Assignment for the sequence analysis module

#1: Make or adapt a Perl implementation of the Needleman and Wunsch algorithm able to report alternative optimal alignments through sampling (you can use non affine gap penalties).

#2: Implement in Perl a routine able to compare the alternative alignments produced by the above routine.

#3: Propose a strategy to measure the stability of pairwise sequence alignments with respect to evolutionary similarity.

Results/questions: cedric.notredame@crg.eu