**Needleman-Wunsch Global Alignment**

**Rules:** In each stepof the algorithm, fill in the cell with the maximum value above, to the left, or above and to the left of it *plus* the match bonus/ mismatch penalty for the two nucleotides if moving diagonally, *or* the gap penalty if moving down or to the right.

What are the match / mismatch scores? A simple version just uses 1 for all matches, and -1 for all mismatches. Similarly -1 for all gaps. It varies: real alignments set these based on properties of nucleotides (e.g. transitions are more common).

