

Sequence Alignment

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?

$x = \text{ACA}$
 $y = \text{ACA}$

$x = \text{G-A}$
 $y = \text{TTA}$

Execute our global sequence alignment algorithm (Needleman-Wunsch) on the strings below ($x = \text{GAGTAC}$ and $y = \text{GTAGCA}$). 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.

What is the runtime of global sequence alignment, in terms of the sequence lengths (n and m)?