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Abstract of presentation

Parsimony, indels, and explanatory power: an update

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At the 22nd meeting of the Willi Hennig Society (NYBG, 2003), I discussed how the conceptual framework of Steve Farris' 1983 paper 'On the logical basis of phylogenetic analysis' can be generalized to deal with unaligned sequence data. An interesting practical result was the recommendation to use what is now commonly called the 3221 parameter set when the aim is to maximize equally weighted explanatory power in analyses of such data (gap opening cost three, transversion cost two, transition cost two, and gap extension cost one). In this follow-up I address some criticisms that have been leveled against this (kind of) approach, review results obtained with the 3221 parameter set in empirical studies, and present some problems with the view that equally weighted explanatory power in such cases is instead maximized by setting all parameters equal. Some of those problems have been known for quite some time and remain unchallenged, some are new.