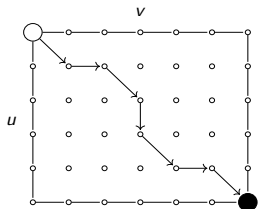


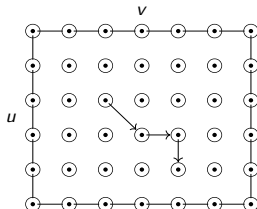
Overview of pairwise distance comparison methods based on dynamic programming

- The sequence comparison methods described so far always compute an $(m + 1) \times (n + 1)$ -table in $O(mn)$ time, given sequences of length m and n , respectively.
- The local alignment method maximizes scores, while all other methods minimize distances.
- We have introduced different tables in which the entry at (i, j) refers to different substrings of the aligned pairs of sequences.
- With respect to the traceback phase the differences of the methods can best be explained by the edit graph they imply.
- Each traceback reconstructs an alignment beginning with a start entry and ending with with a final entry, This is depicted in a schematic way in Figure 1.

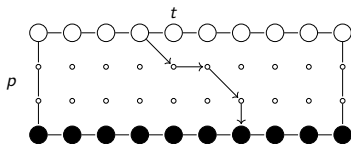
Figure 1: Traceback strategies for different alignment problems in an edit graph. Each traceback strategy is characterized by start entries (i.e. entries where the traceback ends or an optimal alignment starts) and by final entries (i.e. entries where the traceback starts or an alignment ends).



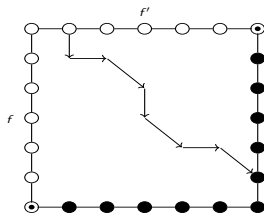
global alignment (table E_δ)



local alignment (table L_σ)



approximate string searching (table D_δ)



fragment overlap (table O_{v_δ})