Needleman-Wunsch and Smith-Waterman Alignment

Group members (1 to 3): ____

(1) Using a scoring system of +3 for a match, -2 for a transversion, -1 for a transition, and -3 for a gap, use the Needleman-Wunsch algorithm to fill in a dynamic programming table and find the best global alignment between the sequences AGTGTAA and AGACATA. If there are ties, list all of the best alignments.

(2) Repeat the above exercise with the Smith-Waterman local alignment algorithm (this is easier).