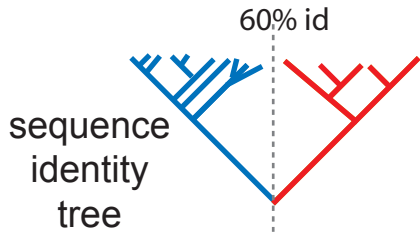
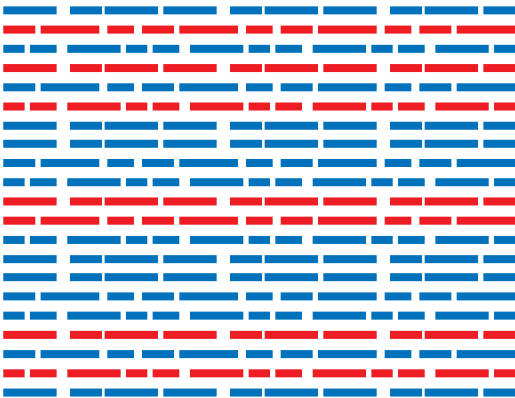
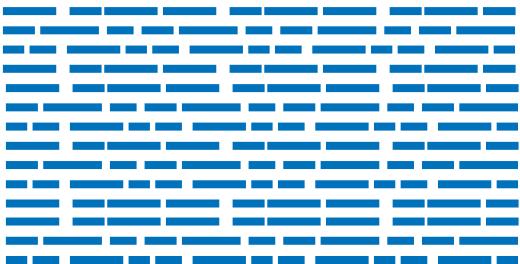


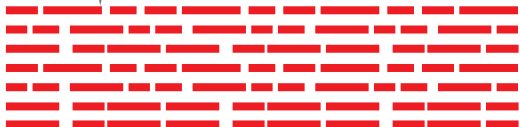
Rfam seed alignment:



training alignment



no train/test sequence pair is > 60% identical



test sequences

profile
(CM or HMM)

BLAST

search

embed in
pseudo-genome



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

E=1E-40 132.53 bits rmark7 OLE 340023 339402 +

...

...

...

...

E=0.0013 32.3 bits rmark3 6S 10135 10261 +

E=0.0026 27.6 bits rmark6 tRNA 789278 789466 +

E= 0.0061 28.3 bits rmark2 Cobalamin 32032 31787 -

E=0.0231 25.4 bits rmark 6 FALSE 673200 673340 +

E=0.0670 25.3 bits rmark6 tRNA 789278 789116 -

...

...

...

...

E=103.3 16.4 bits rmark 4 FALSE 783222 782803 -