Phylogeny Inference by Minimum Conflict

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Abstract

While standard phylogenetic methods like parsimony, maximum likelihood or distance often yield good trees from multiple sequence alignments (Swofford *et al.* 1996), there are situations where these trees contradict the wide body of taxonomic expert knowledge. One reason is that "ancient" character states can persist in a group of taxa, although they are eroded in all other members of a larger monophylum. Then, the group is placed into its own subtree although it may not be monophyletic, i.e. there is no ancestor that is common only to its taxa. We will explain this *erosion trap*, and how to overcome it, using a specific kind of outgroup comparison. The technique is part of a divide-and-conquer tree inference method (Fuellen *et al.* 1998) which tries to find splits with minimum conflicting evidence, guided by the inconsistency patterns triggered by incorrect splits. The method has detected erosion in a number of data sets, including a set of crustacean taxa provided by Spears *et al.* (1994).

References

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