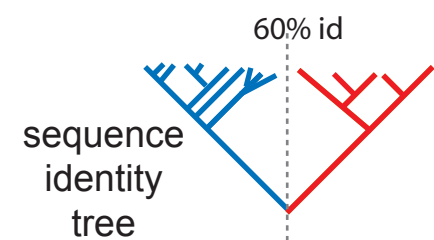
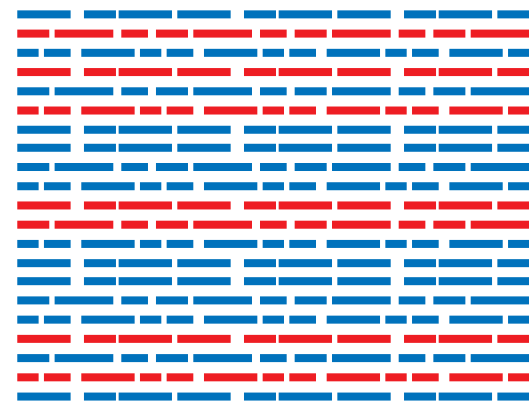
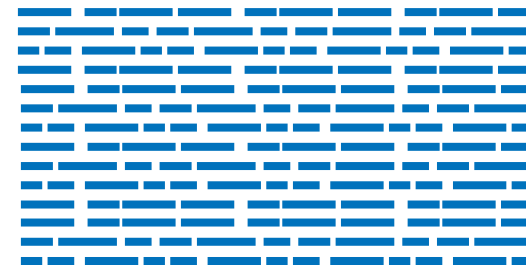


Rfam seed alignment:



training alignment



no train/test sequence
pair is > 60% identical



test sequences

embed in
pseudo-genome



10 1Mb sequences
with 780 embedded
test seqs from 106 families