

Aligns  $s_1$  and  $s_2$  using the following recursion on three matrices:

- $P$  is filled with the best score ending in a deletion on  $s_1$
- $Q$  is filled with best score ending in a deletion on  $s_2$
- $D$  is filled the best score overall score from aligning residues from both sequences,  $P$ ,  $Q$ , and 0 (to allow local alignments to terminate).

$$p_{ij} = \max \begin{cases} d_{i-3,j} + \gamma_1 + g_o, \\ p_{i-3,j} + \gamma_1 + g_e, \\ d_{i-2,j} + \gamma_1 + \delta + g_o, \\ p_{i-2,j} + \gamma_1 + \delta + g_e, \\ d_{i-1,j} + \gamma_1 + \delta + g_o, \\ p_{i-1,j} + \gamma_1 + \delta + g_e \end{cases}$$

$$q_{ij} = \max \begin{cases} d_{i,j-3} + \gamma_2 + g_o, \\ q_{i,j-3} + \gamma_2 + g_e, \\ d_{i,j-2} + \gamma_2 + \delta + g_o, \\ q_{i,j-2} + \gamma_2 + \delta + g_e, \\ d_{i,j-1} + \gamma_2 + \delta + g_o, \\ q_{i,j-1} + \gamma_2 + \delta + g_e \end{cases}$$

$$d_{ij} = \max \left\{ \begin{array}{l} 0 \\ d_{i-3,j-3} + \sigma(a_i, b_j), \\ d_{i-3,j-2} + \gamma_1 + \delta, \\ d_{i-3,j-1} + \gamma_1 + \delta, \\ d_{i-2,j-3} + \gamma_2 + \delta, \\ d_{i-1,j-3} + \gamma_2 + \delta, \\ d_{i-1,j-1} + 2\delta, \\ d_{i-1,j-2} + 2\delta, \\ d_{i-2,j-1} + 2\delta, \\ d_{i-2,j-2} + 2\delta, \\ p_{i,j}, \\ q_{i,j} \end{array} \right.$$

Where:

- $g_o$  is the (amino acid) gap opening penalty
- $g_e$  is the (amino acid) gap extension penalty
- $\delta$  is the frame shift penalty,
- $\sigma(a, b)$  is the substitution cost between amino acids  $a$  and  $b$
- $\gamma_i$  is equal to the stop-codon penalty if the current amino acid in sequence  $i$  encodes a stop codon, 0 otherwise.