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***Parsimony algorithms for characters that are inapplicable in some terminals.*** Jan De Laet, Department of Invertebrates, American Museum of Natural History, Central Park West at 79th Street, New York, New York 10024-5192, USA.

Almost a decade ago, Maddison (1993) discussed the problems that can arise with features that are not applicable across all terminals in a data set. Examples are tail color, when some terminals lack tails, or positions in DNA sequences in which gaps are present. After considering various ways of coding such features for various parsimony algorithms, Maddison concluded that no single coding method was satisfactory in general. Despite the fact that the problem of inapplicable characters has gotten quite some press since then, this conclusion still holds. Following Maddison’s suggestion that a proper solution would eventually entail the development of new algorithms, I discuss modifications of the algorithms of Fitch (1971) (nonadditive characters) and Wheeler (1996) (calculation of ancestral sequences and their costs in optimization alignment) that correctly deal with characters for which some terminals are scored as inapplicable. Maddison’s problems are not restricted to these two algorithms. The extension of Fitch’s (1971) algorithm is easily transferred to the algorithm of Farris (1970) (additive characters). The modification of Wheeler’s (1996) algorithm boils down to the use of a particular sequence distance. As such it can be equally well incorporated in algorithms such as Sankoff and Cedergren (1983) (tree distance of sequences), Hein (1989) (distance between sequence graphs), or Wheeler (1999) (fixed states analysis of sequence data).

#### References

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