

Jan De Laet: Anagallis: a program for minimization of homoplasy in characters that are inapplicable in some terminals.

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In parsimony analysis, the problem of inapplicables can be overcome by maximizing the amount of similarity that can be interpreted as homology, an approach that I first discussed at WHS XXI (Helsinki 2002) and elaborated for the analysis of unaligned sequence data at WHS XXII (New York 2003). For the latter case, in programs such as POY, cost regime 3221 (gap opening cost three, transition and transversion costs two, and gap extension cost one) provides an optimal approximation of that approach when all instances of homology are equally weighted. Here I discuss a generalized notion of homoplasy that covers both cases, and present anagallis, the first computer program for parsimony analysis with an exact implementation of these ideas for inapplicables as they arise in the classic approach. Documentation and a Linux binary are freely available at www.anagallis.be.

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