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
    • $W_k = 1.0 + (1/3) \times k$
    • Also try GCCUCUGCUUAG vs. UGCCGCUGACGG
  – Your alignment and score matrix should match those published in the paper