

Theory and practice of parsimony analysis when some characters are inapplicable in some terminals

Jan De Laet, Göteborgs Botaniska Trädgård, Carl Skottsbergs Gata 22A, SE-413 19 Göteborg, Sweden; email: jan.de.laet@anagallis.be

In parsimony analysis, various problems can arise with features that are not applicable across all terminals of a data set (Maddison 1993, *Syst. Biol.* 42, 576-581). At the XXIst Meeting of the Willi Hennig Society (Helsinki, 2002), I discussed how these can be overcome by imposing constraints on algorithms such as those of Farris (1970, *Syst. Zool.* 19, 83-92; additive characters) or Fitch (1971, *Syst. Zool.* 20, 406-416; non-additive characters); and pointed out that such constraints can break a symmetry that is present in the original algorithms: maximization of homologous similarity and minimization of steps are now no longer equivalent. This can lead to a preference for different trees, an observation that at once made the following fundamental question practically relevant: should we prefer trees that minimize evolutionary events or trees that maximize the amount of similarity that can be interpreted as homology? Here, I reiterate my preference for maximization of homologous similarity and review the corresponding algorithmic modifications that are required when inapplicables are present. These algorithms are available in anagallis, a new computer program for parsimony analysis. It provides an easy and interactive way to specify nested sets of characters that make up an absence/presence character hierarchy; tree searches in which the optimization of such hierarchies is properly constrained; and basic diagnostic functionalities such as plots of final statesets at inner nodes.

**p. 21 in Heraty, J. and C. Weirauch. 2012.
Hennig XXXI. Program and Abstracts.
Riverside, CA.
23-27 June 2012.**