Homework

- Implement the Smith-Waterman algorithm
  - Write a function which accepts the following arguments:
    - 2 sequences
    - a similarity measure between sequence elements (either a function which takes two residue types as arguments, or a two-dimensional matrix)
    - a gap penalty function, which takes the gap length as an argument

Homework

- Implement the Smith-Waterman algorithm
  - Your function should return the common subsequence with the highest score
  - For grading purposes, your function should also print out the score matrix
  - *E-mail both your code and program output to conrad@cgl.ucsf.edu*

Homework

- Input data
  - Apply your code to the example from the Smith & Waterman paper
    - **CAGCCUCGCUUAG** *vs.* **AAUGCCAUUGACGG**
    - $S(A_i, B_j) = 1$ if $A_i = B_j$; -1/3 otherwise
    - $W_k = 1.0 + (1/3) * k$
    - Also try **GCCCUGCUUAG** *vs*. **UGCCGCUGACGG**
  - Your alignment and score matrix should match those published in the paper