In 1763 Adanson (1727-1806) - a contemporary and rival of Linnaeus founded Empiricism in taxonomy.


Method -

- Observe and record as many characters as possible
- Group the species according to the majority of shared characters.
- A species consists of individuals with a maximum number of shared characters.
- A genus consists of species with a maximum of shared characters.
- A family etc....
- Membership in a group did not require sharing all the characters.

More Terminology - From Brooks and McLennan –

**Taxon:** Any named group of organisms.

  - Family
  - Genus

Example: Aves - includes exactly the same organisms whether it is ranked as a

  - Class
  - Order
  - Family

**Natural Taxon:** group of organisms that exists as a result of evolutionary processes. These groups exist whether they are named by us or not.

  2 kinds of natural taxa.

  1) Species - a lineage or group of organisms that share a unique evolutionary history and is held together by cohesive forces of reproduction and development.

     - Every species has a unique historical origin.

  A) **Cladogenesis** - lineage splitting from a parent species into two new daughter species.
B) **Reticulate Speciation** - formation of new species through the hybridization of two ancestral species.

2) **Monophyletic Group** or **Clade**
   - A group of taxa encompassing an ancestral species and all of its descendants.
   
   - Members are bound together with a common ancestral relationship that they do not share with any other taxa.

   *Each monophyletic group begins as a single species, the ancestor of all subsequent members of the clade.*

**Speciation**: The formation of new species via either cladogenesis or reticulate-hybridization.

---

[Diagram: Ancestral species and new species formation via hybridization]

<table>
<thead>
<tr>
<th>A</th>
<th>B</th>
<th>C</th>
<th>D</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>A</td>
<td>B</td>
<td>C</td>
<td>D</td>
</tr>
</tbody>
</table>

Speciation via hybridization
Some observations --

* **Species give rise only to species** - The study of phylogeny is the study of species and their formation via cladogenesis or reticulation (hybridization).

* **Higher level categories** (above the level of the species) are only figments of our imagination. That is, they do not exist in nature. Only species actually exist shown and discussed in the first lectures.

* **Artificial Taxa** - represents an incomplete or invalid evolutionary unit. [Humans produce artificial taxa - evolution does not]

* **Paraphyletic group**: One or more descendants of an ancestor are excluded from the group. See fig 2.4 Brooks and McLennan. P -28

**Genus with species**
- Species a
- Species b

**Genus with species**
- Species d
- Species e
- Species c

* **Polyphtyletic group**: Taxa that are separated from each other by more than two ancestors without including all the descendants OF their common ancestors.

* **Classic example**: a classification that placed birds and mammals as sister taxa in the same clade

* **Ingroup**: Any group of (hypothetically) closely related organisms of interest.

* **Choice of Ingroup**: Constrained only by the rule that it must contain more than 2 species - it is impossible to determine the phylogenetic relationships on only two species.

* **Sister group**: taxon most closely related genealogically to the ingroup.

* **Natural classification**: Contains only monophyletic groups.
The phylogenetic tree can be reconstructed from the classification.

* Artificial classification: Contains one or more paraphyletic of polyphyletic groups. The phylogenetic tree cannot be fully reconstructed from the classification.

* Arrangement: Classification of a group whose phylogenetic relationships have not yet been studied. *cannot convert to a phylogeny then because the relationships are unknown.

* Characters: Can change from ancestor to descendant or can remain the same from ancestor to descendant.

  If the character changes it is novel (new)

    Ancestral character: plesiomorphic character (plesio = close to stem) (morpho = shape)

    Descendant character: apomorphic character (apo = away from stem) (morpho = shape) Derived character.

Synapomorphy: Character that unites two or more derived species.

Autapomorphy: Character that is found only on one species or a terminal taxon on a phylogeny.

Symplesiomorphy: -Character that unites a group of species, -Provides no data on the relationships among the species

Transformation Series: (P 34)

  Collection of 2 homologous character states: 0<—> 1 (Binary)
  Collection of 3 or more homologous character states: 0—1—2—3

Ordered Transformation Series - only one way that state 2 could have come about.
**Unordered Transformation Series** - may be several routes that resulted in state changes observed.

Examples of the possible ordering / polarizing options for character transformation series:

- **Ordered polarized**
  
  \[
  0 \rightarrow 1 \rightarrow 2
  \]

- **Ordered unpolarized**
  
  \[
  0 \rightarrow 1 \rightarrow 2
  \]

- **Unordered - unpolarized**
  
  \[
  0 \rightarrow 1 \rightarrow 2
  \]

- **Unordered polarized**
  
  \[
  0 \rightarrow 1 \rightarrow 2
  \]
Polarized transformation series (Relative apomorphic and plesiomorphic states have been determined). Hypothesis of which character state is the ancestral and which is the derived.

**Character Argumentation:** logical process of determining which characters in a transformation series are plesiomorphic and which are apomorphic based on outgroup comparison.

also called: **Polarizing the Character States:**

**Polarity:** Plesiomorphic or apomorphic states of a character.

**Character Optimization:** how character states should be polarized given a particular tree shape or topology.

Can use 0 for plesiomorphic or 1 for apomorphic states - or vice versa (consistent).

Can use A for ples. Or B for apo.
Paraphyletic groups

Group 1

Species a
Species b

Group 45

Species c
Species d
Species e

Ancestor 4
Ancestor 3
Ancestor 2
Ancestor 1

Polyphyletic groups

Species b
Species a
Species c
Species d
Species e

Ancestor 4
Ancestor 3
Ancestor 2
Ancestor 1

Hennig Argumentation:
Assume a universal tree of life on the planet. All life arose from a single event.

- attempting to construct phylogenetic trees
- taxa are placed in correct genealogical position
- character states are placed where they arose

– Ancestor in which character x arose (and all of its descendants) have character x (in this case stomata).

**Hennigs Auxiliary Principle:** IN THE ABSENCE OF CONTRARY EVIDENCE
– Always presume homology. Never presume convergent or parallel evolution.

Powerful Principle: Without this assertion – we could assume that all
characteristics probably arose multiple times via convergence or parallel evolution.

-Vertebral Column or backbone in Vertebrates.

Argument -
:: All backbones in all species look similar
:: All backbones in all species perform a similar function
:: All backbones develop from the same embryological precursor tissues

Therefore:
:: All backbones are homologous - an a-priori hypothesis that can be tested.

**Empirical Observation**: Replicaiton rates are always higher than rates of mutation - thus this is a very defensible a-priori criterion.

**Kluges Auxillary Principle**: Always presume character independence in the absence of evidence to the contrary.

**Relative Apomorphy Rule** [Outgroup comparison]:

Homologous characters found within members of a monophyletic group that are also found in the sister group are **plesiomorphic**.

Homologous characters found ONLY in the ingroup are **apomorphic**.

Outgroup comparison is used to polarize characters.
**Outgroup Rule:** Given two characters that are homologues and found within a single monophyletic group,

– the character that is also found in the sister group is the plesiomorphic character

– the character found only in the monophyletic group is the apomorphic character

**Outgroup:** Any group of taxa used for comparative purposes in a phylogenetic analysis.

– Choice of an outgroup is constrained by the rule that it cannot contain any members of the ingroup.


**Ingroup:** Group on which we are working. (See p 41)

**Resolved or Unresolved:** (polytomy or dichotomous branching).

**Decisive or Equiocal:** (state of character known at node or unknown at node).

On Monday we will go over pages 43 - 44 - 45 and work through the examples.
Common does not equal plesiomorphic (primitive) in the phylogenetic system.

What happens if we switch outgroups?

1) No change in the transformation series polarities because both outgroups share the same plesiomorphic state with the ingroup for all characters in the analysis.

Or

2) Cannot determine the plesiomorphic and apomorphic states for some characters because the outgroup is too far away from the ingroup.
   Not enough similar characters

Or

3) There will be a change in polarity of some of the TS because the new outgroup shares some homoplasious character states with the ingroup. This might not change the topology of the outgroup, or it might make more polytomys.

The more resilient your tree to changing outgroups, the more confidence you can have in your tree.
Terms that we will know and use in this course.

ancestral taxon
apomorphy
autapomorphy
artificial taxon
branch
branching diagram
branch point
character code
character tree
clade
cladogram
data matrix
genealogical descent
ingroup
ingroup node
internode
monophyletic group
natural taxon
node
outgroup node
paraphyletic group
phylogenetic tree
plesiomorphy
polyphyletic group
polytomy
relationship
root
sister group
symplesiomorphy
synapomorphy
taxon
1) Draw the cladogram (fig. 2.10). Label the nodes.

```
M    N    O    P    Q    R
   /     |     |     |     |
  /      |     |     |     |
 /       |     |     |     |
R
```

Use the data from: page 43.

Character Transformation Series

<table>
<thead>
<tr>
<th>Character 1.</th>
<th>Taxon</th>
<th>Several in</th>
</tr>
</thead>
<tbody>
<tr>
<td>TS</td>
<td>M</td>
<td>N</td>
</tr>
<tr>
<td>1</td>
<td>b</td>
<td>a</td>
</tr>
<tr>
<td>2</td>
<td>b</td>
<td>b</td>
</tr>
</tbody>
</table>

2) Map on the first transformation series to the outgroups and the outgroup node.

3) Make decisions and label the nodes -

- label the node “a” if the 2 closes nodes or branches are both “a” or are “a” and “a,b”
- label the node “b” if the 2 closest nodes or branches are both “b” or “b” and “a,b”
The analysis is over when we reach a decision concerning the outgroup node.

Each decision is made on transformation series at a time
- polarization of each character is independent of each other character.
- final disposition of character states will be subject to an overall analysis
- a series of formal rules that will be used to determine the final states

**Grouping Rule:** Only synapomorphies provide evidence of common ancestry. Sympleiomorphies (shared general homologies do not help in understanding relationships within an ingroup).

How do we combine information from different transformation series to a general hypothesis of relationships for the group in which we are interested?

**Inclusion / Exclusion Rule:** Can combine information if there is either
1) complete inclusion or
2) complete exclusion of groups fromed by the separate TS analyses.

-We will come back to this idea when we talk about tree comparisons.