CSC 314**, Bioinformatics Lab #8: 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 *atacg* with *taca*, which has been partially completed for you.

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  |  | t | a | c | a |
|  | 0 | -4 | -8 | -12 | -16 |
| a | -4 | -1 | 1 |  |  |
| t | -8 | 1 | -2 |  |  |
| a | -12 | **-3** | **6** |  |  |
| c | -16 | **-7** |  |  |  |
| g | -20 |  |  |  |  |

* 1. The highlighted squares with bold scores correspond to the scores that should be used when calculating the optimal global alignment score between *atac* and *ta*. The optimal global alignment score is the maximum of -4, -11, and +2. Show the calculations that yield these 3 values.
  2. What is the score of this optimal alignment (between *atac* and *ta*)?
  3. What is the optimal global alignment (between *atac* and *ta*).
  4. Fill in the rest of the matrix to find the score of the optimal global alignment between the two sequences *atacg* and *taca*.
     1. What is the optimal global alignment score
     2. What is the optimal global alignment?

1. Find the optimal global alignment and optimal global alignment score between the sequences *east* and *hat*, using the scoring system at the top of this assignment, by constructing the appropriate dynamic programming matrix. You must show your dynamic programming matrix to receive credit.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | h | a | t |
|  | 0 | -4 | -8 | -12 |
| e | -4 |  |  |  |
| a | -8 |  |  |  |
| s | -12 |  |  |  |
| t | -16 |  |  |  |

1. What is the optimal global alignment score?
2. What is the optimal global alignment?
3. Find the optimal *local* alignment between *steps* and *toe*, by constructing the appropriate dynamic programming matrix. Refer to your notes for the steps for finding the optimal local alignment. Note that the optimal local alignment is the following which has a score of 6.

t - e

t o e

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | t | o | e |
|  | 0 | 0 | 0 | 0 |
| s | 0 |  |  |  |
| t | 0 |  |  |  |
| e | 0 |  |  |  |
| p | 0 |  |  |  |
| s | 0 |  |  |  |

1. Find the optimal *local* alignment between *rest* and *are*, by constructing the appropriate dynamic programming matrix. What is the optimal alignment and what is the optimal alignment score?

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  |  | a | r | e |
|  |  |  |  |  |
| r |  |  |  |  |
| e |  |  |  |  |
| s |  |  |  |  |
| t |  |  |  |  |