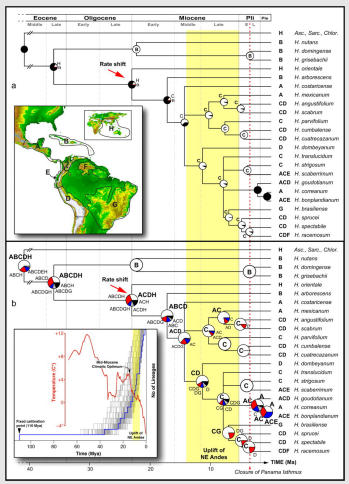
Agenda

- Introduction to Macroevolution and Phylogenies
- Installation Troubleshooting
- Mini R Tutorial

What is Macroevolution?

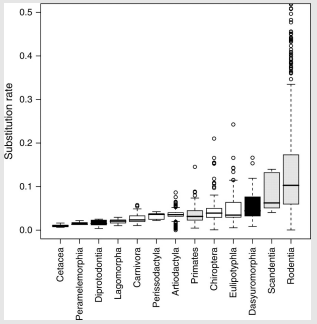
- What was the spatial and climatic environment of ancient angiosperms?
- Did the uplift of the Patagonian Andes drive the diversity of Peruvian lilies?
- How has mammalian body-size changed over time?
- Is diversification in Caribbean anoles correlated with ecological opportunity?
- How has the rate of molecular evolution changed across the Tree of Life?

Historical biogeography



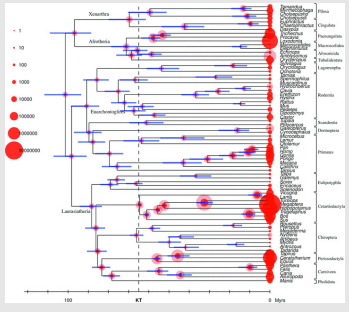
(Antonelli & Sanmartin. Syst. Biol. 2011)

Molecular evolution



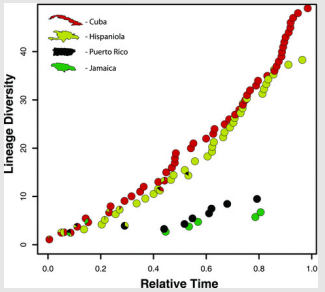
(Nabholz, Glemin, Galtier. MBE 2008)

Trait evolution



(Lartillot & Delsuc. Evolution 2012)

Diversification



(Mahler, Revell, Glor, & Losos. Evolution 2010)

What is Macroevolution?

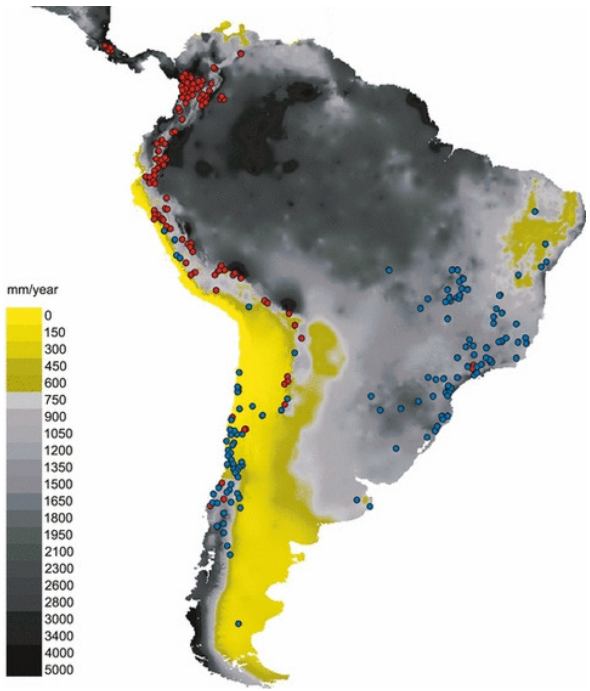
Considers evolutionary processes occurring over deep time, among lineages (i.e., at an interspecies level or above).

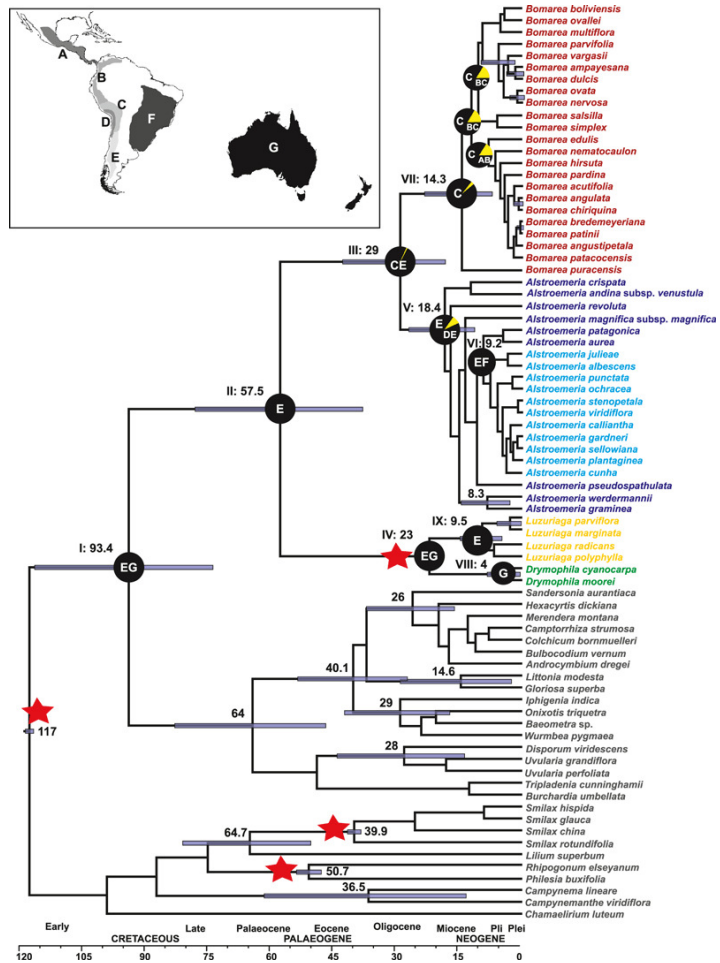
Includes :

- Biogeography
- Lineage diversification (speciation & extinction)
- Morphological evolution
- Co-evolution
- Systematics
- Comparative genomics
- Paleontology
- Development
- History of life
- Evolutionary ecology

Diversification & Historical Biogeography

"From East Gondwana to Central America: historical biogeography of the Alstroemeriaceae"

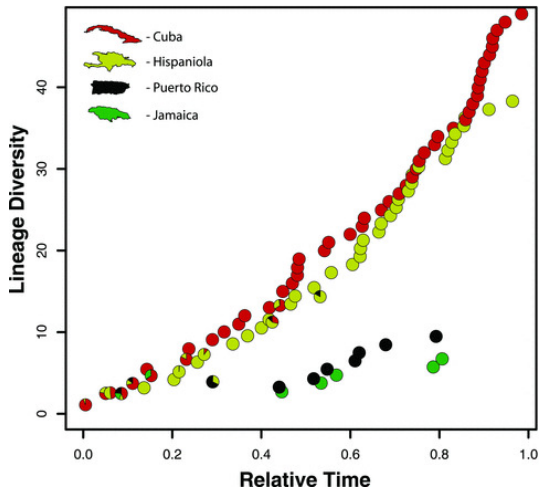




(Chacón et al., *J. Biolgeograpy* 2012)

Relative Times and Diversification

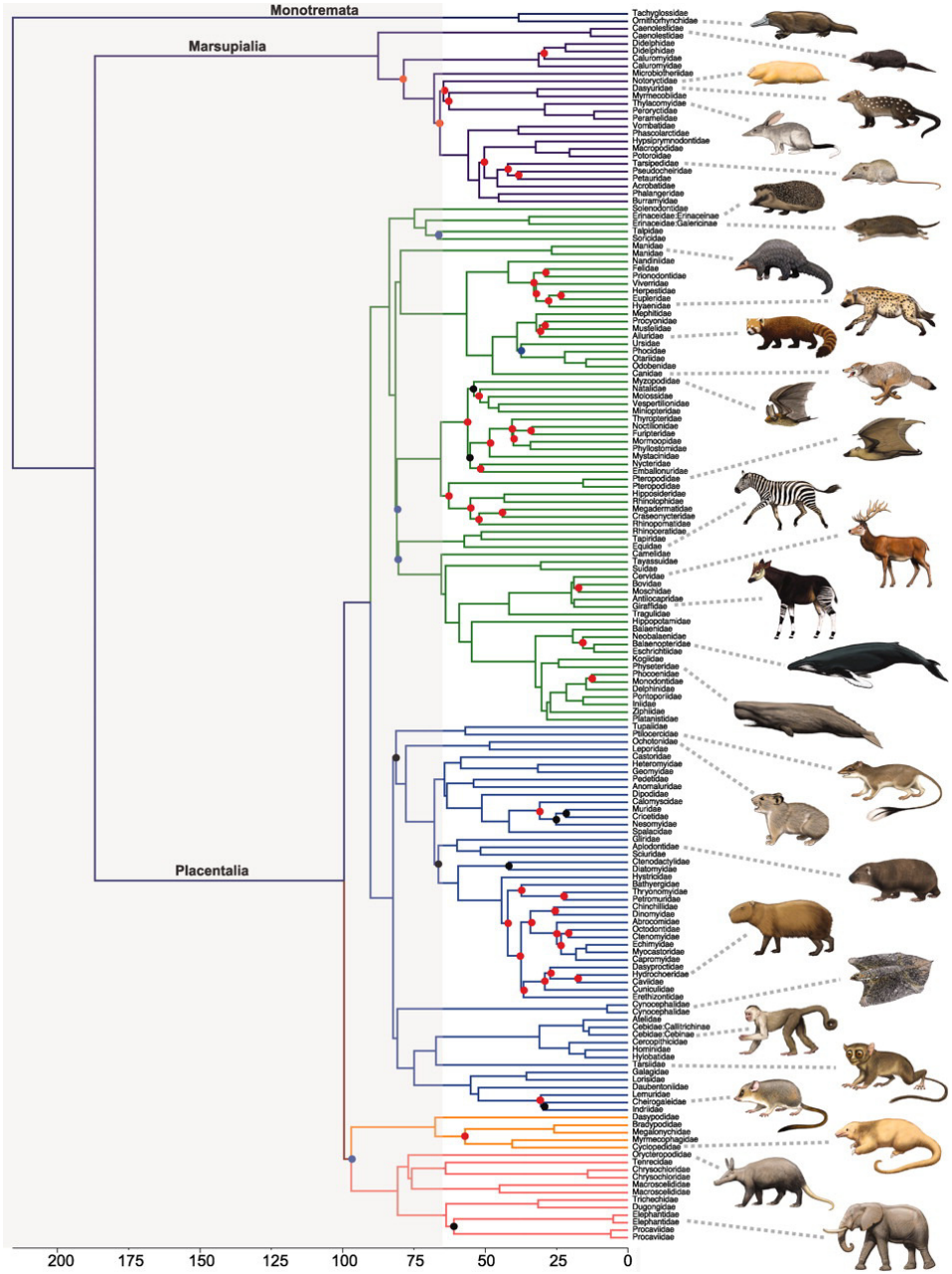
"Ecological opportunity and the rate of morphological evolution in the diversification of Greater Antillean Anoles"




Anolis fowleri (image courtesy of L. Mahler)

(Mahler, Revell, Glor, & Losos. *Evolution* 2010)

Why are Phylogenies Important?



(Meredith et al., *Science* 2011)

Nothing in biology makes sense except in the light of evolution

—Theodosius Dobzhansky, 1973
American Biology Teacher 35:125–129

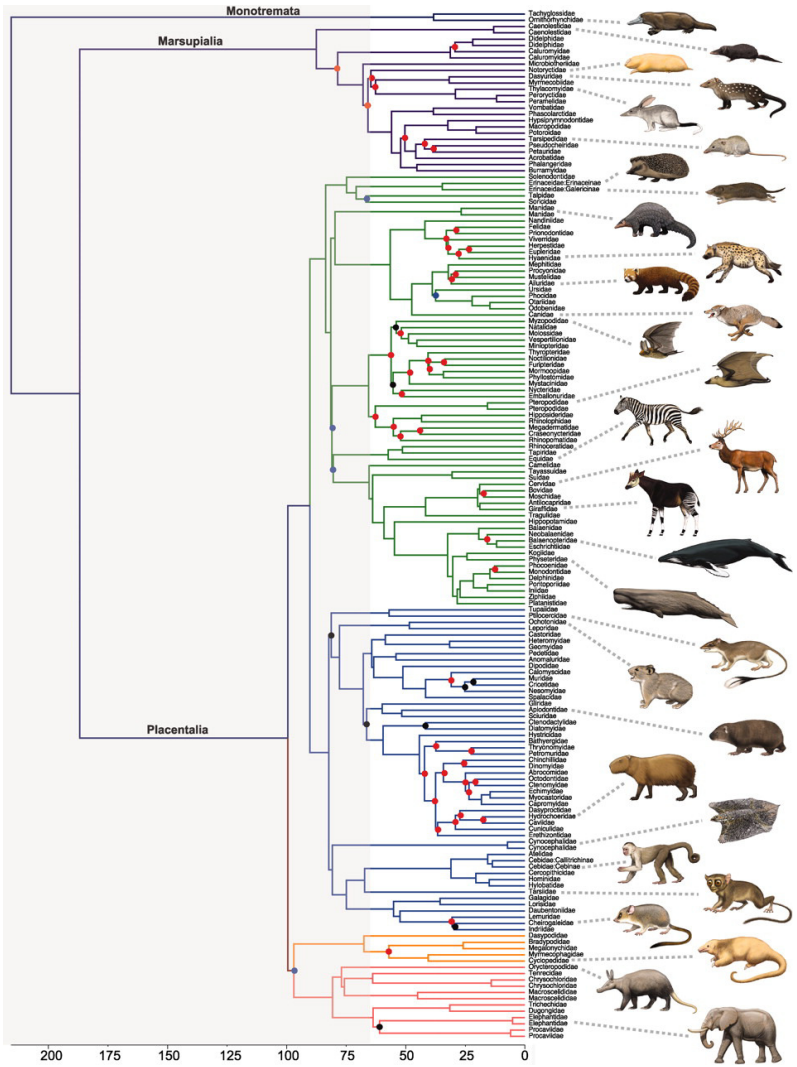
Nothing in evolution makes sense except when seen in the light of phylogeny

—Jay M. Savage, 1997
Soc. of Systematic Biologists Pres. Address

Why are Phylogenies Important?

Provide a time-context for understanding biodiversity

Ask questions like:
What were the "Impacts of the Cretaceous Terrestrial Revolution and KPg Extinction on Mammal Diversification"?



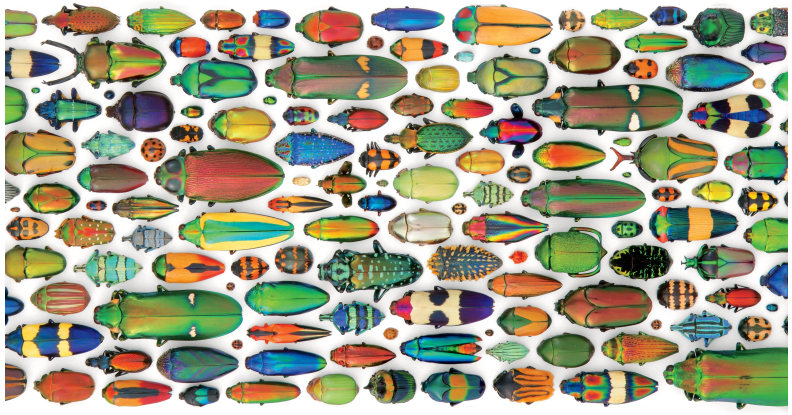
(Meredith et al., *Science* 2011)

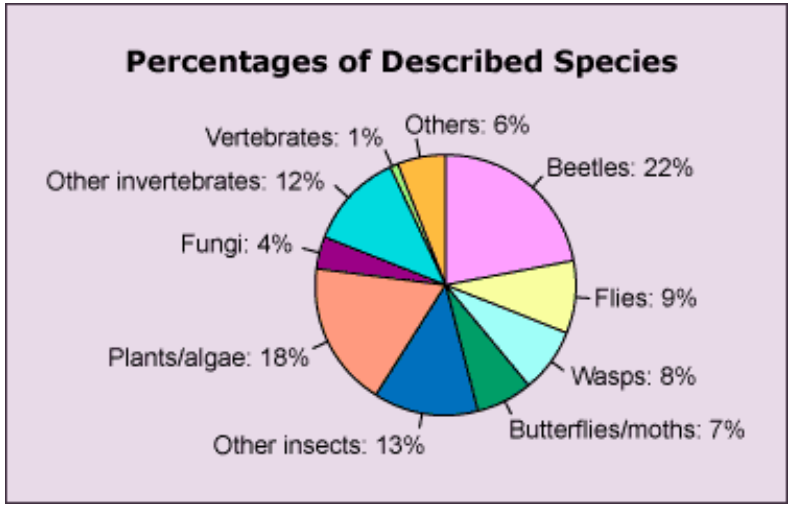
Diversification

Analyses of diversification seek to understand patterns of species diversity

Why are there so many beetle species?

What are the evolutionary processes driving these patterns?





(beetle image from: https://www.audubon.org/magazine/march-april-2009/beetle-mania)

(chart image source: evolution.berkeley.edu/evolibrary/article/phylogenetics_14)

Net Diversification

The rate of diversification (d) is the rate of speciation (λ) minus the rate of extinction (μ)

$$d = \lambda - \mu$$

Diversification in the Fossil Record

The fossil record can give an empirical model of diversity through time

Sepkoski's (1984) Phanerozoic diversity curve shows major trends in taxonomic diversity like mass extinctions and rapid radiations

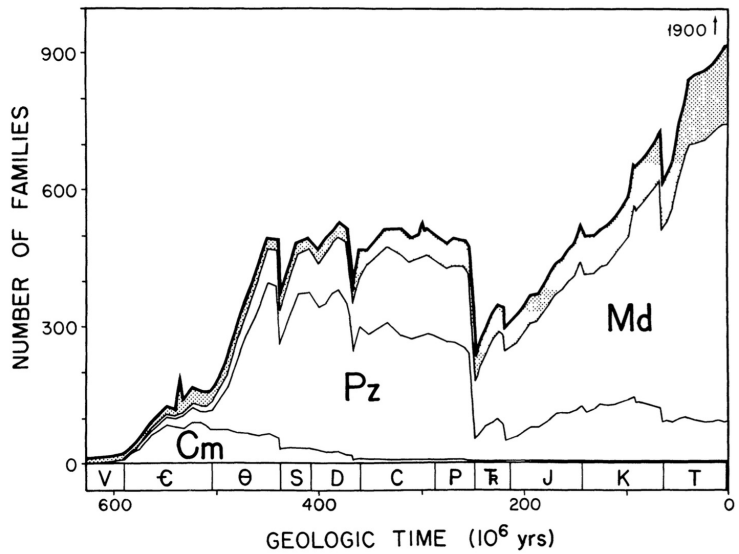


FIGURE 1. The Phanerozoic history of the taxonomic diversity of marine animal families. The upper curve shows the total number of fossil families known from direct evidence or range extension to occur in each stratigraphic stage of the Phanerozoic. The number "1900" in the upper right-hand corner is the approximate number of animal families described from the modern oceans; these include a large portion of soft-bodied and lightly sclerotized groups, such as medusoid coelenterates and many small arthropods, which are only rarely preserved as fossils. The fossil diversity of these "poorly preserved" families (which largely reflects range extension between various exceptional fossil deposits and the Recent) is indicated by the stippled field in the figure. The two curves below the stippled field divide the diversity of heavily skeletonized families into three fields, representing the three "evolutionary faunas" that dominate total diversity during successive intervals of the Phanerozoic (see text). The fields are labeled "Cm" for Cambrian fauna, "Pz" for Paleozoic fauna, and "Md" for Mesozoic-Cenozoic, or Modern, fauna. (The major classes in each of these evolutionary faunas are depicted in Fig. 2.) Symbols along the *x*-axis indicate geologic systems ("V" = Vendian); the time scale is from Harland et al. (1982). Data on fossil families are from Sepkoski (1982).

(Sepkoski, *Paleobiology*, 1984)

Diversification in the Fossil Record

Approaches that only consider the taxonomic diversity in the fossil record are sensitive to the many processes that influence the structure of the fossil record and lead to heterogenous fossil recovery

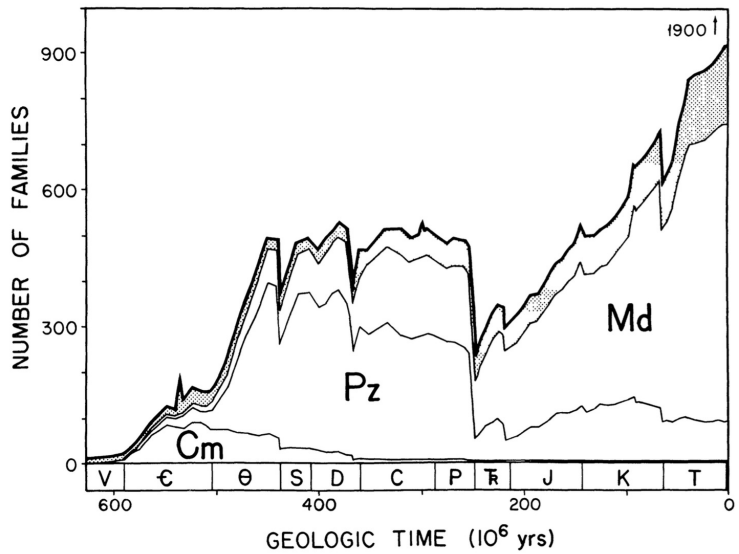


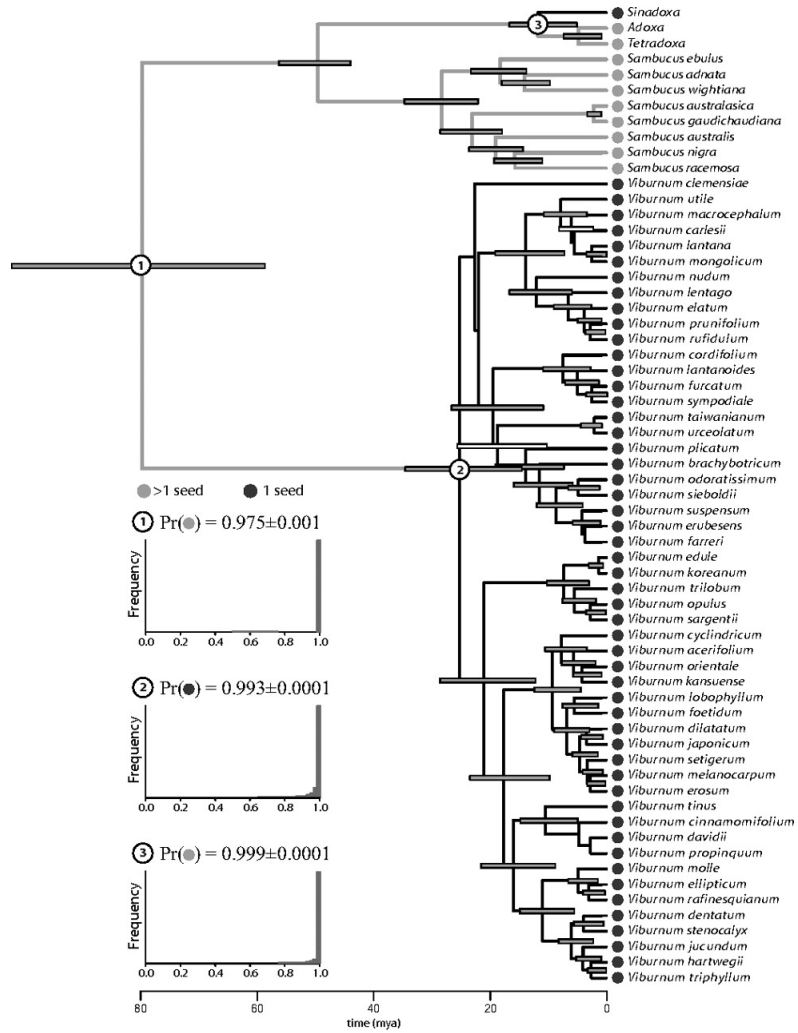
FIGURE 1. The Phanerozoic history of the taxonomic diversity of marine animal families. The upper curve shows the total number of fossil families known from direct evidence or range extension to occur in each stratigraphic stage of the Phanerozoic. The number "1900" in the upper right-hand corner is the approximate number of animal families described from the modern oceans; these include a large portion of soft-bodied and lightly sclerotized groups, such as medusoid coelenterates and many small arthropods, which are only rarely preserved as fossils. The fossil diversity of these "poorly preserved" families (which largely reflects range extension between various exceptional fossil deposits and the Recent) is indicated by the stippled field in the figure. The two curves below the stippled field divide the diversity of heavily skeletonized families into three fields, representing the three "evolutionary faunas" that dominate total diversity during successive intervals of the Phanerozoic (see text). The fields are labeled "Cm" for Cambrian fauna, "Pz" for Paleozoic fauna, and "Md" for Mesozoic-Cenozoic, or Modern, fauna. (The major classes in each of these evolutionary faunas are depicted in Fig. 2.) Symbols along the *x*-axis indicate geologic systems ("V" = Vendian); the time scale is from Harland et al. (1982). Data on fossil families are from Sepkoski (1982).

(Sepkoski, *Paleobiology*, 1984)

Diversification in Extant Phylogenies

Often motivated by observing differences in species diversity in two different clades

Why does the genus *Vibernum* have so many more extant species than *Sambucus*, even though they have similar crown ages?



(Moore & Donoghue, *PNAS*, 2009)

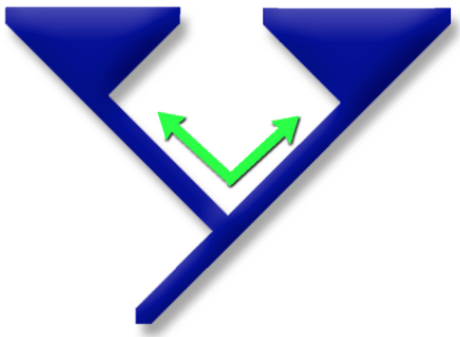
Diversification

When understanding diversification in a phylogenetic context, researchers often ask:

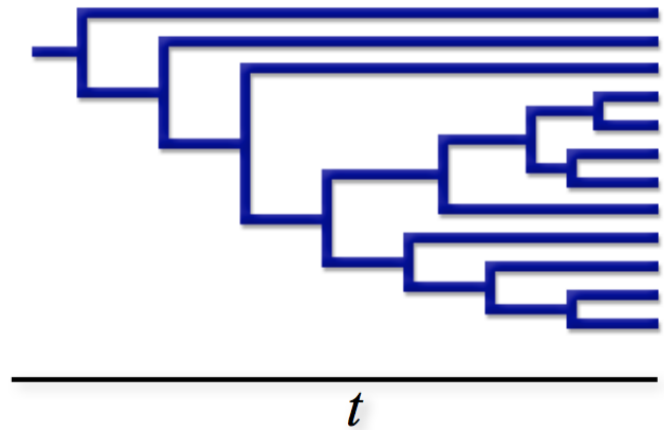
- What are the rates of speciation and extinction (or diversification) for my favorite clade?
- Has the rate of diversification changed over time or across the tree?
- If there were shifts in diversification rate, on what branches or at what time point did they occur?
- Are the rate changes correlated with the evolution of a morphological character, biogeographical event, or ecological change?

Variation in Diversification

Topological Information



Temporal Information

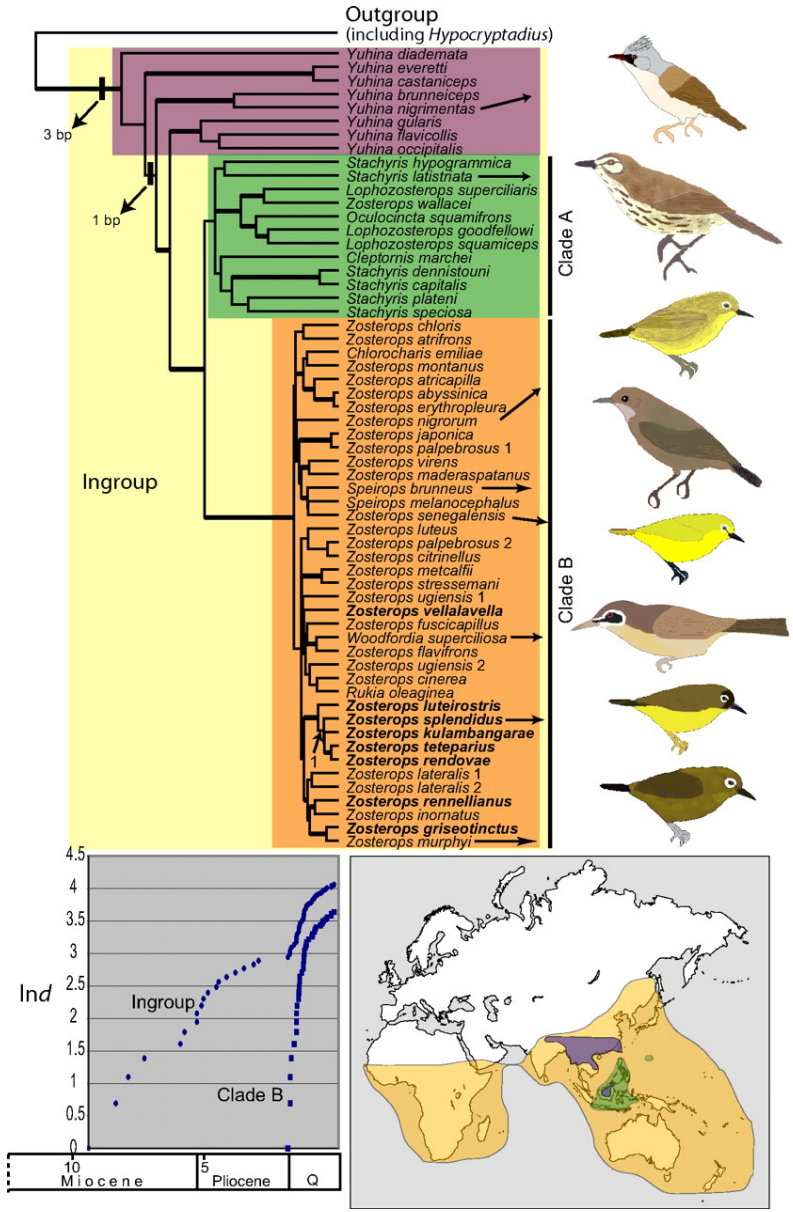


(image souce: from Brian Moore http://treethinkers.org/wp-content/uploads/2014/04/MCMC.pdf)

Diversification in White-Eyes

Used a constant-rate model to estimate speciation by evaluating the distribution of divergence events over time

The lineages through time (LTT) plot shows the accumulation of lineages as a function of time and shows a steep increase followed by a decrease in lineages for Clade B

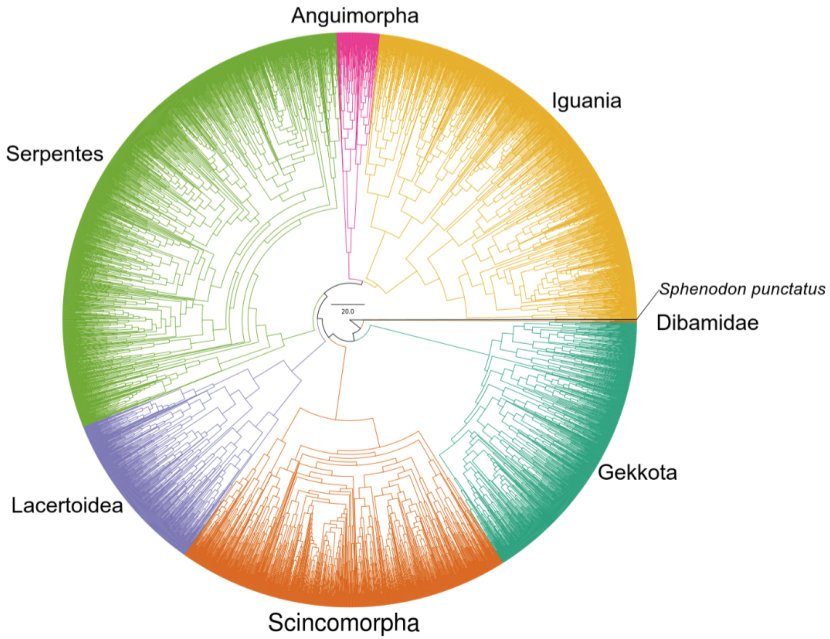


(Moyle et al., *PNAS*, 2009)

Importance of Phylogeny

Analyses of lineage diversification require a phylogeny with branch lengths in proportion to time

Most of these analyses treat the phylogeny as known



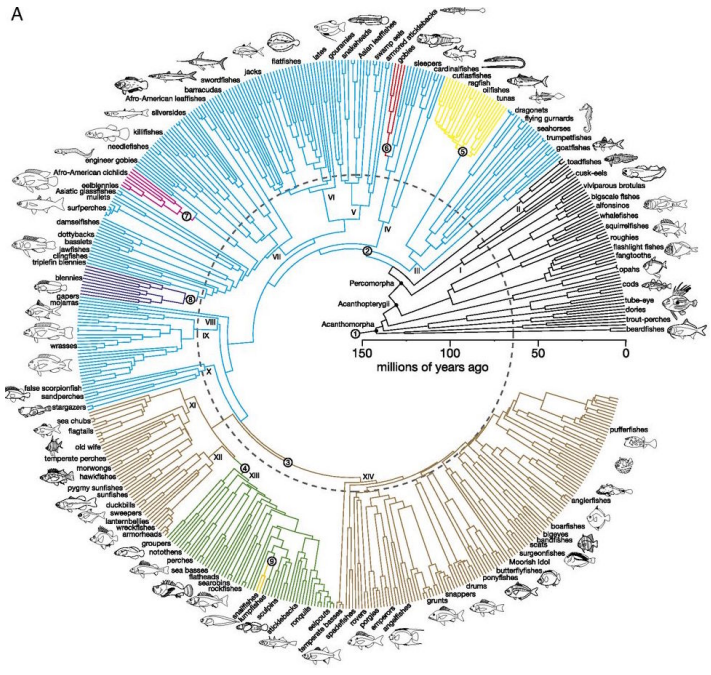
However, the phylogeny is estimated from data (molecular and/or morphological) and has uncertainty

(Wright et al. *JEZ* 2015)

Large-tree Inference

Additionally, diversification methods are sensitive to taxon sampling and are more robust for large trees

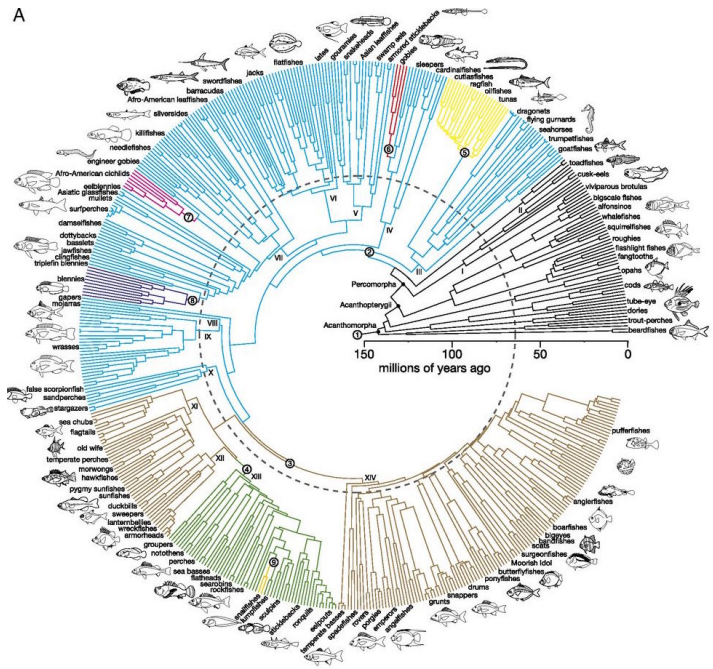
Phylogenetic analysis of large datasets is not trivial and requires complex analysis pipelines



Inferring Phylogenies

Most of the methods we will discuss will assume that we already have a tree

But we will cover, in detail, Bayesian methods for estimating time-calibrated phylogenies



(Near et al. *PNAS* 2013)