Sequence alignment

Goal: find min-cost alignment between two sequences

Example: AATC   Cost
ATCA

- Mismatch

- Gap

Subproblems

as1,as2,cost = align(s1,s2)

- Align s1[0] and s2[0]

    Subproblem:

- Align s1[0] with gap in s2

    Subproblem:

- Align s2[0] with gap in s1

    Subproblem: