

Classification, species concepts and their relation to conservation biology and policy.

Practically, biologists use the species concept all the time. Any journal article will give the Linnean binomial (*Genus species*) of the species studied.

Nonetheless, there is debate about the biological definition of a species, and this has had implications for conservation biology — particularly in policy and law. We would like one simple definition of what a species is, but differences among organisms make this difficult.

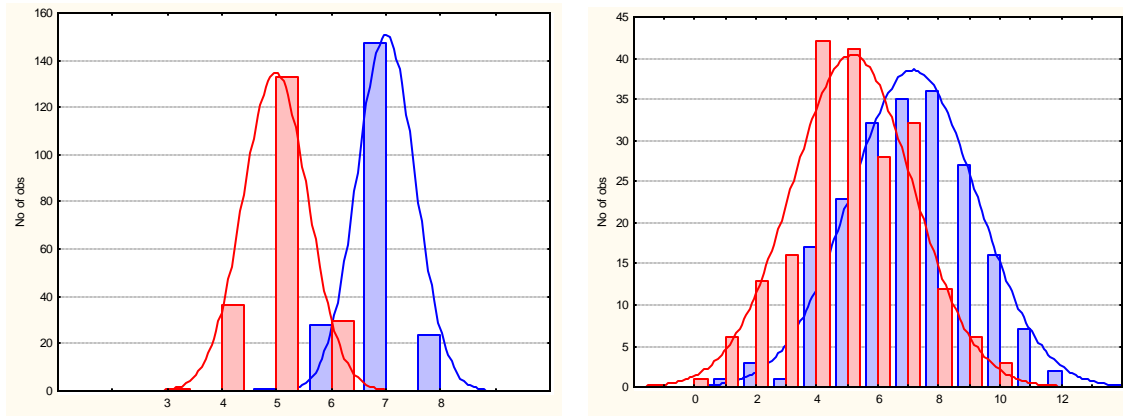
One small semantic issue:

Defining vs diagnostic characteristics. When a species is recognized, it is defined by a set of phenotypic *defining traits*. These traits form the legal definition for that species. If other traits, recognized after the formal definition, can be used to identify the species, they are called *diagnostic traits*.

Species are defined by phenotypic traits. Ideally, can identify set of traits that are:

- clearly defined
- shared by all members of the species
- not shared by other, closely related taxa

Problems arise with variation. Most traits vary among individuals within a population, and among populations.



Frequency distribution on the left shows number of individuals vs bill depth for two hypothetical populations where $\mu = 5$ mm and 7 mm, $\sigma = 0.5$ in each case. On the right, still $\mu = 5$ and 7, but $\sigma = 2$.

Increasing σ from 0.5 to 2 makes the trait far less valuable for recognizing that there are two distinct distributions, even though the mean difference is the same (think about how a t-test works).

Geographic variation in traits creates serious problems, because a character that varies little in one place may vary a lot elsewhere. WHY? (stabilizing selection and/or character displacement by competitors. Recall the bill depth example from Galapagos finches in speciation lecture).

So the problem is to take data and make a working classification of species. We'll cover three aspects of this.

1. Methods of classification
2. Species concepts
3. Implications for conservation

Methods of classification.

1. Phenotypic (= phenetic) classification

Linneus lived before Darwin. The idea of classification into species was established before evolution was understood.

So, the original method of classification is not explicitly evolutionary. It is simply a hierarchical system of putting 'like with like'. You could apply the same logic to musical instruments, for example.

closely similar = same species
less similar = difft species same genus
still less similar = difft genera same family

Some measure of character similarity (there are several such measures) is averaged across many characters to obtain 'overall morphological similarity' (WHY many characters?). Quantitative criteria for the degree of similarity at each level of classification come from comparison to previously established classifications in similar groups.

Strength of phenotypic approach - do not need to know the phylogeny (evolutionary tree) for the organisms to be classified. Phylogenies often have substantial uncertainty, and this is avoided.

To apply phenetic approach:

- measure many characters ($n = \#$ of characters)
- determine phenetic distance for each pair of organisms in n -dimensional plot.
- organize as phenetic tree
- use phenetic distance criteria to classify

(Ohead: Ridley ig 14.5, p 362)

2. *Phylogenetic (= cladistic) classification*

Explicitly evolutionary — classification based on how recently a common ancestor was shared.

(Ohead: Ridley Fig 14.2 p 358)

- Use data to produce a phylogenetic tree (usually molecular genetic data).
- Cladistic classification summarizes the genetic distance between all species in the tree: branch lengths indicate degree of divergence.
- Easy to convert this cladistic classification into Linnean classification, using criteria for degree of divergence at each taxonomic level.

(Ohead Ridley p. 365 Fig 14.6)

E.g. Sequence analysis of mitochondrial cyt b gene of African wild dog (*Lycaon pictus*) identifies it as sole member of a 'monotypic' genus. This is a genus with only one species. Could get a consistent classification with wild dog in same genus (*Canis*) as its closest relatives. But degree of divergence (length of arm in cladistic classification) indicates separate genus.

(Ohead Girman & Wayne Fig. 2.1)

Can apply same logic to finer-scale genetic analysis within a species: e.g. evaluation of subspecies of AWD using mt control loop sequence.

(Ohead Girman & Wayne Figs. 2.2. & 2.3)

To classify by phylogenies, must use certain type of characters:

Analogous characters: characters shared by a pair of organisms due to convergent evolution (wings of flying squirrels and sparrows).

Homologous characters: characters shared by a pair of organisms, inherited from common ancestor (wings of sparrows and finches)

Only **shared, derived homologies** are used in cladistics to determine phylogenies

shared - in all member of a group of species

derived - character has changed from ancestral form seen in other groups

homology - shared by groupmembers due to common ancestry

(Ohead: Ridley fig 14.7 p. 366)

Which of the methods is best? Classification should be:

- a. *Objective & logically justified* - classification by first letter is objective but not logical
- b. *Natural*. - a natural classification is one that gives the same result when characters not used in the classification are considered. An artificial classification does not.

(Ohead: Ridley Fig 14.3 p. 360)

E.g. subfamily Simocyoninae in the family Canidae. Dhole (*Cuon alpinus*), bush dog (*Speothos venaticus*) and African wild dog (*Lycaon pictus*) were grouped on the basis of having 4 toes and no basined cusp on premolar. Not particularly similar in other ways, and genetic data confirm that this was an artificial classification.

(Ohead: Macdonald p 85, 81, 76)

(Ohead: Girman & Wayne p.8)

Applying criteria of objectivity and natural-ness to each method:

Phenetic or Phenotypic Method

- gives very natural classifications if many characters used to generate phenetic distance.
- but is not fully objective

(Ohead: Ridley 14.3 p. 360)

Two *clustering methods: nearest neighbor* and *average neighbor* give different results, with no inherent principle to distinguish which is correct. The main tenet of phenetic classification is that the traits themselves will define unambiguous clusters - but in this example the result is ambiguous.

To be fully consistent, we would have to pick one of the clustering methods. *This choice is arbitrary, not objective.*

Also more than one measure of distance.

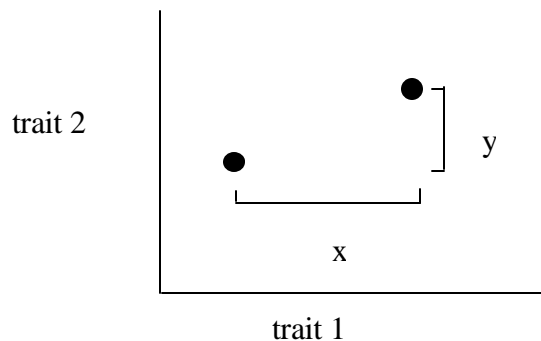
Mean Character Distance = $(x+y)/2$

Euclidean Distance = $\sqrt{x^2 + y^2}$

MCD & ED do not always define identical clusters.

Choice of distance is again *subjective*.

Because phenetic classification gives no logical basis to choose among distance and clustering methods, it is somewhat limited.



Cladistic method

Strengths:

Ridley (1993). "The advantage of the phylogenetic method should be apparent. The *phylogenetic hierarchy exists independent of the methods we use to discover it*, and it is *unique and unambiguous* in form."

Weaknesses:

Can be difficult to distinguish *analogies* and *homologies*.

Some argue that cladistics is too strict a system, because it does not use information from shared ancestral homologies (does not recognize paraphyletic groups, only monophyletic groups)

Summary of Methods

(Ridley Fig 14.7 (again) and Table 14.2, p. 367)

Monophyletic group - common ancestor and *all* descendent species

Paraphyletic group - common ancestor and *some* but not all descendant species

Polyphyletic group - does not contain its common ancestor - arise due to convergence.

Phenetic classification - recognizes polyphyletic, paraphyletic and monophyletic groups
- problem: fails to distinguish convergence and common ancestry

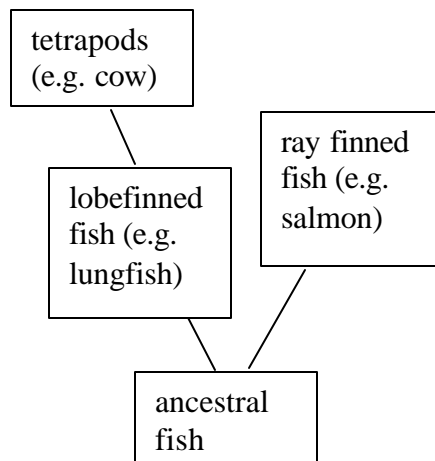
Phylogenetic classification - recognizes only monophyletic groups

- solves the problem of phenetics, but is overstrict by excluding paraphyletic groups, some would argue.

Evolutionary classification - differs from cladistics by recognizing paraphyletic groups

- compromise from strict cladism's focus on monophyletic groups. Broadens to recognize any pattern due to common ancestry, including paraphyletic groups.

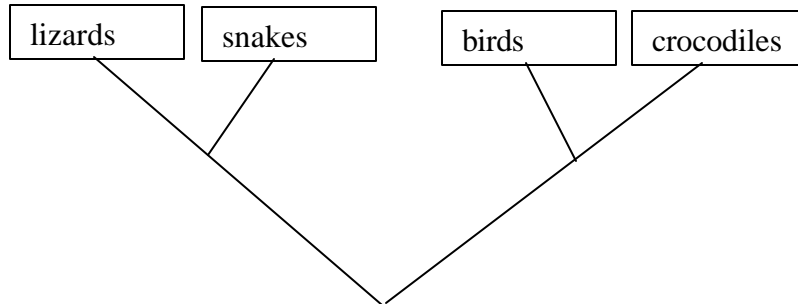
Example of problem this solves: all tetrapods evolved from lobe-finned fish



The group "fish", including salmon and lungfish but excluding cows, does not exist for pure cladism.

The same problem arises for reptiles, b/c crocodiles have a more recent common ancestor with birds than with the rest of the reptiles.

No monophyletic group that contains all reptiles but excludes birds.



There is a paraphyletic group that solves this problem. In general, problems of classification like this arise for pure cladistics when *one lineage has evolved rapidly relative to the other parts of a monophyletic group.*

Eg birds have diverged rapidly relative to crocodiles, tetrapods have diverged rapidly relative to ray-finned fishes.

Evolutionary classification recognizes paraphyletic groups when the phenotypic differences between members of a monophyletic group are big, due to rapid divergence in one subset of the monophyletic group → basically, the cladistic method modified by phenetic method in special cases.

There is considerable debate whether pure cladistics or evolutionary classification is the better system.

Over time, cladistic classification has become more prevalent. Particularly with molecular genetic data (e.g. gene sequences) to infer phylogenies.

Hybridization creates problems for cladistic classification.

Species Concepts.