CSC 314, Bioinformatics Lab #9: **Name:**_____
Dynamic Programming / Pairwise Alignments

Note: For all alignments, we will use a linear gap penalty of 4 points, a match score of +5 points, and a mismatch score of -1 point.

1. Consider the dynamic programming matrix for the optimal global alignment of *ttcag* with *tacaa*, which has been partially completed.

		t	a	c	a	a
	0	-4	-8	-12	-16	-20
t	-4	5	1			
t	-8	1	4			
c	-12	**-3**	**0**			
a	-16	**-7**				
g	-20					

   a. The highlighted squares with bold scores correspond to the scores that should be used when calculating the optimal global alignment score between *ttca* and *ta*. The optimal global alignment score is the maximum of what 3 values?

   b. What is the score of this optimal alignment (between *ttca* and *ta*)?

   c. What is the optimal global alignment (between *ttca* and *ta*). Note: if multiple optimal alignments exist, you can arbitrarily select one.

   d. Fill in the rest of the matrix to find the score of the optimal alignment between the two sequences *ttcag* and *tacaa*. What is the optimal alignment score?

   e. What is the optimal alignment?

2. Find the optimal global alignment between the sequences *east* and *start*, by constructing the appropriate dynamic programming matrix. You must show your dynamic programming matrix to receive credit.

3. Complete the dynamic programming matrix below to find (a) the score of the optimal semiglobal alignment, and (b) the optimal semiglobal alignment. The semiglobal alignment is found in the same way as the global alignment except that (1) the 1st row and 1st column of the matrix are initialized to all 0s (completed for you) and (2) traceback begins from the highest scoring cell in the bottom row or last column, with opening and closing gaps added as necessary.

		t	a	c	c
	0	0	0	0	0
a	0				
c	0				
a	0				
c					

4. Find the optimal semiglobal alignment between *tata* and *caag*.

5. Find the optimal *local* alignment between *east* and *start*, by constructing the appropriate dynamic programming matrix. Refer to your notes for the steps for finding the optimal local alignment.