Stevenson, D. M. 2004. Abstracts of the 22nd Annual Meeting of the Willi Hennig Society. Cladistics 20: 76-100

> *"The 22nd annual meeting of the Willi Hennig Society was held at the New YorkBotanical Garden in the Bronx, New York from July 20–24 [2003]."*

p. 81:

When One and One is Not Two: Parsimony Analysis of Sequence Data. Jan De Laet. Royal Belgian Institute of Natural Sciences, Brussels, Belgium.

When analyzing DNA sequence data, it is common practice to create a multiple alignment prior to tree search, an approach that imposes unnecessary and unwarranted constraints on the analysis. Methods that do not require prior alignment have been available for over a decade. Such methods rely on a cost matrix that specifies the costs of base substitutions and on a gap function that specifies the costs of indel events. It is generally believed that these costs can only be specified or interpreted with reference to the evolutionary processes that generated the data. Observing that minimum mutation trees are not necessarily the trees that maximize similarity that can be interpreted as secondary homology, it is argued that setting substitution and gap costs such that they maximize secondary homology is the proper way to extend parsimony analysis to non-prealigned sequences instead. Some properties of this method are discussed.