Sequence: ACGGATTAGAT

1 → Construct seed matches

GCCGTACG CCCCCTTT GCCGTACG CCCCCTTT GCCGTACG CCCCCTTT

2 → Chain seed matches within *w* nucleotides of each other

① ② ③

Chained seeds and flanking sequence:

① AAAAAAAAATGGGAAGCCGTACGTCCCCCTTTGCATAACTACGACTA
② TTGGCGGGGTGGGAAGCCGTACGCCCCCCTTTGCATAAGTAGGTCTT
③ GCAATACCCTGGGAAGCCGTACGAACCCCCTTTGCATAAGGTCTTACT

3 → Align regions between seeds

① AAAAAAAAATGGGAAGCCGTACGT-CCCCCTTTGCATAACTACGACTA
② TTGGCGGGGTGGGAAGCCGTACGC-CCCCCTTTGCATAACTAGGTCTT
③ GCAATACCCTGGGAAGCCGTACGAACCCCCTTTGCATAAGGTCTTACT

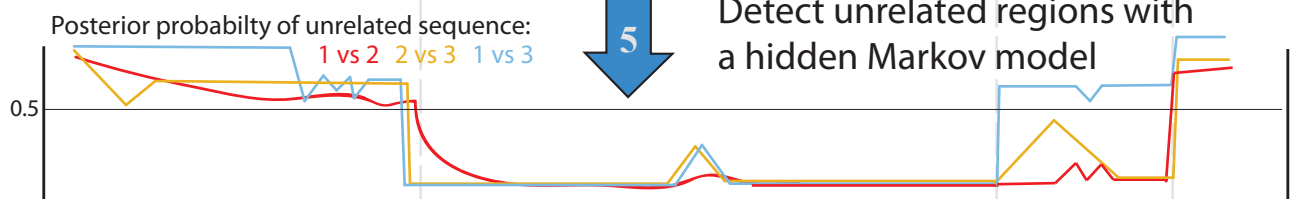**4** → Align regions flanking the chain

① ---------AAAAAAAAATGGGAAGCCGTACGT-CCCCCTTTGCATAACTACGACTA---
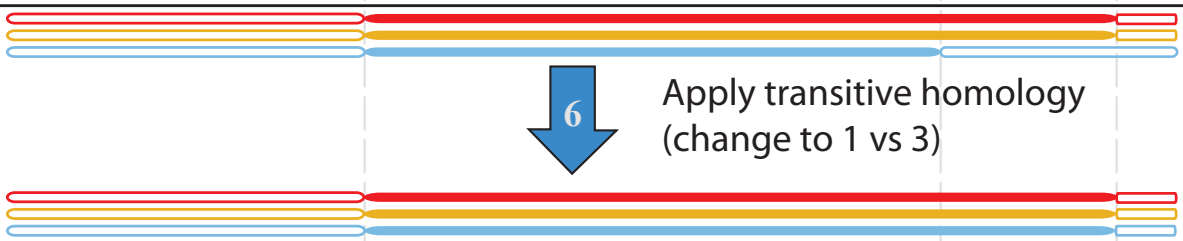② TTGGCGGGG---------TGGGAAGCCGTACGC-CCCCCTTTGCATAACTAGGTCTT---
③ ---GC------AATACCCTGGGAAGCCGTACGAACCCCCTTTGCATAA---GGTCTTACT

Posterior probabilty of unrelated sequence:
1 vs 2 2 vs 3 1 vs 3

0.5

5 → Detect unrelated regions with a hidden Markov model

6 → Apply transitive homology (change to 1 vs 3)

7 → Unalign non-homologous regions and trim alignment boundaries

Final local multiple alignment:

① TGGGAAGCCGTACGT-CCCCCTTTGCATAACTACGACTA
② TGGGAAGCCGTACGC-CCCCCTTTGCATAACTAGGTCTT
③ TGGGAAGCCGTACGAACCCCCTTTGCATAA---GGTCTT