

Jan. 26, 2006. **Homology, or When are two things the same?**

The Hennig principle, as discussed last time, is as elegant and fundamental in its way as was Darwin's principle of natural selection. It is deceptively simple, yet profound in its implications. The controversy surrounding it is reminiscent in many ways of the furor over Darwinism in the 1800's, a conflict over different ways of looking at the world.

This drives home the point that we must pay close attention to both ontology and epistemology, and the feedback relationship between the two: A given method makes sense only if the world really is a certain way, yet the view we have of how the world is organized is dependent on the methods we have used.

For example, if species on earth are related genealogically and evolution is mainly by descent with modification (in a primarily diverging mode), then the Hennig Principle is the best method for reconstructing the history of life. Yet, the discovery of hierarchically nested characters is the best evidence we have on how evolution has occurred.

These concerns are relevant on a local level as well; the mere act of stating that two things are the same, or parts of two things are the same, is loaded with a (perhaps subconscious but nonetheless real) complex theoretical framework.

"Homology"

One of the most important concepts in systematics, but also one of the most controversial. What does it mean to say that two organisms share the same characteristic? [e.g., the Caminalcules-- see handout]

- classes versus individuals (type/token).
- classical, pre-evolutionary views (Cuvier, Owen)
- nominalistic views (many botanists, pheneticists)
- the need for ontology.
- evolutionary views: historical connectedness.
- synapomorphy (Patterson, Stevens)
- historical continuity of information (Van Valen, Roth)**

Ontology:

- Phylogenetic Homology (between organisms)
 - Taxic (= synapomorphy)
 - Transformational (plesiomorphy -> apomorphy)
- Iterative Homology (within one organism), e.g., Serial Homology or Paralogy (in molecular data)

(over)

Epistemology:

How do we recognize homology?

Best early codification of recognition criteria was that of Remane (See Wiley, 1981, pp. 130-158):

- position
- quality of resemblance
- continuance through intermediate forms

Also, an important contribution of the cladists has been the explicit formulation of a phylogenetic criterion:

**** a hypothesis of taxic homology of necessity is also a hypothesis for the existence of a monophyletic group ****

--Therefore, congruence among all postulated homologies provides a test of any single character in question [the central epistemological advance].

--Is this circular? A digression into general concerns in the philosophy of science; reciprocal illumination.

Patterson formulated these epistemological concerns in his three tests of homology:

- similarity
- conjunction
- congruence

Alignment of DNA. A certain prominent paleontologist who was at Harvard (who shall remain nameless, but his initials are S.J.G.) once proclaimed that comparisons of DNA have "solved the problem of homology." Is this true? The very simplicity of molecular characters (i.e., no ontogeny, few possible character states) actually leads to special problems with determining homology! We have essentially a one-dimensional string, although we may also have some additional dimensions added by structural constraints.

Some epistemological concerns:

- mismatches vs. gaps -- gap penalty?

Example: TCAGACGATTG Which is the best alignment?
 TCGGAGCTG [One approach: $D = y + wz$]

- | | | | | | |
|-------|---------------|--------|-------------|---------|--------------|
| (I) | TCAG-ACG-ATTG | (II) | TCAGACGATTG | (III) | TCAG-ACGATTG |
| | TC-GGA-GC-T-G | | TCGGAGCTG-- | | TC-GGA-GCTG- |

Coda: The process of systematics can be defined most simply in three words:
 "*Interpret homologies parsimoniously*" (Patterson)