

Basis for each recommendation:

Accuracy can can often be improved considerably by including closely related sequences, which can then

act as "stepping stones" between distant sequences. Alignment of amino acid sequences is more accurate

which is why aligning their translations is preferable. AlignTranslation works by translating, aligning, and then reverse translating.

decreases false positive homologies by adding gaps. Chained guide trees offer

Iteration and refinement steps are unnecessary when all the sequences are very similar or when a chained

Restricting the alignment space increases speed