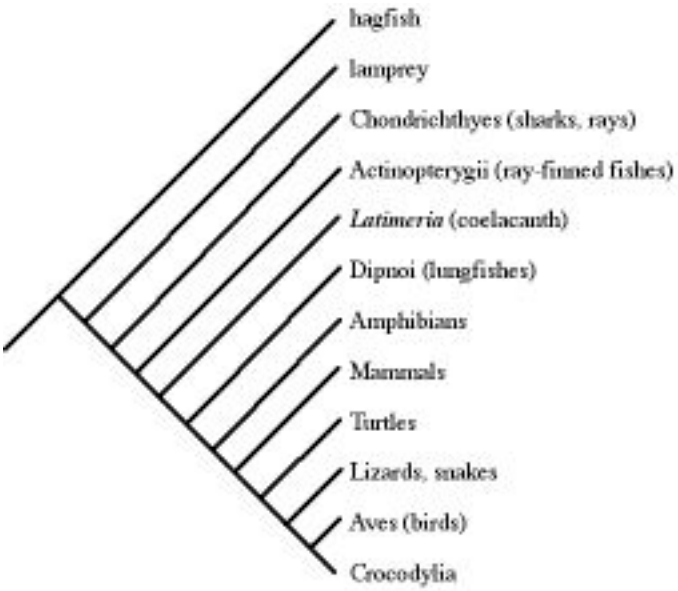
Lecture 2: Systematics: Phylogenetics and Classification

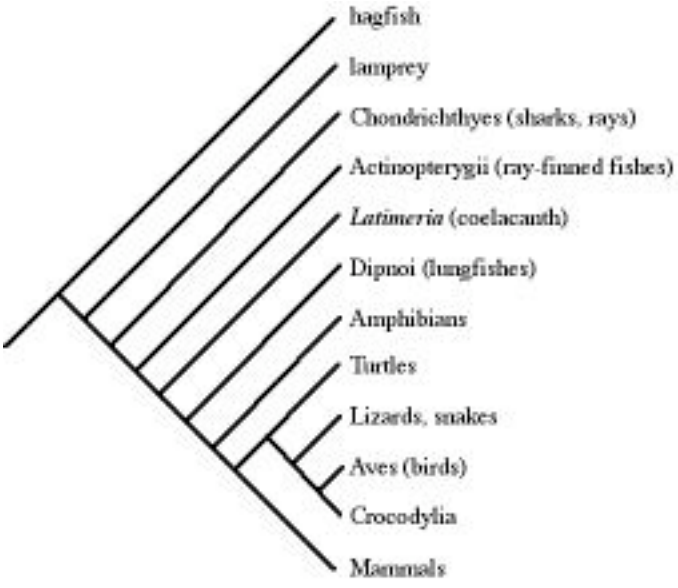
1. Historical classification (Classes) – Universal until about the 1980's
    a. Species
    b. Genus
    c. Family
    d. Order
    e. Class
    f. Phylum
    g. kingdom
2. Historical classification of vertebrate Classes
    a. Fish
        i. Lungfish
        ii. Sharks and rays
        iii. Goldfish
    b. Amphibians
        i. Frogs
        ii. Salamanders
    c. Reptiles
        i. Turtles
        ii. Snakes
        iii. Lizards
        iv. Alligators
    d. Birds
    e. Mammals
3. This classification is unsatisfactory but to understand why we need to look at both how organisms were classified and how modern classification systems work
4. First, a definition: Taxa – a group of organisms that are classified together into a single named group. The group can be at any level (species, genus, family, order, etc. etc.)
5. historical systems of classification were based on one or two criteria:
    a. presence of some character (or set of characters)
    b. absence of some character (or set of characters)
6. For example:
    a. Mammals were defined by presence of hair and nursing behavior
    b. Birds were defined by presence of feathers
    c. Reptiles were defined by presence of amniotic egg (also in birds and mammals) and absence of feathers (birds) and hair/nursing behavior (mammals)
    d. Amphibians were defined by presence of limbs (also in reptiles, birds, and mammals) and absence of amniotic egg
    e. Fish were defined as swimming vertebrates that have fins instead of limbs
7. Isn't it kind of weird to define something by what it doesn't have?
8. Definition break number two: Phylogeny – a graph that illustrates the relatedness among taxa. Phylogenetics is the study of how to make phylogenies or the process of making phylogenies.
9. Phylogenetic trees showing the relatedness of different taxa were used and these trees tended to show some groups arising out of other groups (e.g. birds and mammals arising from reptiles). Also, many classical phylogenetic trees were drawn with a time scale.

10. What we have then is a system with methods that pre-date Darwin and the concept of descent from a common ancestor. Relatedness is not a criteria used to classify because people had no quantitative way to measure relatedness. Instead, biologists understood relatedness based on the classification (conspecifics more closely related to congenerics, congenerics more closely related to confamilials, etc. etc.).
11. This led to a general dissatisfaction with systematics in the 1950s and a revolution in the way systematics is currently practiced.
12. Two different schools of solutions developed. **Importantly both schools reversed the methodological order, so that relatedness was estimated first, and then a classification was developed to reflect this relatedness. Thus the development of phylogenetic systematics, which is a system of classification based on phylogeny.**
    a. Phenetics
        i. The phenetics school based relatedness on overall similarity (presence of shared characters)
    b. Cladistics
        i. The cladistics school based relatedness on presence of shared, **derived** characters
    c. Both of these systemds are quantitative, that is a taxon by character matrix is created and analyed. We will do this in lab.
    d. So, What's the difference?
    e. The logic behind phenetics is that the more characters that are shared by two taxon the more likely they are closely related.
    f. The logic behind cladistics is that only shared, derived characters are evidence of relatedness, while shared primitive characters are not. This makes a lot of sense if we think about evolution of new taxa as a branching process. So for example, Both humans and alligators have limbs with five fingers while horses have limbs with only 1 finger. The presence of five fingers is not informative in this comparison because five fingers is primitive in this comparison (i.e. present in the last common ancestor of horses, humans, and alligators).
    g. The problem with cladistics as a methodology is determining what is derived and what is primitive because to unambiguously know something is derived you have to have some idea of the relatedness but then this is what you are trying to infer.
    h. Phenetics vs. Cladistics was a huge debate in the 70s and 80s that essentially went nowhere until about 1990 when someone came up with the brilliant idea of evolving thousands of virtual organisms with known phylogenies and then applying the different methods and seeing which worked best.
    i. This has led to the ultra-Modern methods of inferring phylogenies based more on statistical methods (likelihood, Bayesian) than some a priori logical model (total similarity vs. shared, derived characters). We will not get discuss these methods.
13. Modern systematics uses trees to illustrate relatedness (phylogenetic trees) but these do not show groups evolving from groups and do not have a time scale. These trees are dichotomously branching diagrams called cladograms. In order to be able to understand anything about modern comparative anatomy, or modern biology in general, you really, really, really need to understand the information in a cladogram – both what it does and does not contain.

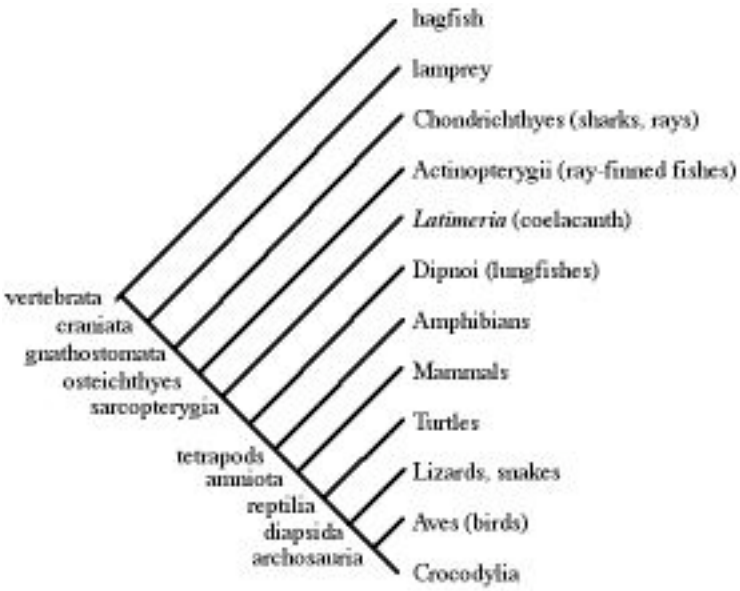
14. Cladograms show the relative degree of relatedness period. They do not show the magnitude of similarity, the timing of lineage splits, or the origins of groups from other groups
15. Modern classification systems are based on the hierarchical organization of the cladogram. This presents three problems that really bothered classical systematists (part of the phylogenetic debates of the 70s and 80s).
    a. As cladograms are revised so is the classification, which would seem to make a phylogenetic classification unstable.
    b. There are literally thousands of hierarchical levels in the tree of life so how to we give each of these levels a name (both generic and specific)
    c. Where to put extinct taxa and the problem of "ancestors"
16. Here is a modern cladogram of vertebrate relatedness



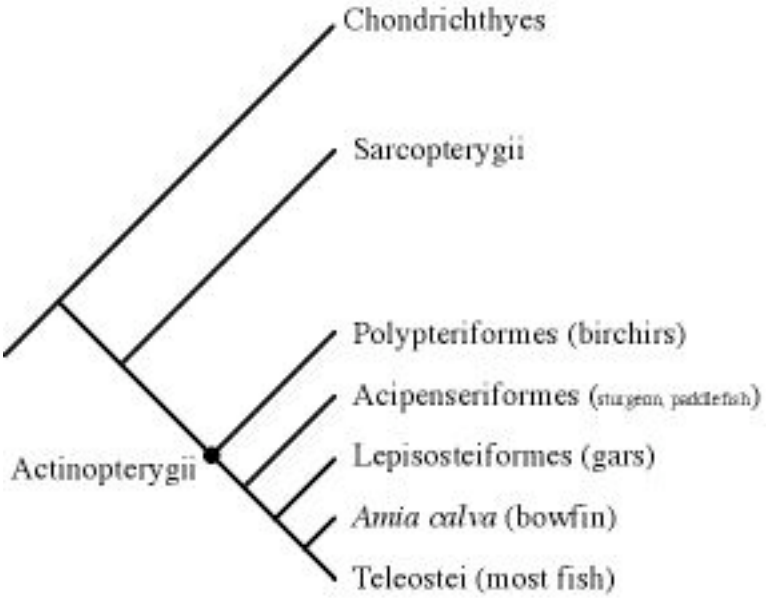
17. is this the same cladogram as above?



18. Yes! It shows the same set of sister taxa
19. Back to classification – names of more inclusive taxa



20. Glossary of terms
    a. Taxa
        i. Sister groups – two taxa that share a common ancestor (Aves and Crocodylia), (Mammals and reptiles)
        ii. Monophyletic group = clade – ancestor and all descendents (Mammals + turtles + lizards/snakes + birds + crocodylia)
        iii. Paraphyletic group – ancestor and some descendents (classic definition of reptilia)
        iv. Polyphyletic group – taxa with more than 1 ancestor
        v. Outgroup – group outside a clade
    b. Characters
        i. Apomorphy – derived character
        ii. Plesiomorphy – primitive character
        iii. Synapomorphy – shared derived character
        iv. Symplesiomorphy – shared primitive character
        v. Homology, homolog, homologous – character shared by common descent
        vi. Homoplastic – Characters that are similar but not homologous (note see incorrect definition in text).
        vii. Convergence – independent evolution of similar characters
        viii. Reversals – reversion to more primitive character state
21. Note that outgroups aren't more "primitive" – they just do not have the derived characters (synapomorphies) of the ingroup. "primitive" can be used to describe a taxa that retains many ancestral traits but realize that all living taxa have derived traits that others don't have. So if we look at the first figure we might think that birds and crocodiles are the most derived but look at this cladogram, which just emphasizes other vertebrates:



22. Now it looks like teleost fishes are the most derived! So don't be fooled by what a cladogram does not tell you!