

Global sequence alignment

(find and work with a partner)

Using the score function: match = 1, mismatch = -1, $g = -1$ (gap), what are the alignments scores for the following two pairs of sequences? Which of the pairs are biologically meaningful?

$x = ACA$
 $y = ACA$

$x = G-A$
 $y = TTA$

Execute our global sequence alignment algorithm (Needleman-Wunsch) on the strings below ($x = GAGTAC$ and $y = GTAGCA$). Use the same scoring system as above (with $g = -1$).

	-	G	T	A	G	C	A
-							
G							
A							
G							
T							
A							
C							

Use back-tracing to find the best alignment(s) for these two sequences.

Local sequence alignment

Execute our local alignment algorithm (Smith-Waterman) on the strings ($x = \text{CGATC}$ and $y = \text{ATCCG}$), with $g = -2$. Use back tracing to find the best local alignment.

	-	A	T	C	C	G
-						
C						
G						
A						
T						
C						

For the two pictures below, the diagonal lines represent a form of optimal alignment between x and y . Draw out what these alignments would look like (i.e. what portion of x aligns to what portion of y)? How could we modify our alignment algorithm to achieve these types of alignments?

