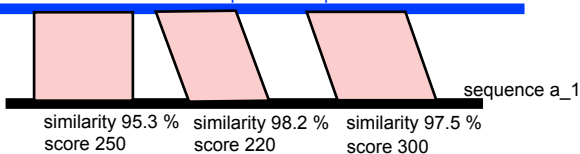


A. Normal case

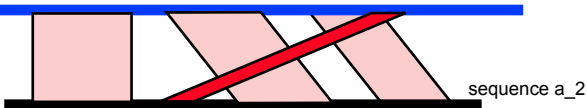
Reference 16S rRNA
sequence of Species A



Average similarity 97 %

Total score 770

B. Strange case



Alignments consistency is broken