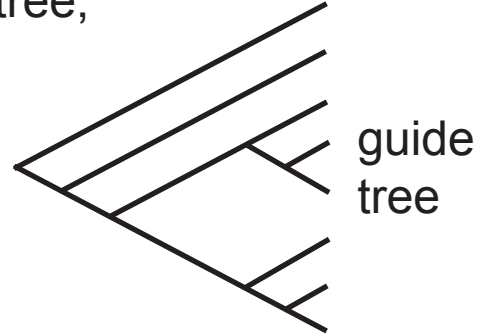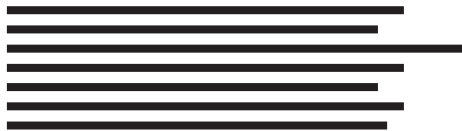N^2 distance matrix

hierarchical clustering
(minimum spanning tree,
UPGMA)

guide tree

N^2 comparisons
(pairwise alignment,
K-mer counting)

input sequences:

Assumption:
These sequences are homologous.