



Basis for each recommendation:

Accuracy can often be improved considerably by including closely related sequences, which can then be removed after alignment. The additional sequences act as “stepping stones” between distantly-related sequences.

Alignment of amino acid and non-coding RNA sequences can be improved by making use of their conserved secondary structure. DECIPHER will automatically predict secondary structures if the input is an `AAStringSet` or `RNAStringSet`. For coding (nucleotide) sequences, `AlignTranslation` will align the sequences in amino acid space.

Staggering the alignment decreases false positive homologies by separating independent insertions.

Chained guide trees offer a viable alternative when aligning hundreds of thousands of unique sequences, as the default requires $O(n^2)$ time. Refer to the section of this vignette entitled “Building a Guide Tree”.

Iteration and refinement steps are unnecessary when all of the sequences are very similar or when a chained guide tree is being used.

Setting `normPower` to zero will weigh all columns of the alignment equally, regardless of column occupancy. This helps with aligning partial-length sequences because many columns of the alignment are expected to have low occupancy.