

### **Algorithm: Feng–Doolittle progressive alignment**

- (i) Calculate a diagonal matrix of  $N(N - 1)/2$  distances between all pairs of  $N$  sequences by standard pairwise alignment, converting raw alignment scores to approximate pairwise ‘distances’.
- (ii) Construct a guide tree from the distance matrix using the clustering algorithm by Fitch & Margoliash [1967a].
- (iii) Starting from the first node added to the tree, align the child nodes (which may be two sequences, a sequence and an alignment, or two alignments). Repeat for all other nodes in the order that they were added to the tree (i.e. from most similar pairs to least similar pairs) until all sequences have been aligned. ◁