Programming Assignment – II

**Deadline: 6th Oct**

1. Dynamic Programming Algorithm for Global Alignment: implement Needleman-Wunch algorithm (for both DNA and Protein Sequences).
2. Dynamic Programming Algorithm for Local Alignment: implement Smith-Waterman algorithm using linear gap cost (for both DNA and Protein Sequences).

Use linear gap cost (default BLAST value). Use default scoring matrices in BLAST for DNA and Protein Sequences.

Compare the results of your program with that of EMBOSS “needle” and “water” and submit the results for two DNA/protein sequences (along with the accession id of the sequences used).