Global Alignment with Dynamic Programming

Align the protein sequences S₁ and S₂ with a gap penalty of 2 and the "H₂O" substitution cost defined as:

For amino acids x and y,

+5, if x=y

+1, if x≠y, x,y are both hydrophobic

 $H(x,y) = {$ -5, if only one is hydrophobic

0, if x≠y, neither are hydrophobic

S₁ = GWWPDT S₂ = WRRKHY

Write down the Dynamic Programming (DP) recursion for global alignment of S₁ and S₂. Form and fill out the DP table with traceback indices. Trace the path and form your alignment. Discuss the resulting alignment with respect to the substitution metric H.

Amino Acid Properties

