CBB/CPSC Programming Assignment #1: Smith-Waterman

Background: The Smith-Waterman local alignment algorithm is one of the simplest and most fundamental algorithms for sequence alignment in bioinformatics.

Assignment: The first programming assignment is to implement the Smith-Waterman alignment algorithm for protein sequences using the provided similarity matrix (BLOSUM62). Sequence pairs are provided on the class website (Discussion Section page). The file containing the sequence pairs should be read in via a command-line argument.

For each sequence pair, the test run must include the completed scoring matrix (including the sequences themselves and in tab-delimited format), the score for the best local alignment (please label this), and a print-out of the local alignment such as the following:

```
T C W A F P L N
  |   | | | | |
S C - A W P L N
```

where | represents amino acid identity and – represents a sequence gap.

For general instructions refer to the **General Requirements for Programming Assignments** document.

DUE DATE: February 12, 2010 by 5 PM.