

Problem 1. Global alignment

You are given two sequences AGATT and AGTT. Assume a match score of 1, a gap penalty of 3 and a substitution score of -1. Using these scores, obtain the global alignment of these two sequences in the following two steps:

- (a) Fill in the entries of the F matrix by applying the recurrence relationship for global alignment to these sequences. Please show the back pointers to the matrix entry/entries that give you the maximal score for any entry.
- (b) Apply the trace back procedure to obtain an optimal alignment. If there are multiple possible alignments, please show all of them along with their traceback paths.

Problem 2. Local alignment

Using the same scores above perform a local alignment for the sequences, GAAGAG and AAGC in the following two steps:

- (a) Fill in the entries of the F matrix using the recurrence relationship for the local alignment of these sequences. Show back pointers to matrix entry/entries that give you the maximal score.
- (b) Apply the trace back procedure to generate a local alignment.

Problem 3.

You are required to read and solve problems 3 and 4 from the webpage:

http://personal.tcu.edu/yryu/50133/bioinformatics_exercises.pdf)