

## Affine (extension) gaps for pairwise sequence alignment

Consider the alignment of X = ACCG and Y = AGAACCGG shown below

X = ACCG----  
Y = AGAACCGG

The score of an alignment is just the sum of the scores of aligned pairs of nucleotides and gaps. For example let the score of a match be 8, the score of a mismatch be 2, and the score of a gap be -5. Then the score of the alignment

ACCG----  
AGAACCGG

is given by  $8 + 2 + 2 + 2 - 5 - 5 - 5 - 5 = -6$

In the affine gap model we call the first gap encountered from left to right an **open** gap. Any gaps that follow an open gap are **extension** gaps. Both have their own scores. For example suppose the gap open score is -5 and extension is -.1. Then the score of the alignment

ACCG----  
AGAACCGG

is given by  $8 + 2 + 2 + 2 - 5 - .1 - .1 - .1 = 8.7$

To identify an open gap we simply look the aligned pair immediately to the left of the gap. If there is a match or mismatch there then our gap is an open one and otherwise it is an extension. Some more examples of affine gap scores are

Alignment	Score
AG----TTGA--- AACCGGGTGTAAAG	$8 + 2 - 5 - .1 - .1 - .1 + 2 + 8 + 8 + 2 - 5 - .1 - .1 = 19.5$
AG----TTGAAAA AACCGGGTG---A	$8 + 2 - 5 - .1 - .1 - .1 + 2 + 8 + 8 - 5 - .1 - .1 + 8 = 25.5$