

"PRINCIPLES OF PHYLOGENETICS: ECOLOGY AND EVOLUTION"

*Integrative Biology 200B*  
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A. The value of biodiversity:

- ethical: each lineage is a thread in an heirloom fabric that we have the responsibility to pass on to future generations.
- intellectual: we have a basic need to understand the world, how it came to be, and where we fit in it.
- ecological: a diversity of interactors is needed for proper function of ecosystems, and a diversity of replicators is needed as the raw material for natural selection (future evolutionary potential).
- economic: natural lineages are a potential source for a myriad of products of direct economic benefit (medicines, food, esthetics, shelter, etc.).

B. Criteria that can be used for prioritizing conservation:

Taxon-based

- threat of extinction
- ecological importance ("keystone species")
- rarity
- phylogeny

Landscape and Habitat-based ("communities")

- threat of extinction
- ecological importance (ecosystem services, resilience to climate change)
- rarity
- phylogeny

C. Key concepts behind conservation planning tools (Sarkar et al. 2006)

Complementarity – 'quantitative contribution to the biodiversity features of a site that are not adequately represented in the existing set'

Irreplaceability – the contribution of a given site in a potential set of targets to achieve a particular goal

Vulnerability – probability of persistence of a population or other features of an area

D. Phylogenetics and conservation

As we have discussed, there has been tremendous recent progress in understanding the relationships of organisms at all levels, due to two different advances, whose cumulative impact has been great. One advance is theoretical and methodological -- a revolution in how any sort of data can be used to reconstruct phylogenies and interpret evolution and ecology. The other is empirical -- the sudden availability of copious new data from the DNA level. Unfortunately, these advances have not made their way fully into applied biology and the critical task of conserving biodiversity.

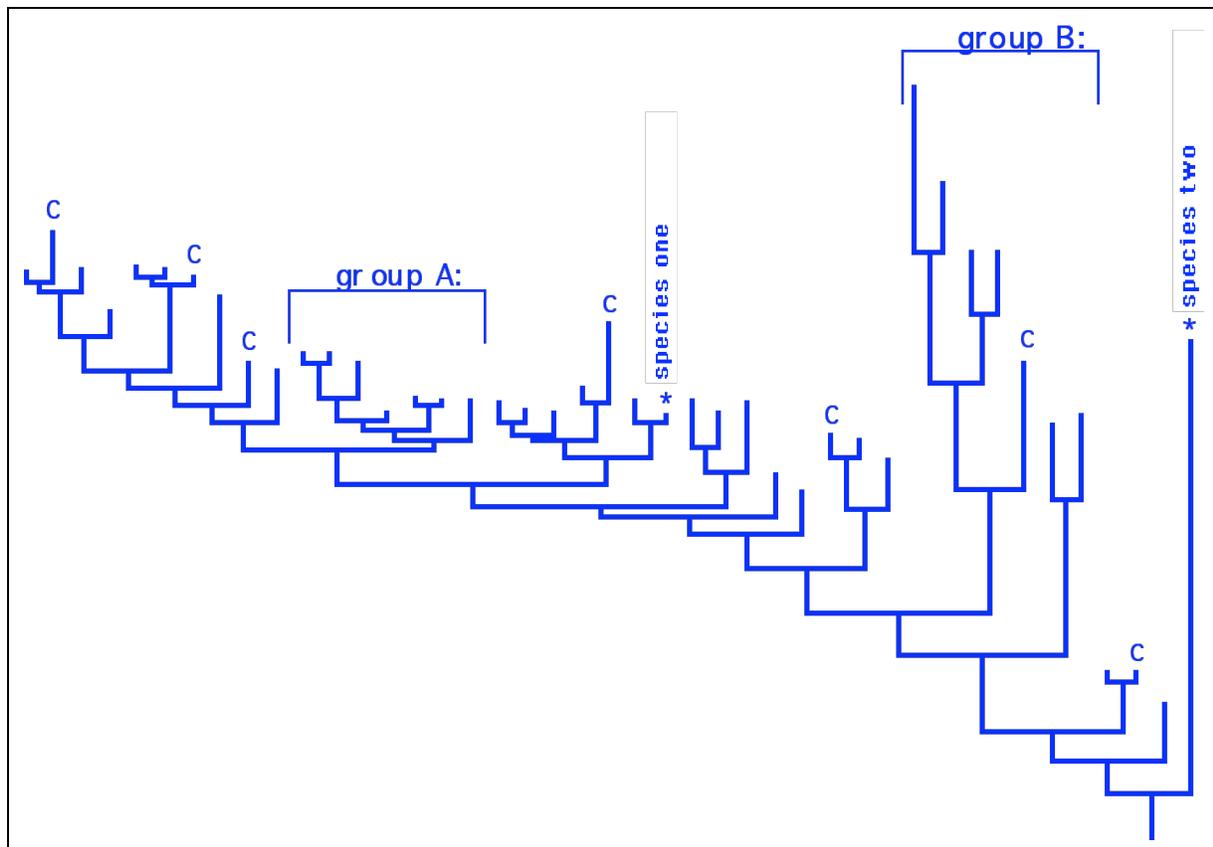
We systematists understand now that biodiversity is the whole tree of life, not just the named species. There are lineages smaller and larger than the traditional species level. Furthermore, species are not comparable between lineages in any manner. Thus counting species or measuring their ranges and abundances is a poor measure of biodiversity; we must develop measures of the actual diversity of lineages taking into account their evolutionary properties and phylogenetic position. New quantitative measures for phylogenetic biodiversity, which take into account the number of branch points (and possibly branch lengths) separating two lineages have been developed, which can be applied to rarity assessment and conservation planning. This relatively new phylogenetic worldview can clarify greatly what "rarity" means: *rarity fundamentally means not having many living close relatives*. We can now quantitatively define what we mean by "many" and "close."

As discussed in an earlier lecture, all "species" are not equal in a phylogenetic sense (or any other sense for that matter). As has been pointed out by a number of pioneering cladistic conservation biologists, conservation priorities can best be set by a consideration of the phylogenetic relationships among species. This is because all attributes of organisms (genetic similarities, ecological roles, morphological specializations) tend strongly to be associated with phylogeny. From the standpoint of preserving the maximum phylogenetic diversity (and its associated attributes), saving a "long-branch" species (i.e., one such as the Coast Redwood or Santa Lucia Fir with much change along the terminal branch, either due to extinction or rapid evolution) should carry a higher priority than saving a "short-branch" species (i.e., a dandelion differing in only a few minor features from near relatives). Furthermore, saving a community of 100 species of diverse phylogenetic relationships should carry a higher priority than saving a community of 200 species belonging to only a few large genera (see the figure below for an illustration of these points). Thus, phylogenetic considerations should play a much more important role in conservation biology than they have to date.

In an ideal world all species could be preserved -- in this world of limited resources (time, money, and public goodwill) indices based on phylogeny are being developed to help us preserve the maximal genetic, morphological, chemical, and ecological diversity. The general public will be much more supportive of species preservation efforts that are carefully focused and justified in this way, rather than of uncritical, across-the-board efforts. Phylogeny reconstruction is thus not just an academic exercise, but rather the fundamental basis of a truly practical taxonomy.

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*Next page.* A hypothetical cladogram illustrating the potential role of phylogeny in setting conservation priorities. Shown is a phylogeny of 43 "species"; the branch lengths are proportional in the vertical direction to the number of evolutionary character changes along that branch.

Small group exercise: if you were offered three alternative conservation scenarios that would save either group A or B or C, how would you rank them? How would you explain your ranking to a biodiversity manager who is not familiar with phylogenetic concepts?



## E. Literature

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## F. Quantitative methods

*Phylogenetic diversity:*

PD = sum of branch lengths of subtree incorporating set of selected taxa.

*Abundance-weighted PD*, also known as Rao's entropy (Hardy and Senterre 2007):

$$D^p = \sum_i \sum_j \delta_{ij} f_i f_j$$

$\delta_{ij}$  = phyletic distance between individuals taxa i and j

$f_i, f_j$  = relative abundance of taxa i and j

$D^p$  = average phyletic distance between two randomly chosen individuals from a community

Rao's entropy can be calculated within communities (phylo-alpha diversity) or between communities (phylo-beta diversity) (see Graham and Fine 2008)

### A few R tools

*ape* library:

*cophenetic.phylo* - gives phylogenetic distance matrix, used in Rao's entropy

*picante* library:

*pd* - Faith's phylogenetic diversity

*psc/psd/pse/psr/psv* - phylogenetic species diversity metrics of Helmus et al. 2007

*specaccum.psr* - rarefaction curve for phylogenetic species richness (psr)

*vegan* library:

*diversity* - general diversity and rarefaction metrics

*betadiver* - general beta diversity metrics

*taxondive* - taxonomic diversity indices using a distance matrix (you can substitute a phylo distance or trait distance matrix)