## **Homework 2 Writeup**

## **DP Matrix**

Output from my script, including the DP matrix and resulting alignment, is shown below.

```
S1:
    GWWPDT
S2:
    WRRKHY
h() matrix:
                Ρ
                   D
                       Т
     G
        W
            W
  -2 -2 -2 -2
                   -2
                       -2
W -2 1
        5
            5
               -5
                   -5
                      1
R -2 -5 -5 0
                   0
                       -5
R -2 -5 -5 -5
                   0
                       -5
               0
K -2
     1
            1
                -5
                   -5
        1
                      1
H -2 1
            1
        1
                -5
                   -5
                       1
Y -2 1
            1
                -5
                   -5
                      1
DP matrix:
                Ρ
                       Т
     G
            W
                   D
     -2 -4 -6
               -8 -10 -12
W -2 1
        3
            1
                   -3
                      -5
                -1
     -1 1
R -4
            -1
               1
                   -1
                      -3
R -6
    -3 -1
           -3
               -1
                   1
                       -1
K -8 -5 -2 0
               -2
                   -1 2
H-10 -7 -4 -1 -3
                   -3
                      0
Y-12 -9 -6 -3 -5 -5 -2
GWWPDT - -
--WRRKHY
```

## Discussion

Several alignments are possible; the script I wrote produces only one. Looking at the matrices above, one can see the below alignments are also valid. The first two simply shift S1's T to align with either S2's H or Y, instead of aligning it with K. Because T, H, Y, and K are all hydrophobic and gap length is penalized linearly, these alternate alignments will have no effect on total score. The latter three alignments are variations with S2's W aligning with either S1's first or second W. Again, because both W-W alignments score equally and gap penalties are linear, these alignments will not affect the score.

```
GWWPD-T-
--WRRKHY

GWWPD--T
--W-RRKHY

GWWPDT--
-W-RRKHY

GWWPD-T-
-W-RRKHY
```

The decision to choose one alignment instead of another occurs in the DP matrix backtrace routine. When checking which sub-alignment was used to find the current alignment, two or more may be possible. Different methods of resolving these ties is what gives different alignments. My script compares the value of up (a gap in S1), diagonal (a match in S1 and S2), and left (a gap in S2), in that order, and uses the first sub-alignment possible. Alternatively, a program may choose to use several, even all, possible paths. Imagine a program did follow all paths. Without somehow validating its input, a malicious user may be able to craft two sequences such that all possible paths are ties, thus executing a DoS attack. An ameliorative measure may be to track the number paths followed until some threshold is reached, choosing the first matching sub-alignments thereafter.