1830's

- 1. homology the "same organ" in different organisms
- 2. analogy structures with the same function. Potentially "different" organs.

Reaction to Dowling paper

- 1. interest in snake phylogeny (first page, second column, last para)
- 2. interest in ranks (39 first paragraph ordinal rank discussion)
- 3. interest in anagenesis wrt ranks (39 second para comparison to mammals)
- 4. superfamilial categories phyletic units or "merely adaptive"? (39 second column)
- 5. want to find the primitive groups based on which "presumed primitive characters should be given the most phyletic weight" (39 second column)
- 6. lots of discussion of whether traits might be adaptive detecting homoplasy caused by convergence.
- 7. Textual, vague description of characters no character matrix. Table of character state distributions is nice, but even it has phrases like "absent in some Scincidae"
- 8. Page 41 ideal morphology approach. Lots of discussion about how traits could have evolved. On one hand it is thoughtful character analysis, but it is also *ad hoc* and would be hard to formalize or repeat.
- 9. Page 43 second column top. At times he seems to be aware that it is dangerous to group based on primitive states (discussion of Typhlopidae and Leptotyphlopidae).

- 1. Build the matrix: "score" characters states for each OTU.
- 2. Proceed to analysis/classification.
- 3. Pheneticists: objectivity, equally weighting, and large # of characters \rightarrow **similarity**
- 4. Cladists: emphasized homology of characters states, but objectivity and clarity too.

"deriving a conclusion based solely on what one already knows" $^{\rm 1}$

- logical
- statistical

¹definition from Wikipedia, so it must be correct!

Deductive reasoning:

- 1. start from premises
- 2. apply proper rules
- 3. arrive at statements that were not obviously contained in the premises.

If the rules are valid (logically sound) and the premises are true, then the conclusions are *guaranteed* to be true. All men are mortal. Socrates is a man.

Therefore Socrates is mortal.

Can we infer phylogenies from character data using deductive reasoning?

Premise: The following character matrix is correctly coded (character states are homologous in the strict sense):



Is there a valid set of rules that will generate the tree as a conclusion? Instances of the filled character state are homologous Instances of the hollow character state are homologous



Instances of the filled character state are homologous Instances of the hollow character state are NOT homologous



Instances of the filled character state are NOT homologous Instances of the hollow character state are homologous



Rule: Two taxa that share a character state must be more closely related to each other than either is to a taxon that displays a different state.

Is this a valid rule?

Here is an example in which we are confident that the homology statements are correct, but our rule implies two conflicting trees:

	placenta	vertebra
Homo sapiens	Ζ	Α
Rana catesbiana	Y	А
Drosophila melanogaster	Y	В

Z = "has placenta" Y = "lacks placenta"

A = "has vertebra" Y = "lacks vertebra"

Hennig's correction to our rule: Two taxa that share a **derived** character state must be more closely related to each other than either is to a taxon that displays the **primitive** state.

Here we will use 0 for the primitive state, and 1 for the derived state.

	placenta	vertebra
Homo sapiens	1	1
Rana catesbiana	0	1
Drosophila melanogaster	0	0

Now the character "placenta" does not provide a grouping, but "vertebra" groups human and frog as sister taxa. prefixes:

- "apo" refers to the new or derived state
- "plesio" refers to the primitive state
- "syn" or "sym" used to indicate shared between taxa
- "aut" used to indicate a state being unique to one taxon

Hennigian rules

- synapomorphy shared, derived states. Used to diagnose monophyletic groups.
- symplesiomorphy shared, primitive states. Diagnose icky, unwanted paraphyletic groups.
- autapomorphy a unique derived state. No evidence of phylogenetic relationships.
- constant characters columns in a matrix with no variability between taxa. **No** evidence of phylogenetic relationships.

We must:

- use the same character state only for homologous conditions,
- correctly polarize the character states (identify the directionality of the transformations – which state is plesiomorphic and which is apomorphic).

Homology: Remane's criteria

- Position,
- "special similarity", and
- continuity through ancestors

Practical rules, but not a theoretical advance.

How does one determine continuity if we don't know the tree?



We polarize based on:

- on developmental considerations,
- paleontological evidence,
- biogeographic considerations,
- **outgroup polarization** \leftarrow most common method