Examples: Smith-Waterman Local Sequence Alignment

The most time-consuming step of the dynamic programming approach to sequence alignment (as implemented in the Smith-Waterman algorithm), is constructing the similarity matrix. Use the formula given in class and in the assignment to compute the matrices. The first example also illustrates the use of the "trace-back" method to specify the optimal alignment.

Example 1

Sequence (s):   G A T A T G C A
Unknown (t):   A T A G C T

```
        A  T  A  G  C  T
     0  0  0  0  0  0  0
G    0  0  0  0  1  0  0
A    0  1  0  1  0  0  0
T    0  0  2  0  0  0  1
A    0  1  0  3  1  0  0
T    0  0  2  1  2  0  1
G    0  0  0  1  2  1  0
C    0  0  0  0  0  3  1
A    0  1  0  1  0  1  2
```

max = 3, i = 7, j = 5 (if more than 1 maximum → give lowest, rightmost location)

```
s:    G A T A T G C A
t:      A T A - G C
        1 1 1 -2 1 1        Σ = 3
```

Example 2

Sequence (s):   A A T C G G A T T C
Unknown (t):   G A C G G T T C G T

```
        G  A  C  G  G  T  T  C  G  T
     0  0  0  0  0  0  0  0  0  0  0
A    0  0  1  0  0  0  0  0  0  0  0
A    0  0  1  0  0  0  0  0  0  0  0
T    0  0  0  0  0  0  1  1  0  0  1
C    0  0  0  1  0  0  0  0  2  0  0
G    0  1  0  0  2  1  0  0  0  3  1
G    0  1  0  0  1  3  1  0  0  1  2
A    0  0  2  0  0  1  2  0  0  0  0
T    0  0  0  1  0  0  2  3  1  0  1
T    0  0  0  0  0  0  1  3  2  0  1
C    0  0  0  1  0  0  0  1  4  2  0
```

max = 4, i = 10, j = 8