Understanding and Creating Phylogenetic Trees

I. What is a phylogenetic tree?
A. What is a phylogenetic tree?
   1. The evolutionary history of a group of taxa is called its phylogeny.
   2. The phylogenetic tree is a graphical, representation of those relationships.
      a. Think of it as a family tree.

B. Brief history of phylogenetic trees.
   1. Phylogenetic analysis has historically associated with classification and the naming of organisms (known as taxonomy).
      a. However, phylogeny is something that occurred,
      b. Whereas classification is an artifact of people – it is creation of the mind to categorize.

II. Characteristics of Phylogenetic trees.
A. Some terminology.
   Character state – One of the variant conditions of a character (e.g. melanic or typical moth color. Or presence and absence of a trait. ).
   Derived character state - same as apomorphy; a derived character / trait is inferred to be a modified version of a more primitive condition of that character and therefore inferred to have arisen later in the evolution of the clade

   Clade - a group of organisms that share a common ancestor; lineage; a monophyletic group.

   Monophyletic group - terms applied to a group of organisms that includes an ancestral species and all of its descendants; e.g. Aves, Mammalia. This group is a complete branch of the tree of life, the phylogeny of life. Such a branch is called a clade.

   Homologous (homology)- Possession by two or more species of a character state derived, with or without modification, from their common ancestor.

   Synapomorphies – A derived character state that is shared by two or more taxa and is postulated to have evolved in (been modified by) their common ancestor.

   Synapomorphies are integral to studying phylogenetic trees because:
   a) they identify evolutionary branch points
   b) they are nested. As you proceed from the base of the tree to the tips, each branching event adds one or more shared, derived traits.

   Cladogram (syn. dendrogram, phenogram)– A phylogenetic tree inferred by clustering synapomorphies. Cladograms only show the branching order. They display no information on the relative timing of events leading to the branch points (nodes –where a branch ends. Nodes at the tips of branches represent taxa (sequences if it’s DNA data)). A cladogram displays only the topology of the tree.
**Phylogram** – A phylogenetic tree (a type of **dendrogram, or phenogram**) that not only displays branching order, but conveys a sense of time as to when the branching events occurred. Branch lengths are proportional to the amount of inferred evolutionary change.

III. Difficulties in Creating Phylogenetic trees – Homoplasies

A **homoplasy** is a character state that has independently evolved two or more times and does not have a unique origin. (It is written that a character state is homoplasious.)

A. Convergent evolution.
   1. Two taxa may share a similar traits, but are they homologous?
      a. E.g. the flipper of shark and a penguin were derived separately.
      b. We can develop a degree of confidence about this by examining the synapomorphies of penguins (or sharks) and realize that they share many more traits with other birds than they do sharks.
      c. The evolution of similar features independently in different taxa is called **convergent evolution**.

B. Reversals
   1. A derived trait can revert to an ancestral trait either through a mutation, or selection.
   2. Reversals provide misleading evidence about the order in a phylogeny and they can remove similarity that is caused by descent from a common ancestor (the reversal means that the two descendants of an ancestor do not share the derived trait.)

III. Resolving conflicts –

A. A cladistic approach.
   2. Hennig pointed out that taxa may be similar because they share:
      a. Uniquely derived character states
      b. Ancestral character states.
      c. Homoplasious character states.
   3. When inferring a phylogenetic tree, we can rule out homoplasious characters.
      a. Hennig said that evidence that species share a more recent ancestor with each other than they do with any other species is provided only by shared derived (advanced) characters that evolved in the species’ common ancestor.
      b. Thus, they form a monophyletic group.
      c. E.g. the placenta is a derived character that provides evidence of the common ancestry of horses, humans, and other eutherian mammals;
      d. But the primitive character state (lack of a placenta) does not tell us that animals without a placenta (birds, reptiles, fishes, and for that matter, insects and sponges) are more closely related to each other than they are to mammals (as they indeed, are not).
5. To make a phylogenetic tree, we can only consider the similarity due to uniquely derived character states. But this presents a problem.
   a. How can we tell which state of a character is derived?
   b. How can we tell whether it is uniquely derived or homoplasious?

6. Hennig’s approach is the root of **cladistics**.

7. Contrast with **Phenetics** – A system of classification of species based on the degree of overall similarity based as many features as possible.
   a. A **phenogram** does not necessarily represent phylogenetic relationships – it is a representation of how species are grouped based on the number of character states that they have in common.

B. **Parsimony** –

1. Parsimony is the principle that the simplest explanation which requires the fewest undocumented assumptions should be the preferred over more complicated hypotheses.
   a. The preferred tree is the one that minimizes the total amount of evolutionary change that has occurred.

2. The rationale for invoking parsimony is simple –
   a. Convergence (evolution) and reversals should be relatively rare compared to taxa that are similar due to modification from a common ancestor.
   b. That is, synapomorphies are likely to be more common than convergent evolution or reversals.
   c. By assuming that convergence and reversals are rare, a phylogenetic tree is made that minimizes the amount of homoplasy.

3. Parsimony results in the **best estimate** of the actual phylogenetic relationships, but there is no “correct” or “right” phylogenetic tree.