

Algorithm: CLUSTALW progressive alignment

- (i) Construct a distance matrix of all $N(N - 1)/2$ pairs by pairwise dynamic programming alignment followed by approximate conversion of similarity scores to evolutionary distances using the model of Kimura [1983].
- (ii) Construct a guide tree by a neighbour-joining clustering algorithm by Saitou & Nei [1987].
- (iii) Progressively align at nodes in order of decreasing similarity, using sequence–sequence, sequence–profile, and profile–profile alignment. \triangleleft