

# WHAT THE HECK IS CLADISTICS?

Adapted from (UC Berkeley Museum of Paleontology) <http://www.ucmp.berkeley.edu/clad/clad4.html>

**Phylogenetics** = inferred reconstruction of evolutionary history (See excellent expansion at UCMP website)

## A. 3 methods of reconstructing phylogenies:

1. Phenetics (numerical taxonomy)
2. Evolutionary taxonomy
3. Cladistics - used to determine relative timing of divergences. The hierarchy, or ranking, of groups derives logically from their genealogical position. For example, birds and crocodiles derive from a common reptilian stem ancestor and are considered by cladists to be sister groups of equal rank in the taxon Archosauromorpha. Note that cladists do not follow the usual classification of ranking birds (Aves) as a class separate from the class of reptiles (Reptilia). Easiest and most commonly used technique today.

## B. 2 major goals of constructing phylogenetic relationships:

1. Clarify evolution of a group
2. Aid in the classification of the group

## C. Assumptions in cladistics:

1. The group of organisms to be studied is related by descent from a common ancestor
2. Descent follows a bifurcating pattern (ancestral form splits into 2 sister taxa, ancestor goes extinct). This is controversial. Many biologists hold that multiple new lineages can arise from a single population.
3. Change in characteristics occurs in lineages over time

## D. How to construct a cladogram:

1. Choose taxa (organisms must be "clades" = ancestor + inferred descendants)
2. Determine characters (this step is important and often the most difficult. Are similarities derived homologies or the result of convergent evolution?)
3. Determine polarity (characteristics defined as either ancestral ("plesiomorphic") or derived ("apomorphic").
4. Group by shared derived characters (called synapomorphies), homologies that have evolved after a branch diverged. Use nested sets called Venn diagrams)
5. Build cladogram. This is NOT an evolutionary tree showing which organism is descended from whom. Follow these rules: 1) All taxa go on the endpoints of the cladogram, never at nodes. 2) All nodes must have a list of synapomorphies which are common to all taxa above the node (unless character is later modified). 3) All synapomorphies appear on the cladogram only once unless the character state was derived separately by evolutionary parallelism. For example, anteater-like features have appeared in different lines of mammals that were descended from non-anteater mammalian groups.

## E. Resources/Background

VIDEO. "The case of the Flying Dinosaur" (NOVA). About \$20. Attempts to answer the question about the ancestry of modern birds. covers cladistics nicely, but briefly.

Golden Guide: *Dinosaurs*. A very portable, usable treatment of the anatomy and evolution of dinosaurs. Uses a cladistic approach. Great diagrams. About \$5.00.

1. Daniel R. Brooks and Deborah A. McLenna (1991). *Phylogeny, Ecology and Behavior*. University of Chicago Press. Chicago, USA 434 pgs.
2. Niles Eldridge and Joel Cracraft. (1980). *Phylogenetic Patterns and the Evolutionary Process*. Columbia University Press, New York, USA, 348 pgs.
3. Paul H. Harvey and Mark D. Pagel (1991). *The Comparative Method in Evolutionary Biology*. Oxford University Press, Oxford & New York, 239 pgs.
4. Wayne P. Maddison and David R Maddison. (1992). *MacClade: Analysis of phylogeny and character evolution*. Version 3.0. Sinauer Associates, Sunderland, MA, USA.
5. D.L. Swofford (1991). *Phylogenetic Analysis Using Parsimony (PAUP)*, version 3.0s. Illinois Natural History Survey. Champaign, Illinois, USA
6. E.O. Wiley, D. Seigel-Causey, D.R Brooks, & V.A Funk. (1991). *The Complete Cladist: a primer of phylogenetic procedure*. U. of Kansas Museum of Natural History, Spec Pub #19.