Phylogenetic Analysis
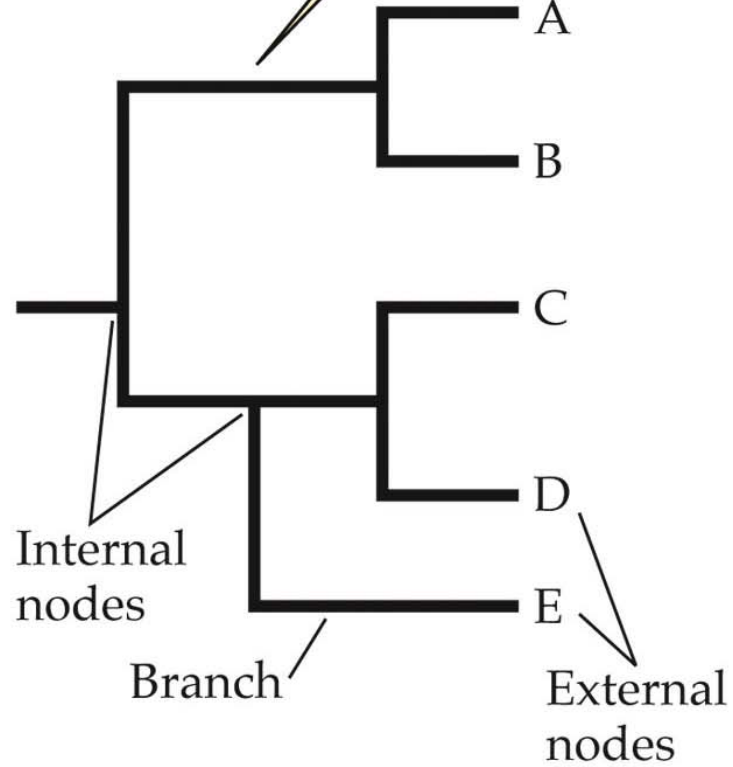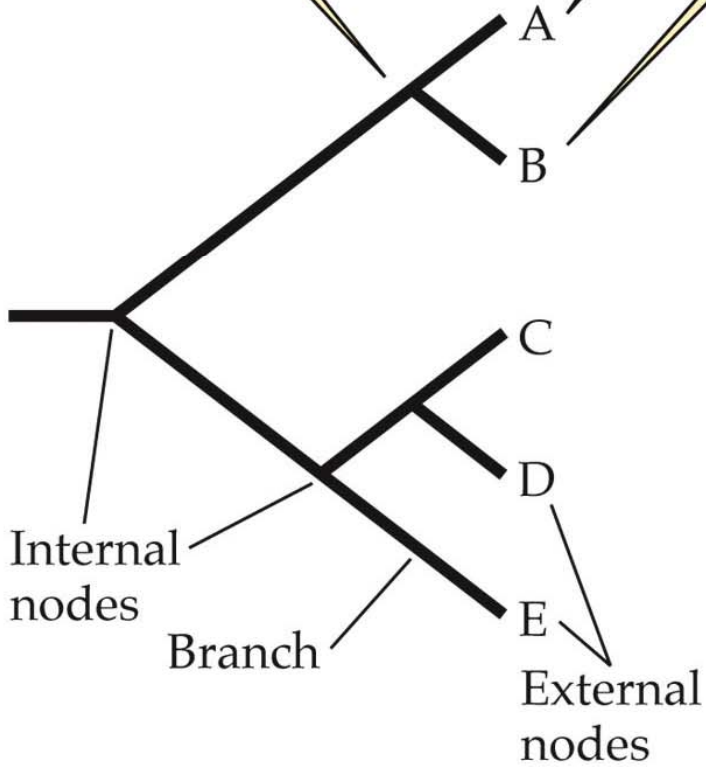
The phylogeny and classification of life a proposed by Haeckel (1866).
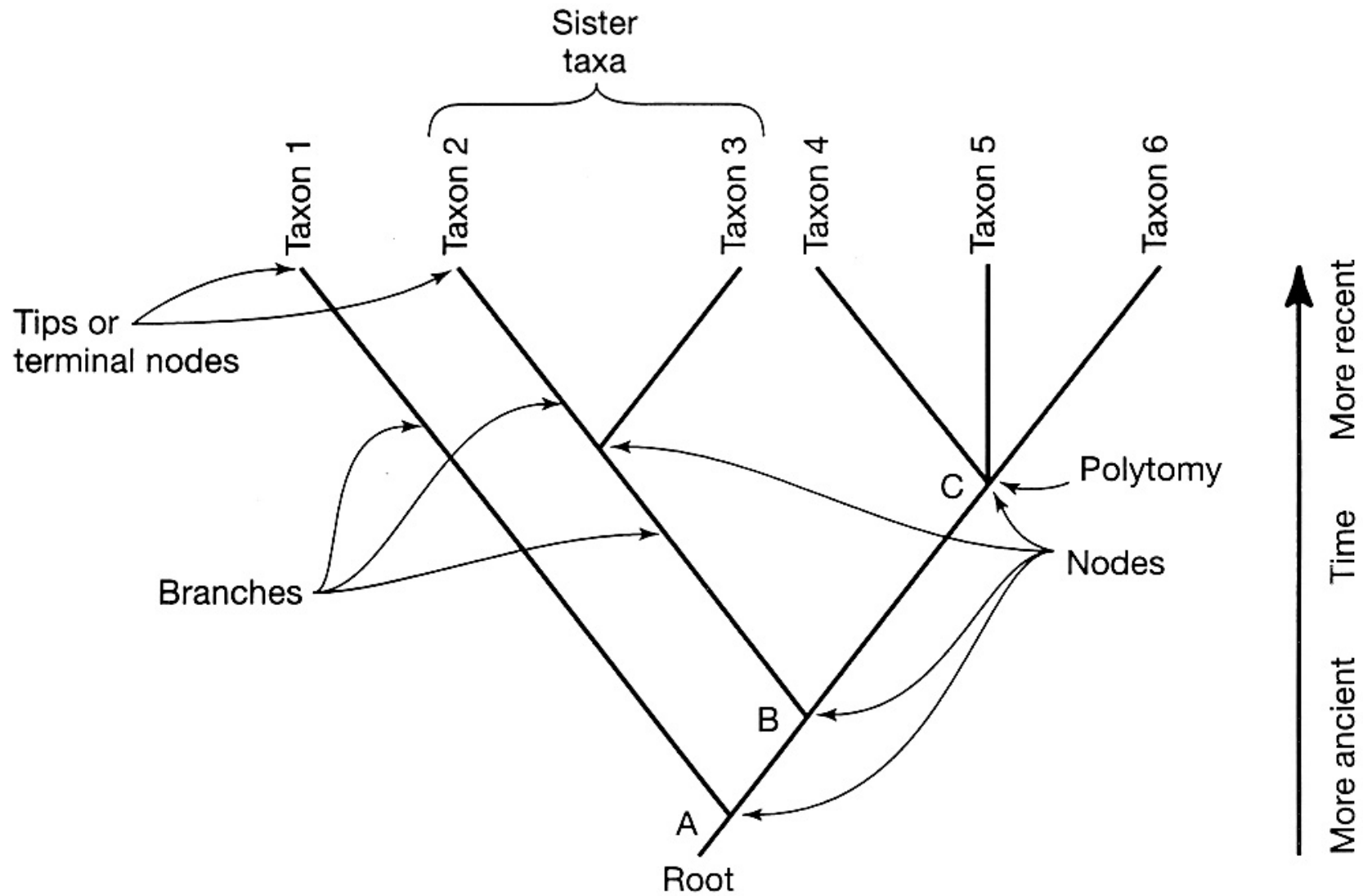
Internal nodes represent ancestor species…

…**external nodes** represent extant, known species…

…**branch** lengths represent evolutionary distance between species.

A

B

C

D

E

Internal nodes

Branch

External nodes

A

B

C

D

E

Internal nodes

Branch

External nodes

Parts of a phylogenetic tree In this hypothetical phylogeny, node A defines a monophyletic group, or clade, comprising taxa 1–6. Node B defines a monophyletic group comprising taxa 2–6. Node C defines a monophyletic group comprising taxa 4–6.

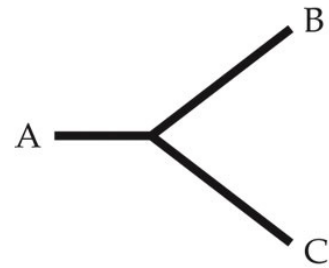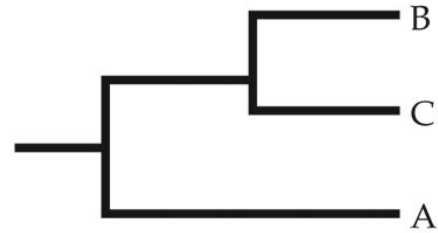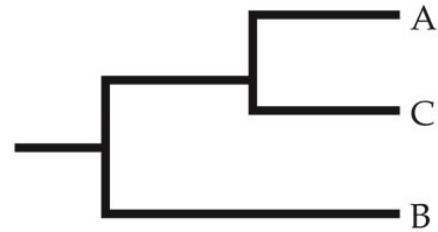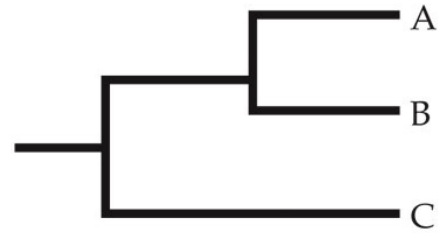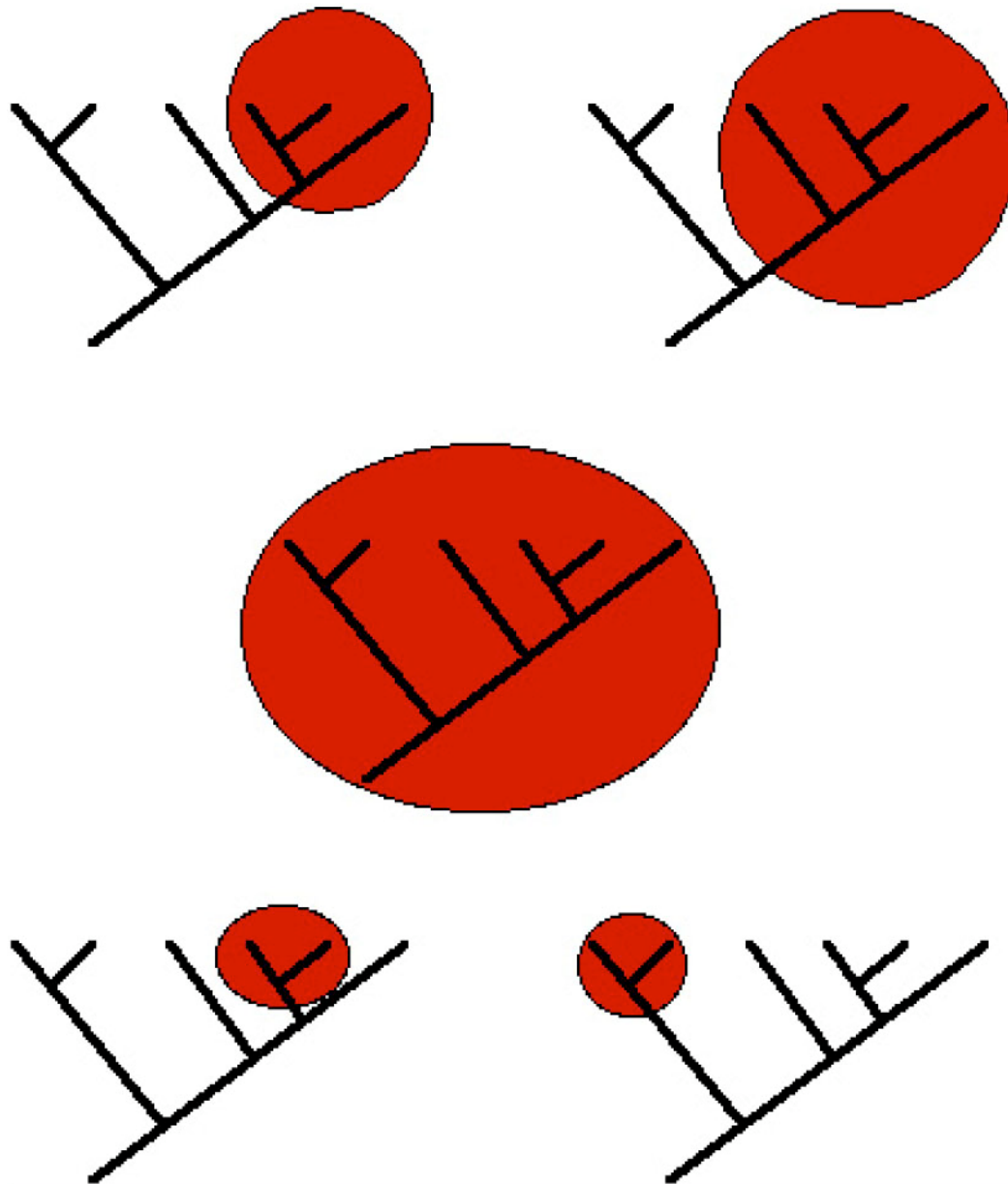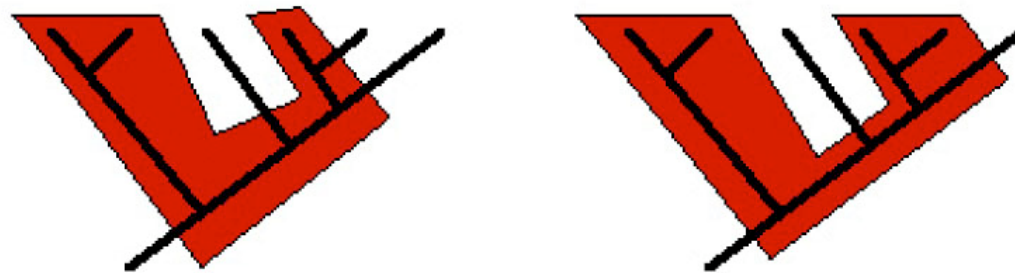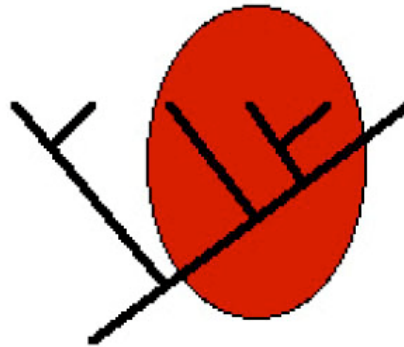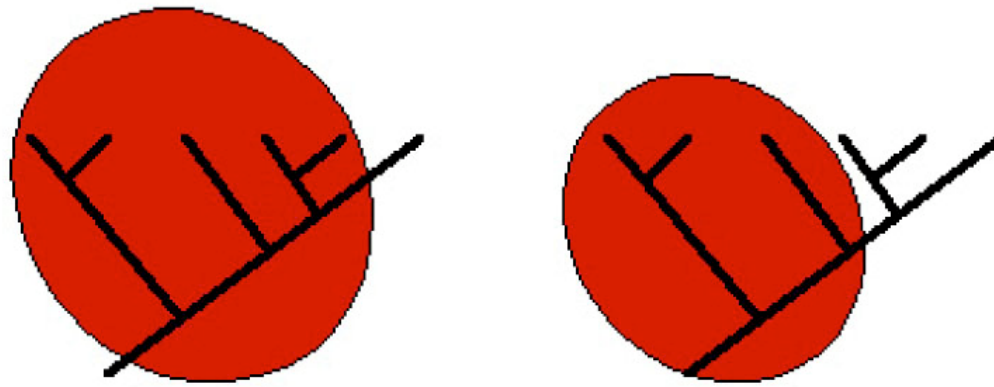# Trees - Rooted and Unrooted

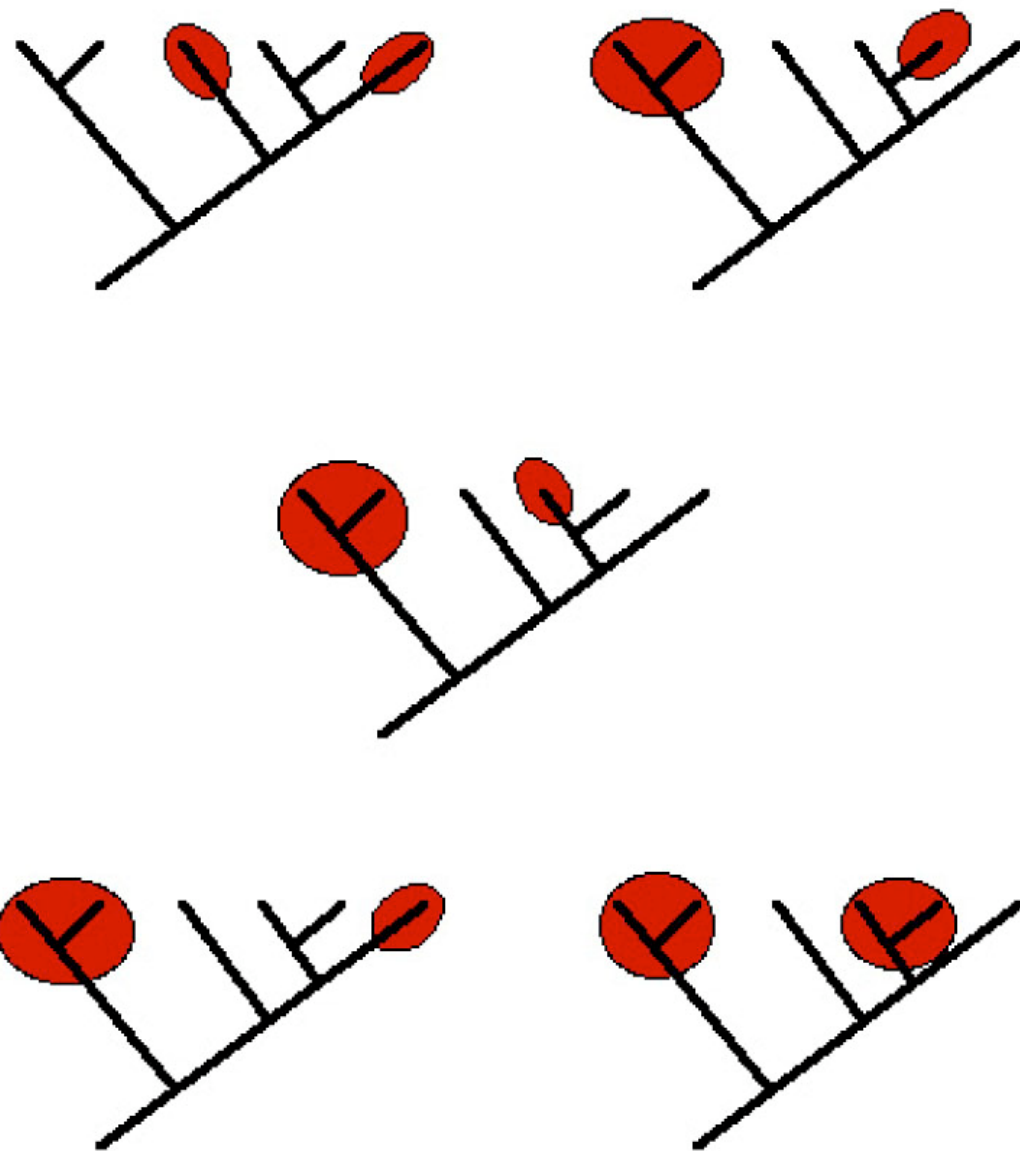(A) Unrooted trees
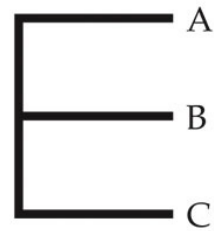
(B) Rooted trees

Monophyletic Groups

Paraphyletic Groups

Polyphyletic Groups

Monophyletic

one and
only one cut

One branch

Paraphyletic

one cut below the
group and one or more
cuts higher up

A piece of a branch

Polyphyletic

more than one cut
below the group

More than one
piece of a branch
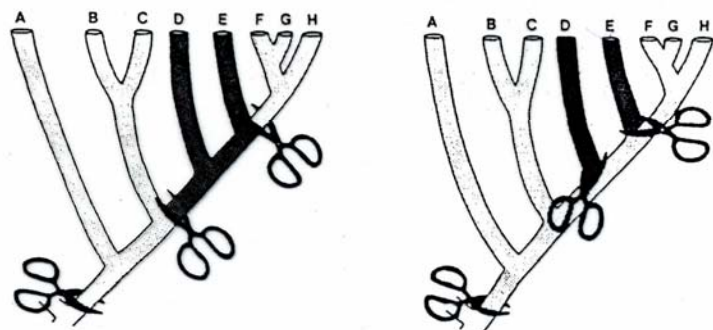
In the left-hand classification the group A-B-C-F-G-H is polyphyletic. It consists of two pieces of the tree diagram separated by two cuts above the stem line. The group D-E is paraphyletic. In the right-hand classification, the two monophyletic groups D and E are ranked equal with A-B-C-F-G-H, which then becomes paraphyletic. It is a clade with two subclades taken out but still a coherent piece of the diagrammatic tree.

Monophyletic: A group composed of a collection of organisms, including the most recent common ancestor of all those organisms and all the descendants of that most recent common ancestor. A monophyletic taxon is also called a clade.

Paraphyletic: A group composed of a collection of organisms, including the most recent common ancestor of all those organisms. Unlike a monophyletic group, a paraphyletic group does not include all the descendants of the <u>most recent</u> common ancestor.

Polyphyletic: A group composed of a collection of organisms in which the most recent common ancestor of all the included organisms is not included, usually because the common ancestor lacks the characteristics of the group. Polyphyletic groups are considered "unnatural", and usually are reclassified once they are discovered.

Character Evolution

- **Heritable** changes (in morphology, gene sequences, etc.) produce different character states.

- **Variability** in terms of similarities and differences in character states provide the basis for inferring phylogeny (i.e., provide evidence of relationships).

- **Independent** occurrence of different character states is a necessary requirement. The more frequent the better the resolution.

Theoretical advances in areas such as **phenetics** and **cladistics** have provided improved, empirical methods for framing and testing evolutionary hypotheses.
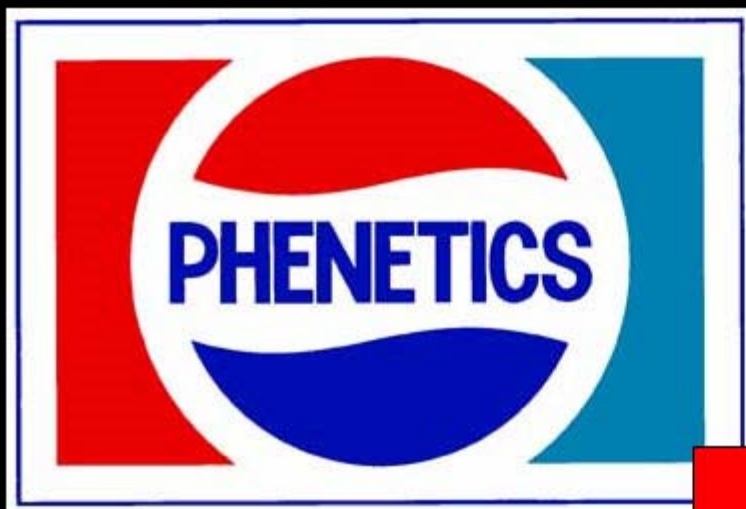
"overall similarity"

R.R. Sokal & P.H.A. Sneath (1963),
Principles of numerical taxonomy

W. Hennig (1963), *Phylogenetic Systematics*

"shared, derived characters"

(Designs by D. Maddison)

Numerical Taxonomy aka Phenetics

- Based on a numerical comparison of similarities and differences of a group of organisms.

- Gave a new sense of rigor. (eventually used computers!)
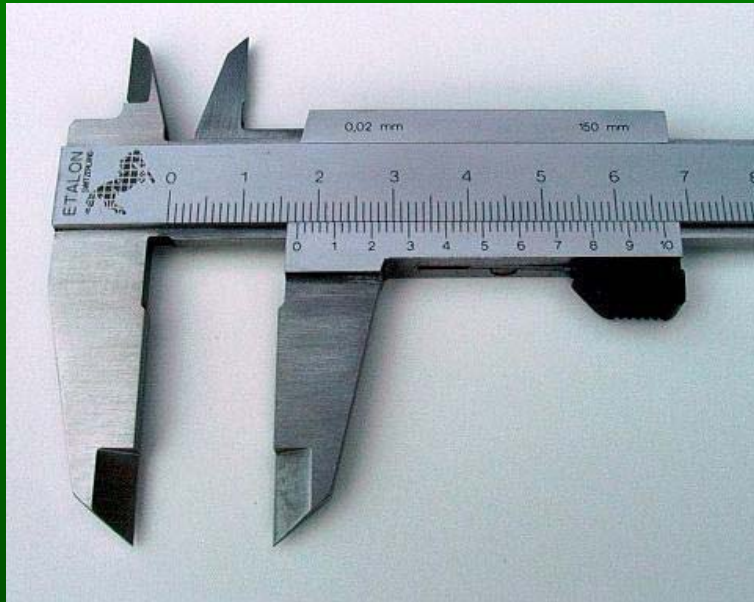
- The source of data: characters and character states.

1. CHOICE OF SPECIMENS

2. DISCOVERY & MEASUREMENT OF CHARACTERS

3. CODING OF CHARACTERS

n x t table

n characters	t OTU's					
		1	2	3	4	5
1	3	0	4	5	1
2	2	7	3	2	5
3	9	2	8	8	4
4	4	5	3	2	6
5	6	9	6	7	9

4. CALCULATION OF AFFINITY (SIMILARITY) BETWEEN SPECIMENS

% Affinity OTU's

OTU's	1	2	3	4	5
1	100				
2	51	100			
3	88	54	100		
4	85	53	86	100	
5	52	66	54	52	100

5. CLUSTERING OF SPECIMENS INTO PHENONS

% Affinity OTU's

OTU's	1	3	4	2	5
1	100				
3	88	100			
4	85	86	100		
2	51	54	53	100	
5	52	54	52	66	100

% Affinity
100
90
80
70
60
50

6. EXTRACTION OF DATA ON TAXA

Diagnostic Key

Ear with notch — tail ratio <0·9... 1
" " 0·9–1·1... 3
" " >1·1 ... 4
Ear without notch — Dorsal fur grey... 2
" " brown 5

7. IDENTIFICATION OF SPECIMENS

The Terminology of **Cladistics**

Synapomorphy: a shared, <u>derived</u> character state.
These are the basis of cladistics!

Autapomorphy: a unique, derived character state.

Symplesiomorphy: a shared, <u>ancestral</u> character state.

Only synapomorphies are used in order to avoid or minimize homoplasy.

Symplesiomorphy
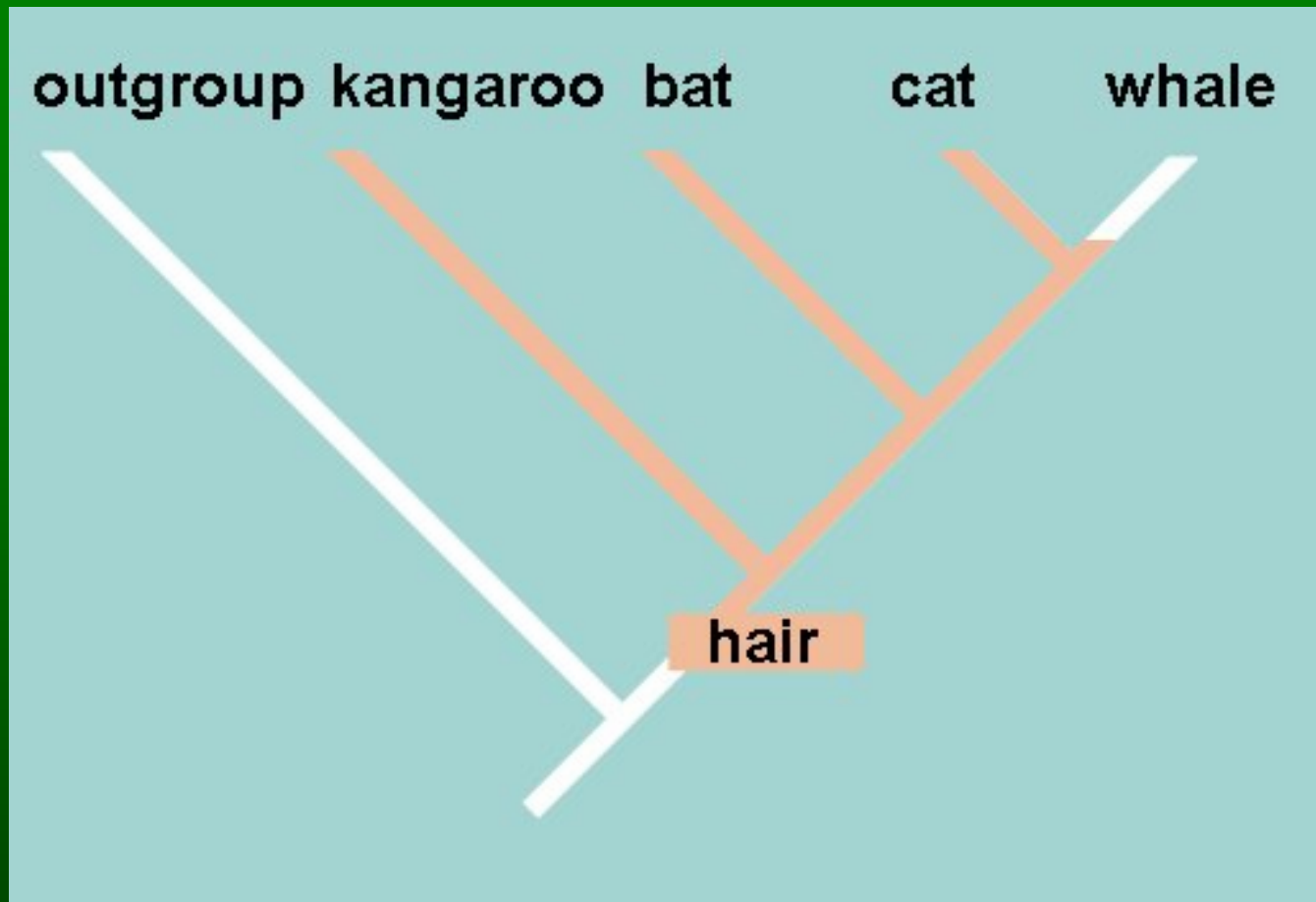
Within this taxon set, hair is a **shared ancestral character** (**symplesiomorphy**) of non-cetaceans. It would *not* indicate a close relationship of marsupial and placental mammals.

Cladogram of Mesozoic Birds
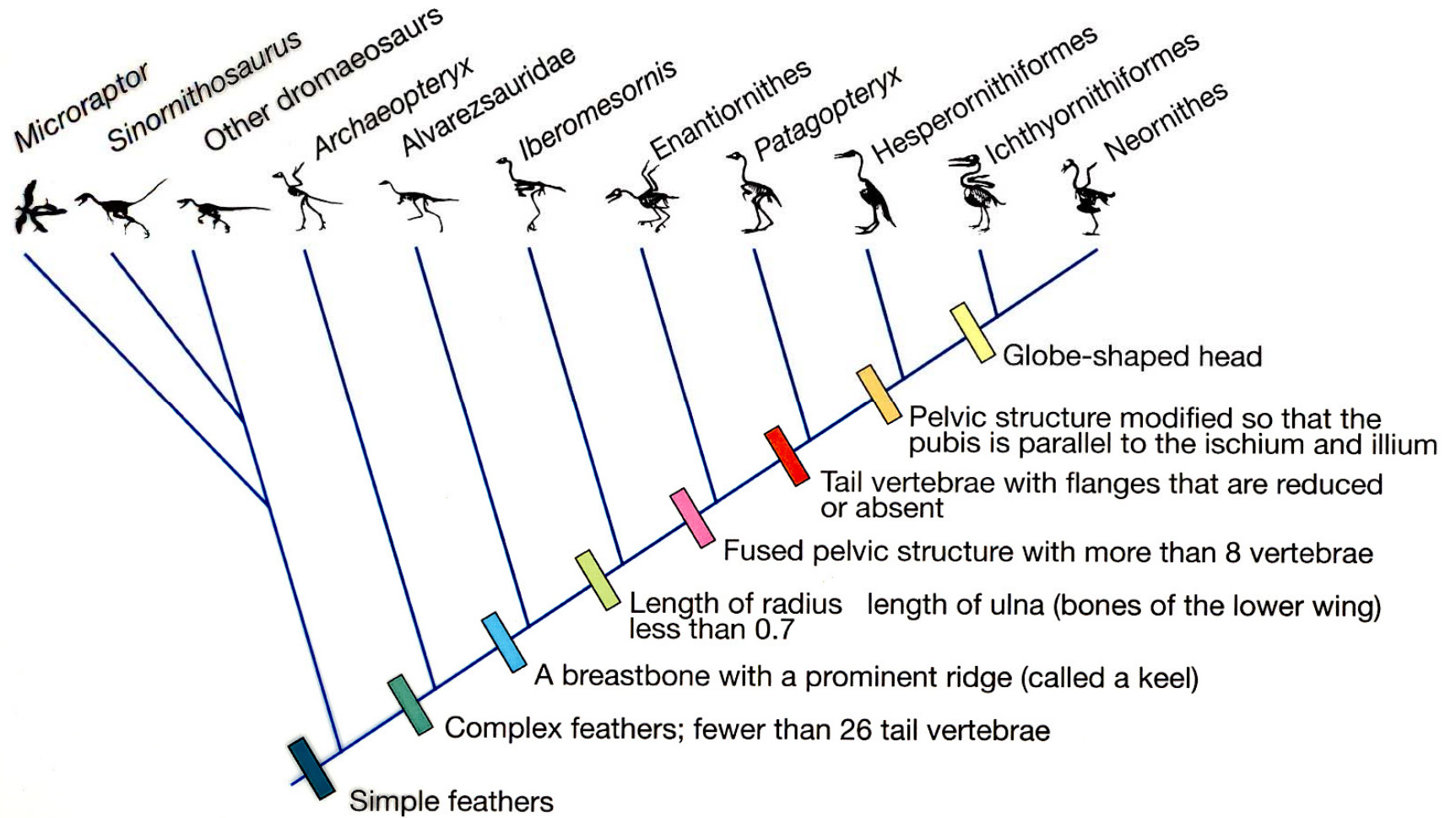

Microraptor

Sinornithosaurus

Other dromaeosaurs

Archaeopteryx

Alvarezsauridae

Iberomesornis

Enantiornithes

Patagopteryx

Hesperornithiformes

Ichthyornithiformes

Neornithes

Globe-shaped head

Pelvic structure modified so that the pubis is parallel to the ischium and illium

Tail vertebrae with flanges that are reduced or absent

Fused pelvic structure with more than 8 vertebrae

Length of radius length of ulna (bones of the lower wing) less than 0.7

A breastbone with a prominent ridge (called a keel)

Complex feathers; fewer than 26 tail vertebrae

Simple feathers

Why Might Similarities and Differences Be Unreliable for Inferring Phylogenies?

Homoplasy: similarity that is not homologous (not due to common ancestry). Can provide misleading evidence of phylogenetic relationships (if mistakenly interpreted as homology). Remember same as analogous structures or traits.

Parallelism refers to the independent evolution of the same derived trait via the same developmental changes.

Convergence refers to superficially similar traits that have a distinct developmental basis.

Reversal refers to return to the ancestral state. More problematic when considering molecular character data.

How Do We Improve on Cladistics?

• **Ockham's Razor** - "entities should not be multiplied unnecessarily" aka the KISS system.
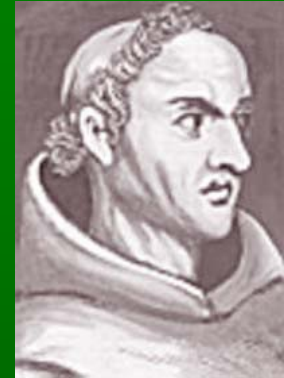
• **Parsimony** - the best estimate of phylogeny requires the fewest evolutionary changes to explain the distribution of shared derived character states (synapomorphies) in the organisms.

• **Maximum Parsimony** – exhaustive examination of all possible trees, where trees with the fewest inferred changes between character states are the maximum parsimony trees.