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Abstract of presentation

Self-calibrated character weighting

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A cladistic analysis consists of two main activities. The first one, character analysis, results in a dataset that encodes similarities among a group of terminals. These encoded similarities are grounded in empirical observation and constitute possibly conflicting a priori hypotheses of identity through common descent and inheritance (homology). The second activity, parsimony analysis, determines the set of trees that maximizes the number of independent pairwise such similarities that can simultaneously be interpreted as homology. It is discussed how this view can provide an answer to the following two questions: (1) exactly what should be weighed when using tree-based character weights in parsimony analysis; and (2) what should the weighting function look like. The resulting weighting method optimizes a particular quadratic function of the amount of homoplasy of a character on a tree. It is dubbed self-calibrated weighting because it automatically adapts weighting strength to data set size. Using results obtained with random bipartitions of published empirical datasets, this new method is compared to implied weighting and range weighting.