Maximum Parsimony

- Input: Set *S* of *n* aligned sequences of length k
- Output:
 - A phylogenetic tree T leaf-labeled by sequences in S
 - additional sequences of length k labeling the internal nodes of T

such that

$$\sum_{i,j)\in E(T)} H(i,j)$$

is minimized, where H(i,j) denotes the Hamming distance between sequences at nodes i and j