.c)

```
./global_alignment
Score matrix:
          Α
               Т
                    Α
                         C
                              G
         -2
                   -6
                        -8
                            -10
              -4
                                 -12
   -2
          2
                   -2
                             -6
                                  -8
               0
                        -4
Α
          0
                    2
    -4
               4
                             -2
Т
                         0
                                  -4
               2
                    3
                              2
         -2
C
   -6
                         4
                                   0
  -8
                              6
G
         -4 0
                    1
                         2
                                   4
              -2
  -10 -6
                    2
                              4
                         0
                              2
Т
   -12
         -8
              -4
                    0
                         1
AT-CGAT
ATACG-T
Percent identity: 71.43%
Hamming distance: 2
```

Output of question 4 (local_alignment.c)

```
./local_alignment
Score matrix:
                 D
                                         W
                                                      Н
                                                                 Q
            Н
                        Α
                             G
                                    Α
                                                G
                                                            Ε
     0
           0
                  0
                              0
                                                0
                                                           0
                                                                 0
                       0
                                    0
                                          0
                                                      0
     0
           0
                  0
                       0
                             0
                                    0
                                         0
                                                0
                                                      0
                                                           0
                                                                 0
Ρ
                        2
                              0
                                    2
                                                0
                                                      0
                                                           0
                                                                 0
      0
            0
                  0
                                          0
Α
W
     0
           0
                  0
                       0
                              1
                                    0
                                         4
                                                2
                                                      0
                                                           0
                                                                 0
                                                           2
                                                3
Н
     0
           2
                  0
                       0
                             0
                                          2
                                                      4
                                                                 0
                                    0
                                                1
                                                           6
Ε
     0
           0
                  1
                       0
                             0
                                    0
                                          0
                                                      2
                                                                 4
                       3
                                    2
                                                           4
                                                                 5
Α
     0
           0
                  0
                              1
                                          0
                                                0
                                                      0
                                                                 3
Ε
            0
                        1
                              2
                                    0
                                                0
                                                           2
      0
                  0
                                          1
                                                      0
alignment_length: 5
AW-HE
\Pi
AWGHE
Percent identity: 80.00%
Hamming distance: 1
```

Output for question 5 (levenshtein.c)

```
./levenshtein
Score matrix:
                          C
                               G
                                     Т
          Α
               Т
                     Α
     0
         -2
                    -6
                         -8
               -4
                              -10
                                   -12
          2
Α
    -2
                0
                    -2
                         -4
                               -6
                                    -8
Т
                     2
    -4
          0
                4
                               -2
                                    -4
                          0
                     3
C
    -6
         -2
                2
                          4
                                2
                                     0
    -8
         -4
G
                0
                     1
                          2
                                6
                                     4
                                     5
   -10
                     2
Α
         -6
               -2
                          0
                                4
Т
   -12
         -8
                     0
                          1
                                2
                                     6
               -4
AT-CGAT
\Pi
ATACG-T
Percent identity: 71.43%
X: ATCGAT
Y: ATACGT
Levenshtein distance between initial strings X and Y: 2
Levenshtein distance between aligned sequences: 2
```

```
./6_and_7
Score matrix:
          Α
               Τ
                    Т
                                    Α
         -2
     0
              -4
                   -6
                         -8
                             -10
                                  -12
    -2
         2
              0
                   -2
                        -4
                              -6
                                   -8
         0
Т
    -4
               4
                   2
                         0
                              -2
                                   -4
    -6
               2
Т
                    6
                         4
                              2
                                    0
         -2
    -8
               0
                         5
                               3
         -4
                    4
                                    4
Number of optimal alignments: 6
Optimal Alignment Number: 1
A--TTA
1 111
ATTTTA
Optimal Alignment Number: 2
A-T-TA
I + I + II
ATTTTA
Optimal Alignment Number: 3
AT--TA
\Pi
ATTTTA
Optimal Alignment Number: 4
A-TT-A
| | | |
ATTTTA
Optimal Alignment Number: 5
AT-T-A
\Pi
ATTTTA
Optimal Alignment Number: 6
ATT--A
\Pi \Pi = \Pi
ATTTTA
```