

A Bootstrapping

Alignment of sequences

Species 1	ATGTTGGATGGT GAT
Species 2	ATGTTGGAAGGAGAA
Species 3	ATGTTAGGAGAAGAA
Species 4	ATGTCAGCAGCCGCC

Bootstrapping alignment #1

Species 1	ATGTTGGAGGGTAAT
Species 2	ATGTTGGAGGGAAAA
Species 3	ATGTTAGGGGAAAAA
Species 4	ATGTCAGCGGCCCC

Bootstrapping alignment #2

Species 1	ATGGGGGATGGT GAT
Species 2	ATGGGGGAAGGAGAA
Species 3	ATGGGAGGAGAAGAA
Species 4	ATGGGAGCAGCCGCC

B Jackknifing

Alignment of sequences

Species 1	ATGTTGGATGGT GAT
Species 2	ATGTTGGAAGGAGAA
Species 3	ATGTTAGGAGAAGAA
Species 4	ATGTCAGCAGCCGCC

Jackknifed alignment 1 (10 columns kept)

Species 1	AT-T-GGA-GG-GA-
Species 2	AT-T-GGA-GG-GA-
Species 3	AT-T-AGG-GA-GA-
Species 4	AT-T-AGC-GC-GC-

Jackknifed alignment 2 (10 columns kept)

Species 1	--GTTGG--GGT-AT
Species 2	--GTTGG--GGA-AA
Species 3	--GTTAG--GAA-AA
Species 4	--GTCAG--GCC-CC

FIGURE 27.21. Bootstrapping. (A) Bootstrapped alignment #1. The columns in *green* and *light blue* are not part of the new alignment and the columns in *yellow* and *red* are present twice. Bootstrapped alignment #2. The columns in *green* and *light blue* are present but the two columns in *dark blue* are not and the column in *pink* is represented three times. (B) Jackknifing. Alignments are resampled without replacement such that the new alignments have fewer columns than the original.