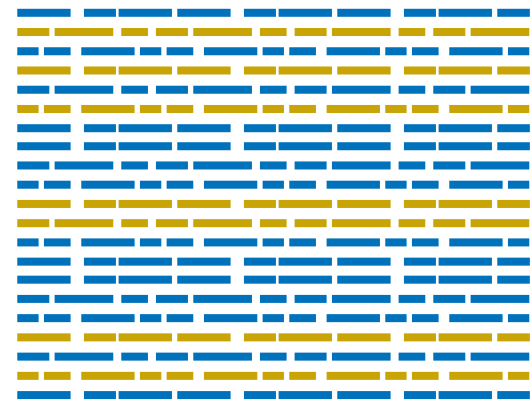


trusted “gold standard”
alignment (152 sequences):



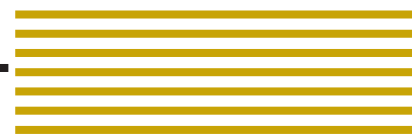
seed alignment
(101 sequences):



**construction
procedure**

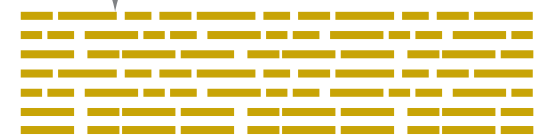
profile
(CM or HMM)

51 test sequences:



alignment

no seed/test sequence
pair is > 80% identical



test alignment
(51 sequences)

Test: How similar
are these alignments?

