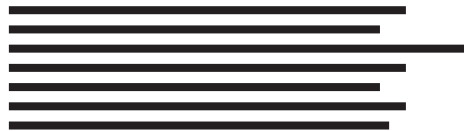


N^2 comparisons
(pairwise alignment,
K-mer counting)

input sequences:



Assumption:
These sequences are homologous.