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Panbiogeography: A Cladistic Approach

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Apparently several cladists regard their dendrograms as final scientific achievements, but what precisely must the taxonomists do with them — frame them to hang them on the wall? [A. D. Meeuse]

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Abstract

This thesis develops a quantitative cladistic approach to panbiogeography. Algorithms for constructing and comparing area cladograms are developed and implemented in a computer program. Examples of the use of this software are described.

The principle results of this thesis are:

(1) The description of algorithms for implementing Nelson and Platnick's (1981) methods for constructing area cladograms. These algorithms have been incorporated into a computer program.

(2) Zandee and Roos' (1987) methods based on "component-compatibility" are shown to be flawed.

(3) Recent criticisms of Nelson and Platnick's methods by E. O. Wiley are rebutted.

(4) A quantitative reanalysis of Hafner and Nadler's (1988) allozyme data for gophers and their parasitic lice illustrates the utility of information on timing of speciation events in interpreting apparent incongruence between host and parasite cladograms.

In addition the thesis contains a survey of some current themes in biogeography, a reply to criticisms of my earlier work on track analysis, and an application of bootstrap and consensus methods to place confidence limits on estimates of cladograms.