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## Implementation as theory, hierarchy as transformation, homology as synapomorphy

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### Abstract

Presently cladistics is based on, and justified by, a computer implementation (Wagner Parsimony) rather than sound methodological or theoretical foundations. In this paper, the recent goals of cladistics that are derived from computer implementations and ‘tree-thinking’ are discussed. The discussion raises a critical point, namely whether one can dispense with these recent goals and adopt a wholly systematic approach, one herein termed systematic thinking.

**Key words:** Cladistics, computer programs, homology, synapomorphy, systematic thinking, tree thinking

### Introduction

Cladistics developed from the works of Willi Hennig (1950, 1966) and Lars Brundin (1966) and has, over the last 30 years, created several conflicting hypotheses, but with one overarching methodology, namely Wagner Parsimony (see Williams & Ebach 2008; Schuh & Brower 2010).

Divorced from such methodology, cladistics is founded on a simple premise: two or more taxa are more closely related to each other than they are to any other taxon. Where this premise conflicts is when the term relationship (i.e., homology) is defined. This is clearly illustrated in the definition of homology given by Brower and de Pinna (2012):

*“Homology is the relationship among parts of organisms that provides evidence for common ancestry”* (Brower & de Pinna, 2012, p. 537, their italics)

Brower and de Pinna offer four properties:

*“This definition expresses the real world praxis of phylogenetic inference and applies to both layers of homology assessment, primary and secondary. Also, it places evidence where it belongs: before models. It does not specify that a hypothesized relationship is corroborated through parsimonious accounting of character-state transformations, although that is the method that we advocate. Nor does it assume a priori an evolutionary causal mechanism, although it implies that evolution is the best explanation for the observed pattern”* (Brower & de Pinna 2012, p. 537)

While none of this seems controversial, their final ‘property’ offers scope for further discussion:

*“Those familiar with phylogenetics are welcome to abbreviate our definition by replacing ‘synapomorphy’ for all that follows the verb ‘is’.”* (Brower & de Pinna, 2012, p. 537)

That is:

Homology = Synapomorphy.