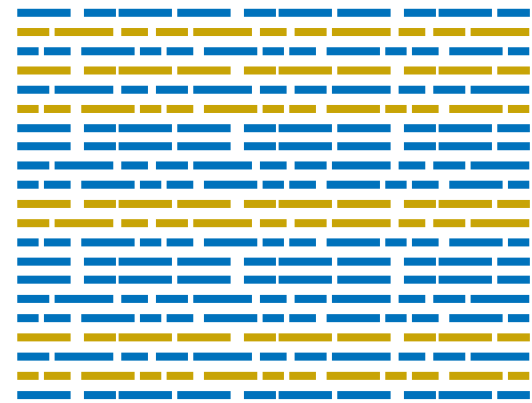
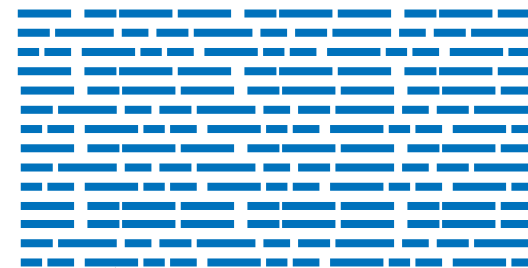


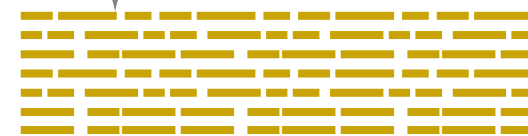
trusted “gold standard”
alignment (152 sequences):



seed alignment
(101 sequences):



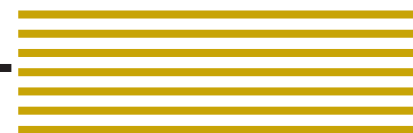
no seed/test sequence
pair is > 80% identical



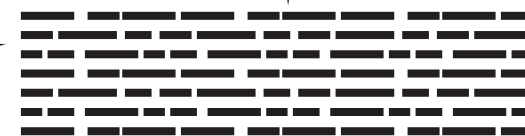
test alignment
(51 sequences)



51 test sequences:



alignment



Test: How similar
are these alignments?

