

The Effect of Multiple Sequence Alignment Guide Tree Choice on the Topology of the Alignment-Based Phylogeny

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Phylogenetic trees of evolutionary relationships are vital to understanding evolution. Phylogenetic tree inference involves the construction of a multiple sequence alignment, which itself depends on the construction of a guide tree. Guide trees have no evolutionary significance but guide the reconstruction of multiple sequence alignment and are expected to influence the construction of phylogenetic trees. In this paper we investigate the relationship between the choice of guide tree and the resulting phylogeny. Using three clustering methods of varying precision (Neighbor-joining, UPGMA, and UPGMB) as well as the true tree, we constructed and analyzed alignments and phylogenies to determine their accuracy and similarity. Results showed a very strong correlation between guide tree accuracy and phylogenetic tree topology, and suggest that the phylogeny may tend to be similar to the guide tree used in its creation process.