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"The XXV annual meeting of the Willi Hennig Society, organized by the Instituto de Biología, Universidad Nacional Autónoma de México, took place from August 14th to 17th 2006, in Oaxaca City, México."

p. 87:

POY and the art of jackknife support justification. Jan De Laet. Leuvenstraat 20, Veltem-Beisem B-3020, Belgium

In phylogenetic analyses of datasets of unaligned DNA sequences by means of tree alignment methods (available in programs such as POY), base-level correspondences among observed sequences are not hypothesized prior to the analysis but instead arise as part of the results. This poses a problem when trying to assess group support by means of character jackknifing: positional characters, which would be the units of prior resampling, are not available until after the analysis. POY's jackboot command patches this problem by using an exclusion mask, a mask that is fixed within a given pseudoreplicate and that consists of a (long enough) sequence of zeroes and ones in which zero stands for exclusion and one for inclusion. When calculating the cost of a tree alignment during analysis of the pseudreplicate, this mask is applied to the positional correspondences as they are reconstructed in that particular tree alignment, and steps in positions that are excluded are not counted. One of the problems with this approach is that positional correspondences may be different between different tree alignments. Therefore, different trees that are considered optimal for a given pseudoreplicate may in fact have been evaluated with respect to different sets of included residues; trees that are optimal for a given pseudoreplicate are only guaranteed to have their exclusion mask in common, not the included residues on which their evaluation was based. In a less used approach, sequences are resampled at the level of individual residues: a pseudoreplicate dataset is constructed by randomly turning a given fraction of the observed residues into ''n'', indicating the presence of a further unspecified residue. In this approach, readily applicable to aligned datasets and morphological datasets as well, the resulting support values can be understood in terms of independent pair-wise similarity statements that can be explained as homology, an interpretation that is at a higher level of resolution than in the original parsimony jackknife procedure. Interestingly, this view allows for different support values for groups that are supported by the same number of characters but that differ in size, which raises the general question of calibration of jackknife support values.

[*I didn't make it to that meeting, so this never got presented.*]