

Some general ideas:

What is a reptile?

What is an amphibian?

Taxonomy:

Fundamental to any course like this is taxonomy.

We need a way to talk about the different animals; after all, “Herpetology” includes reptiles, amphibians and ???

This course covers what are commonly known as amphibians and reptiles.

The big problem, though, is that pretty much everyone agrees that amphibians and reptiles are two somewhat unrelated groups.

Two other issues:

Lately a lot of stuff has been reclassified (details below)

A lot of scientific names have changed (see below).

From a cladistic point of view (also below), a lot of stuff doesn't make sense.

[Here's a lizard]

Your text makes a big deal about this - yes, all snakes are lizards.

This doesn't make sense to anyone except a cladistic taxonomist.

[Here's a reptile]

Your text even says it won't cover these kinds of “reptiles”.

We will say more about this below.

Before anyone gets the wrong idea - some parts of cladistics do make sense, but it does make some subjects impossible to teach.

Traditional taxonomy:

Traditional taxonomy - based on Linnaeus' system.

System divides everything into increasingly similar groups:

Kingdom
 Phylum
 Class
 Order
 Family
 Genus
 species

Most of you should be very familiar with this system.

Using this system, we divide Chordates into a number of different classes, including *Amphibia* and *Reptilia*.

Here is a complete classification of the American Toad:

Kingdom:	Animalia
Phylum:	Chordata
Class:	Amphibia
Order:	Anura
Family:	Bufonidae
Genus:	<i>Anaxyrus</i>
species:	<i>americanus</i>

The problem with this system is that it doesn't reflect evolutionary relationships very well.

The cladists are quite correct in one regard when they classify snakes as lizards, or birds as reptiles:

Snakes are an offshoot from the lizards, so why should they have the same taxonomic level?

Traditionally, snakes are in the suborder Serpentes, and lizards in the suborder Sauria (both in the order Squamata).

Do birds really deserve to be a class if they obviously branched off from the “class” Reptilia?

Traditionally, these criticism have been answered by saying that groups such as birds are:

- a) highly derived, and therefore different from most other reptiles.
- b) instantly recognized as homogenous group similar to the reptile “group”.

As such, birds “deserve” class status. Besides, it is true that this makes it much easier to teach and understand, particularly for the lay-person.

Modern (??) taxonomy (partly based on the cladistic approach):

Modern taxonomy tries to classify organisms based solely on their evolutionary relationships.

In other words, birds are reptiles, and snakes are lizards.

While it does reflect evolution, it makes it ridiculously difficult to teach a course like this (unless it's specifically dedicated to taxonomic relationships).

Let's look at table 1.4 or figure 1.12 for example.

What on earth are all the various names?

They're not any of the traditional Linnean taxa.

They define branching points based on a specific character or set of characteristics

Diapsida, for example, refers to “two” openings in the skull (more on that later).

Unless we want to spend all our time defining these “taxa”, this doesn't provide a coherent approach to teaching.

It's also totally unnecessary unless you really are doing taxonomy, in which case it's obviously important.

The approach used in this class is to stick with the traditional Linnean system, while keeping in mind that it is hardly perfect. We'll need to make reference to modern taxonomy many times.

Analyzing relationships:

There are actually several different ways of doing this:

1) Phenetics:

Measures as many different characters as possible, then tries to establish relationship based on the similarities of these characteristics.

Often uses fairly complicated statistical techniques such as cluster analysis.

The problem is that a “blind” phenetic approach does so without regard to the relationships of the characters.

In other words, what is causing the similarities? Evolution? Convergence? Homologies?

A blind phenetic approach can lead to classifications based on similarities, regardless of where those similarities come from.

2) Cladistics:

Uses “shared derived” characteristics to determine relationships.

If two organisms have the same characteristic due to homologies, then they are in some way related.

Supposedly, this provides an objective approach.

Unfortunately, what happens in practice is that there is a lot of argument over:

- which characters are homologous

- and which characters should be used
- also, many of the algorithms used to do cladistic classification allow one to rate characters on an importance scale before analysis.
 - for example, if the researcher believes that two skull openings is more important than color pattern, then he or she can “assign” relative weights to these characters.
 - this can obviously remove the objectivity (although the example above seems reasonable).

Cladistics is partly responsible for the state of modern taxonomy. Whether that's a good or bad thing is for other people to decide.

3) Traditional:

There is a third approach that is sometimes still used. It's the “expert” approach.

Someone will study a particular group of organisms for a long time and become an acknowledged expert in the field.

Based on his or her knowledge, he or she puts together a taxonomy.

This may or may not be combined with one of the two approaches above.

Regardless of what approach one uses, one ought to be able to explain what happened or is happening.

For example, someone decides to subdivide two species of lizard.

Why? Just because? Is there a reason for doing so (not just because “cladistics tells me so”)

Is there some type of geographic barrier that can explain why there should be two species?

Characters used:

Morphology:

Basically, the appearance of individuals. Various measurements are taken. For example:

Snout-vent length, skull shape, Shell length, various ratios, number of labial scales, etc.

All of these can be used to differentiate different species. You will be using some of these in lab.

Biochemistry/genetics:

Using proteins, DNA, immune system responses, or other techniques to differentiate species and/or groups.

These days a lot of taxonomy is done using DNA sequences.

Obviously, the more similar DNA sequences, the more related.

This is without a doubt the most powerful approach to establishing relationships and usually works very well.

However, there are two problems in using this blindly:

1) Sometimes the people doing the analysis have no idea what the organisms even look like.

a) if you are trying to establish the relationship between x and y, you ought to make sure you can identify x and y to begin with!!

2) It is not always clear what a specific difference in DNA means. Does a difference of “x” imply two different species?

a) Recently, someone decided to elevate *Chrysemys picta dorsalis* from a subspecies to a species based on DNA analysis.

b) This totally ignored the fact that *C.p.d.* hybridizes regularly with the other subspecies of *Chrysemys picta*.

In other words, it shouldn't be a species.

Still, doing DNA analyses intelligently is probably one of the best methods for establishing taxonomic relationships.

Has been used successfully many, many, times.

(DNA is one of many techniques. Not the only one!)

We will not learn how to do this in this course.

Some taxonomic nomenclature:

Monophyletic - all members of a taxon are in the same group and descended from a single “node” or individual.

Paraphyletic - Not all members of a taxon are in the same group

This is the issue with birds vs. reptiles

Cladists do not like to see paraphyletic groups

Polyphyletic - Members of the same taxon have different ancestors (really screwed up).

No one likes to see polyphyletic groups

An example of all three using mammals (but see figure 1.16 in your text for a herp example).

Recent taxonomic changes:

One final problem is the current state of taxonomy.

In recent years much of the taxonomy has changed.

This is not just in herpetology, but also in mammalogy and other similar courses.

Unfortunately, the current nomenclature is a real mess, and not all of it is accepted yet.

Some simple examples:

Rana --> *Lithobates*

Bufo --> *Anaxyrus*

What does that mean for us?

Two things are obvious:

Scientific names are not stable. They should be. But what you learn today may change tomorrow.

English (=common) names seem more stable than anything else.

As a result, you will be required to learn English names as well as current scientific names.

We'll use the scientific names as current on the SSAR web page:

http://www.ssarherps.org/pages/comm_names/Index.php

(Previous editions were also be available in pdf, but I haven't found this one yet)

Finally, what will the course actually cover?

Despite the arguments about what a reptile or amphibian is, this course covers:

Amphibians - in the traditional sense of the word:

Frogs, salamanders, caecilians

Reptiles - in the traditional sense of the word:

Crocodiles, turtles, tuataras, "lizards & snakes"

We may occasionally (particularly next week) discuss some material related to dinosaurs and other "reptiles".

Other than today, we will not cover taxonomic methods. Feel free to read through chapter 1 in more detail if you're really interested.

Go through syllabus.