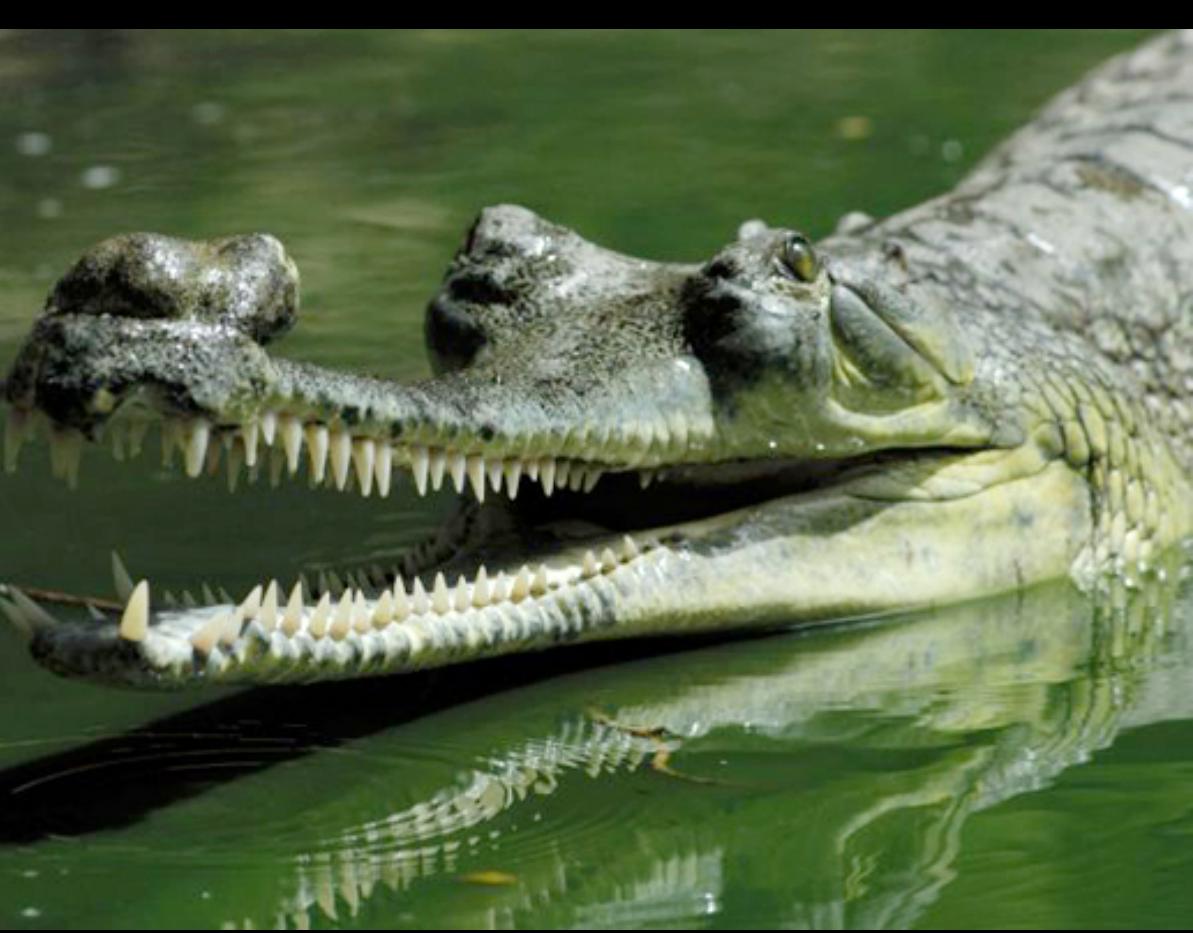


“Mister!” he said with a sawdusty sneeze,
“I am the Lorax. I speak for the trees.





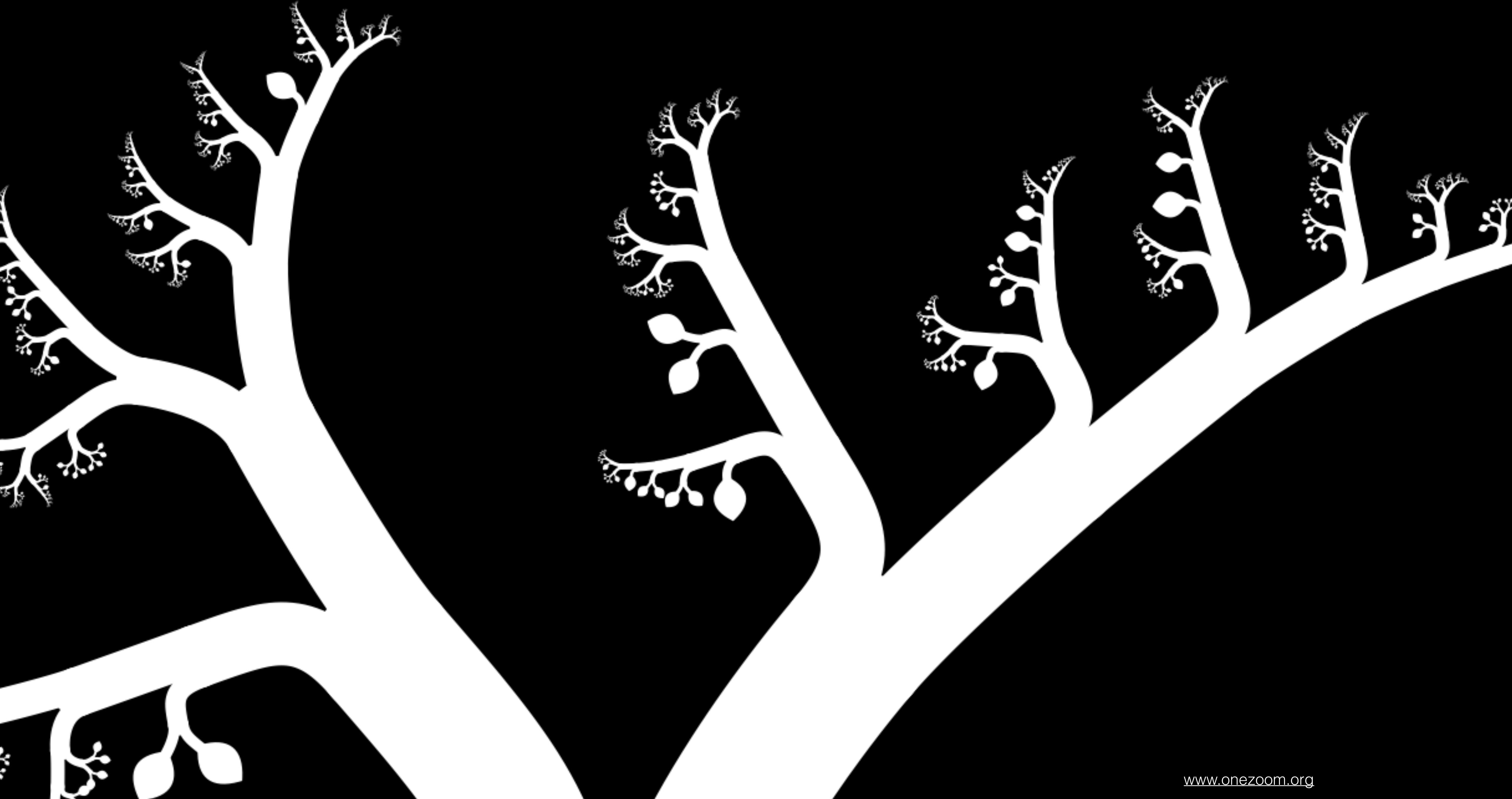
NASA



NASA



NGC 2818



Learning about Deep Time

from the

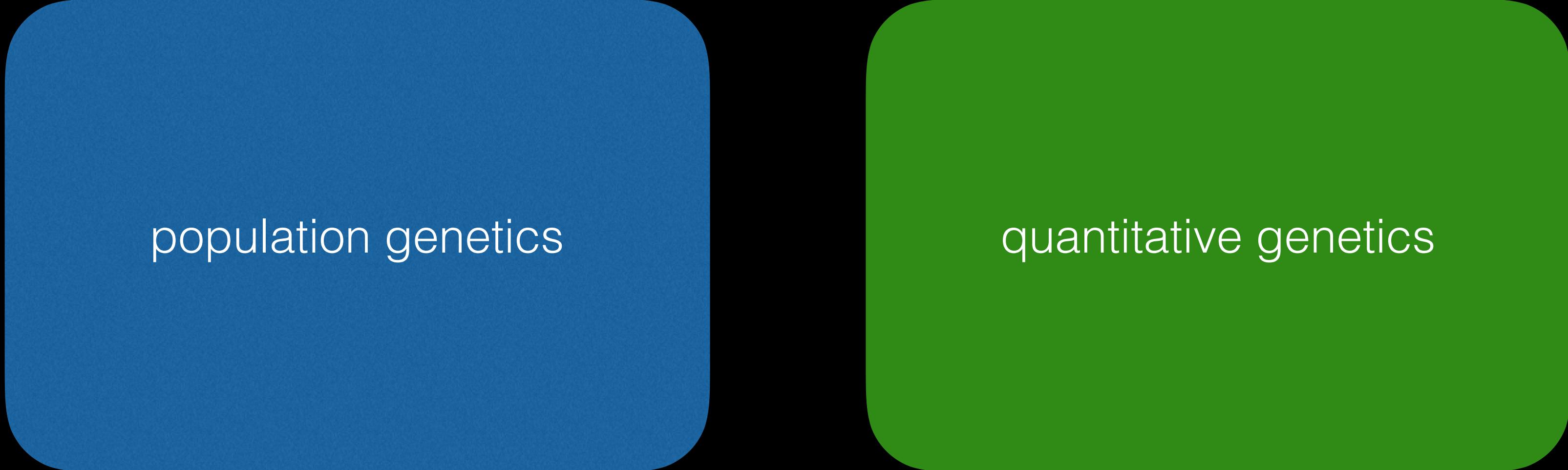
Tree of Life

How are there **so many** species?
Why are they **so different** from one another?

How are there **so many** species?
Why are they **so different** from one another?
And is any of this **predictable**?

Phylogenetic comparative methods

population genetics



population genetics

quantitative genetics

population genetics

quantitative genetics

paleobiology

population genetics

quantitative genetics

paleobiology

phylogenetics

comparative
methods



Scholar



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Joe Felsenstein

Phylogenies and the comparative method

[PDF] from harvard.edu

Authors Joseph Felsenstein

Publication date 1985/1/1

Journal The American Naturalist

Volume 125

Issue 1

Pages 1-15

Publisher University of Chicago Press

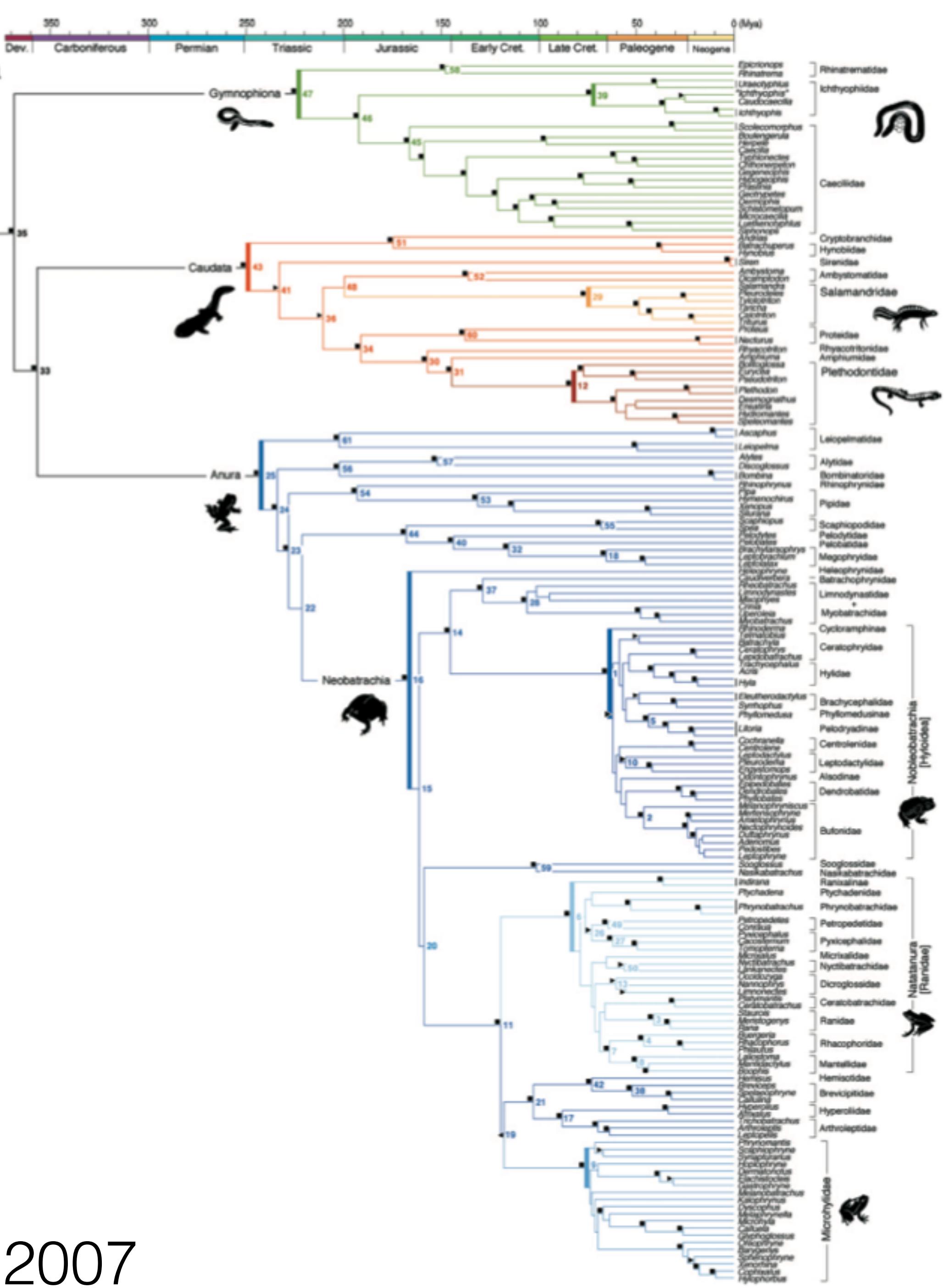
Description Comparative studies of the relationship between two phenotypes, or between a phenotype and an environment, are frequently carried out by invalid statistical methods. Most regression, correlation, and contingency table methods, including nonparametric methods, assume that the points are drawn independently from a common distribution. When species are taken from a branching phylogeny, they are manifestly nonindependent. Use of a statistical method that assumes independence will cause overstatement of the ...

Total citations Cited by 6716

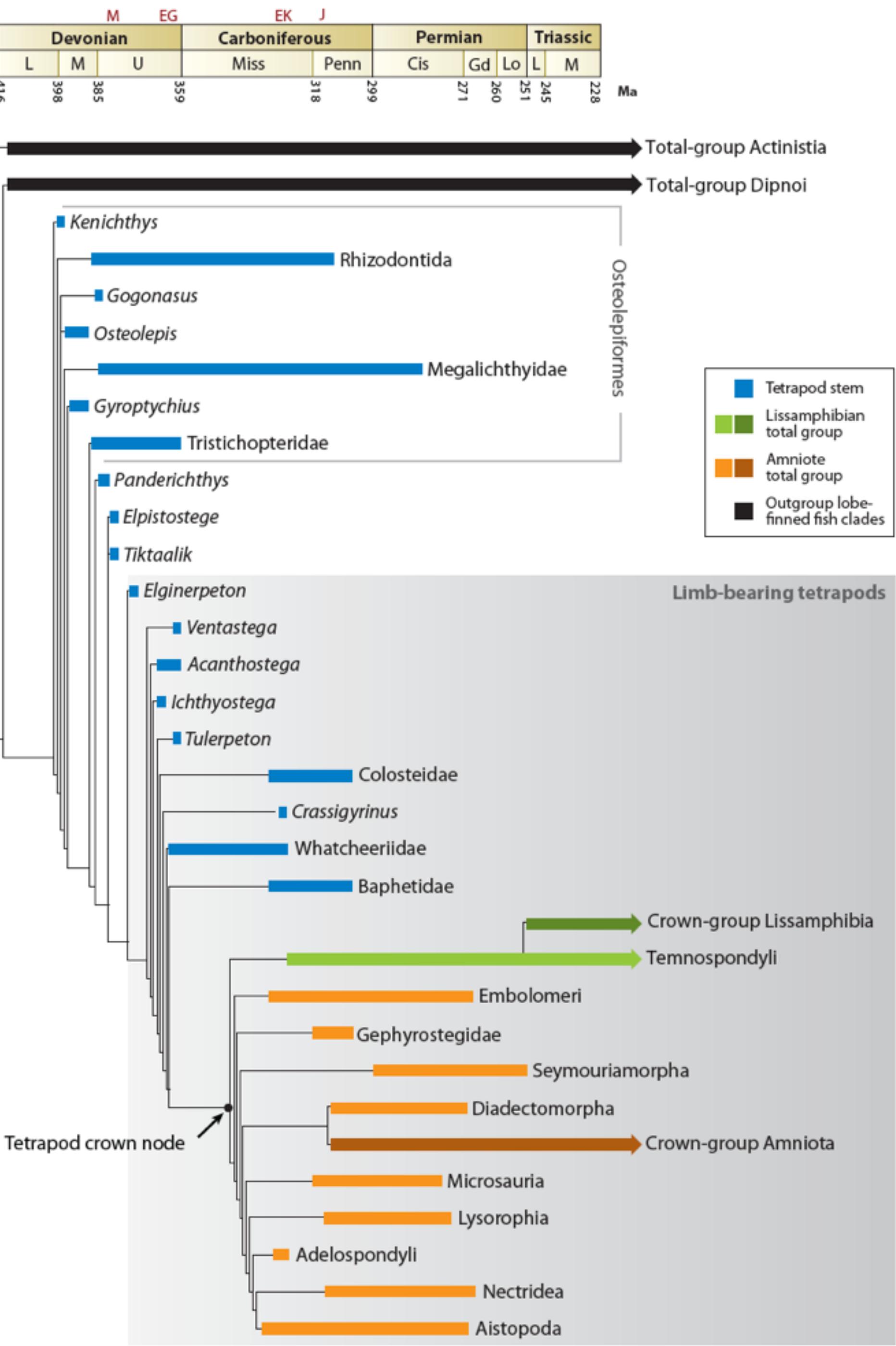


Phylogenetic trees are **difficult** to reconstruct...

... because they are **full of information**



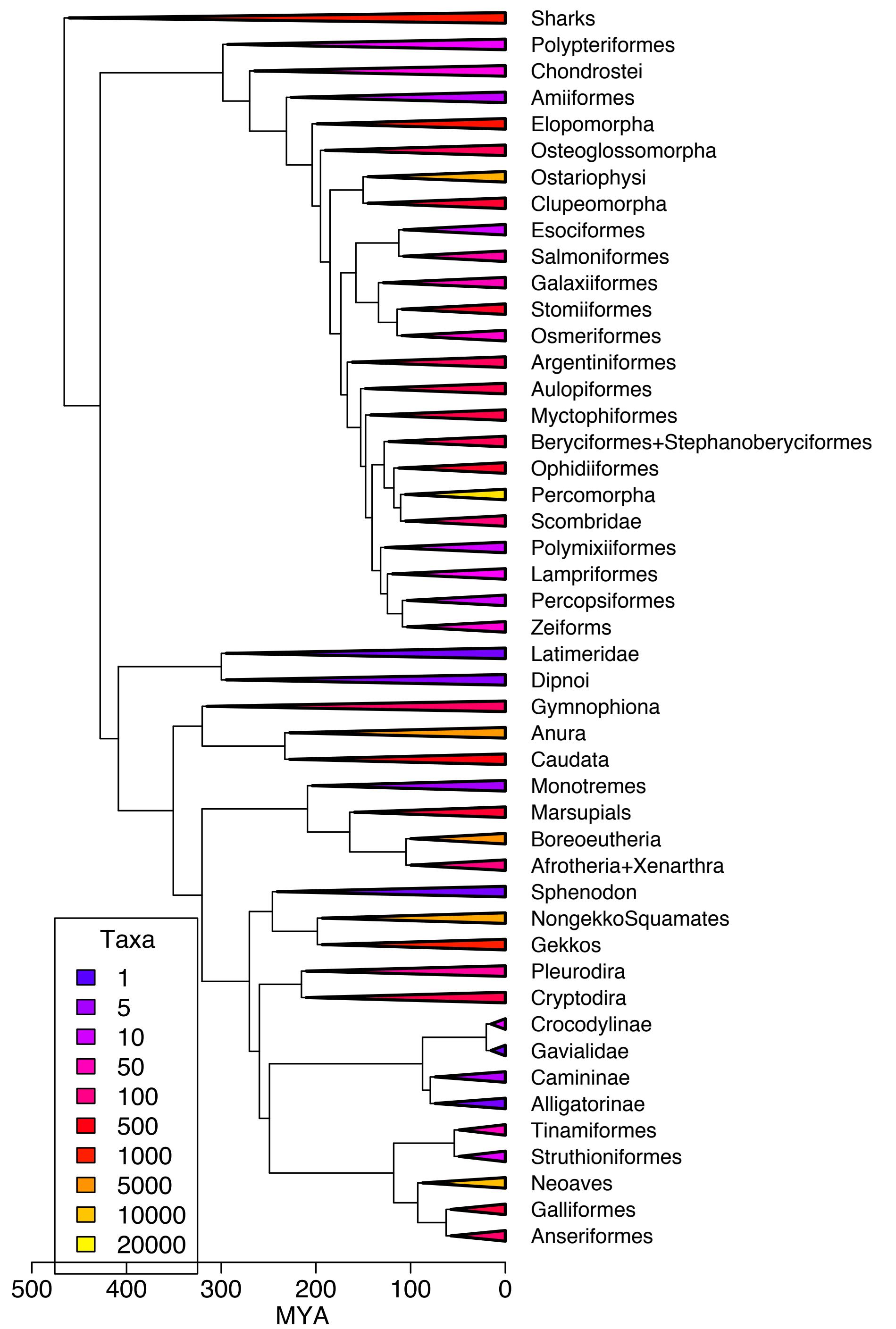
Roelants et al. 2007

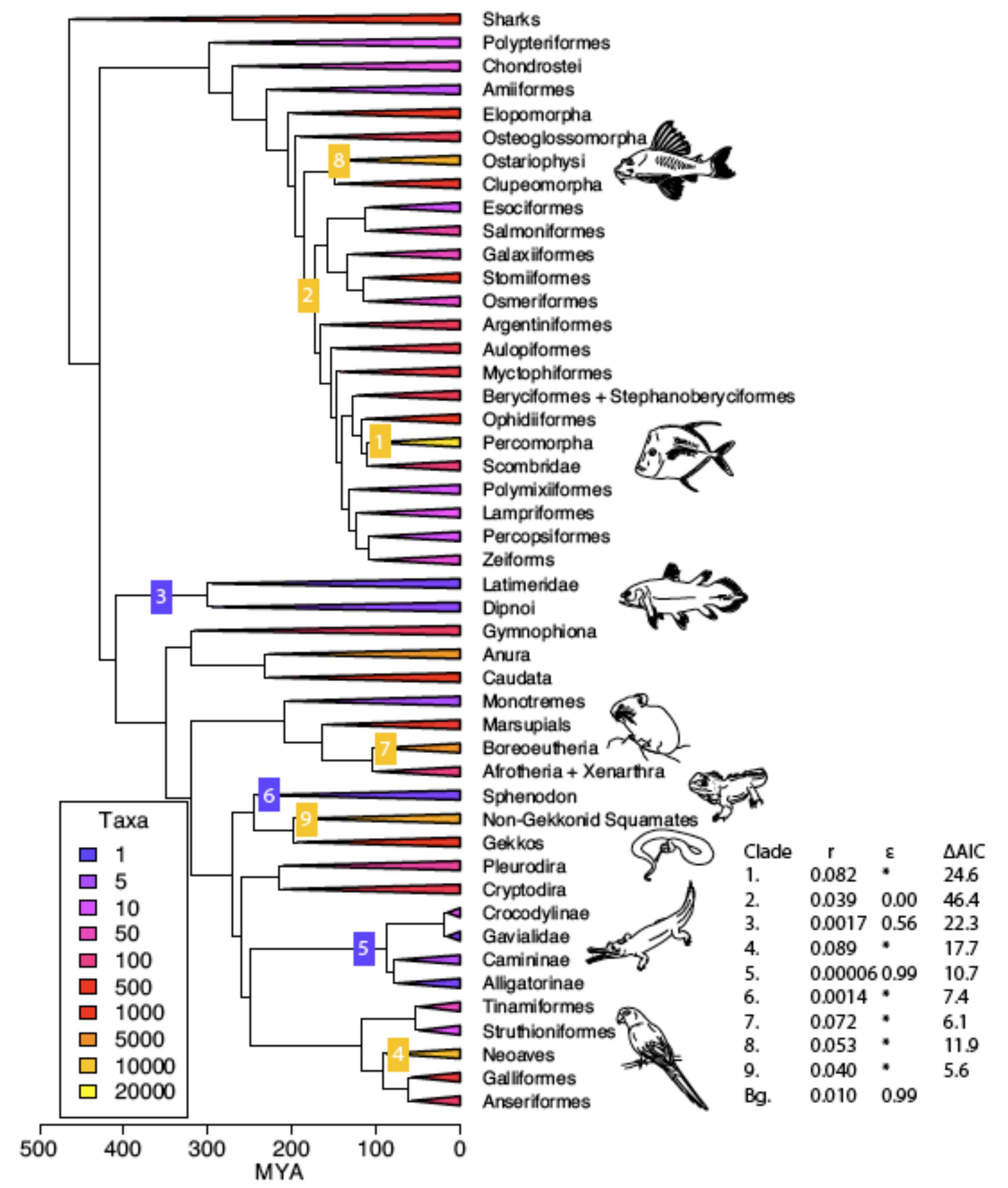


What can you do?

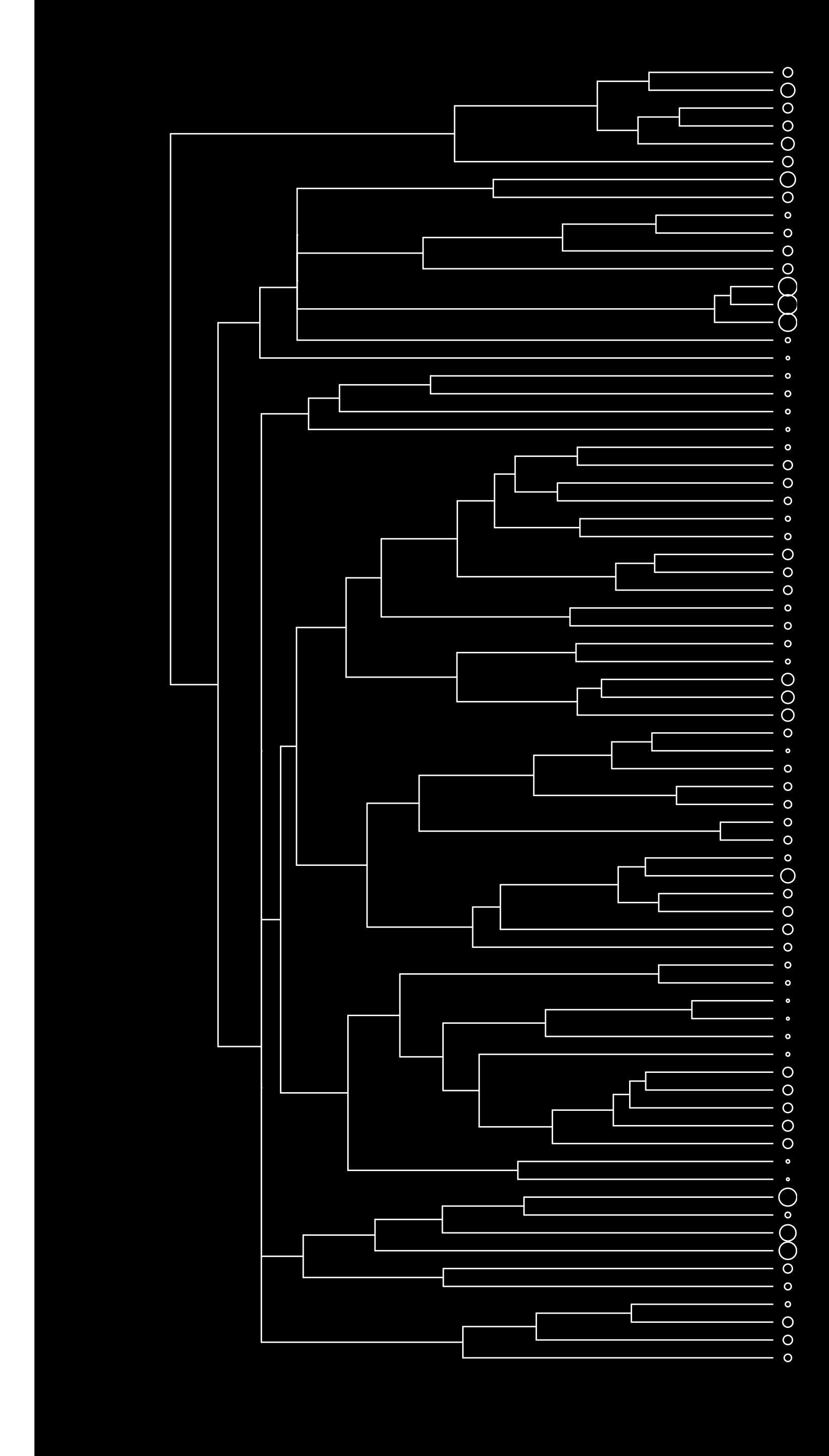
- Diversification (speciation and extinction)
- Character evolution
- Characters and diversification
- Biogeography
- Testing complex evolutionary models

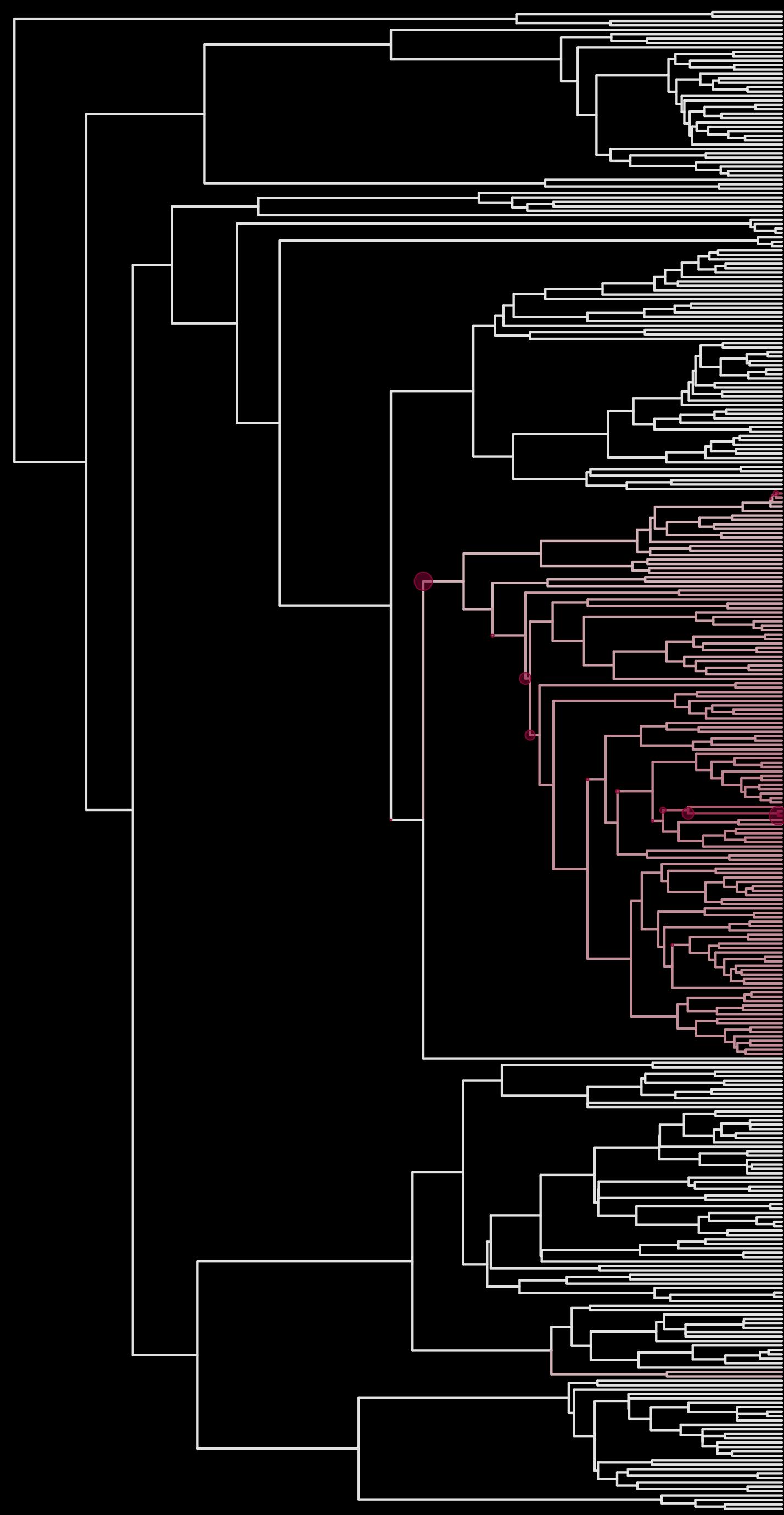
Diversification (speciation and extinction)



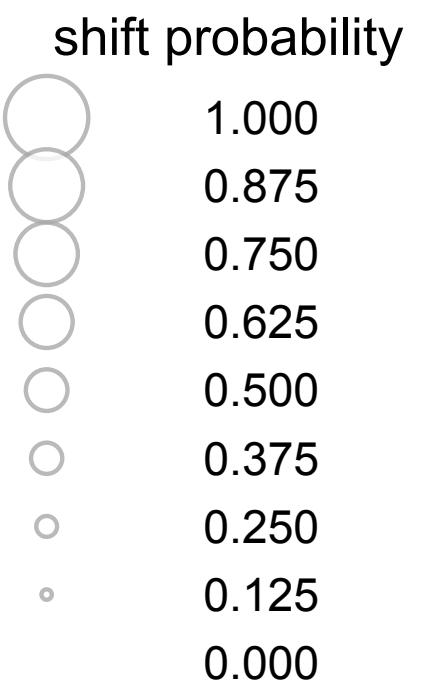
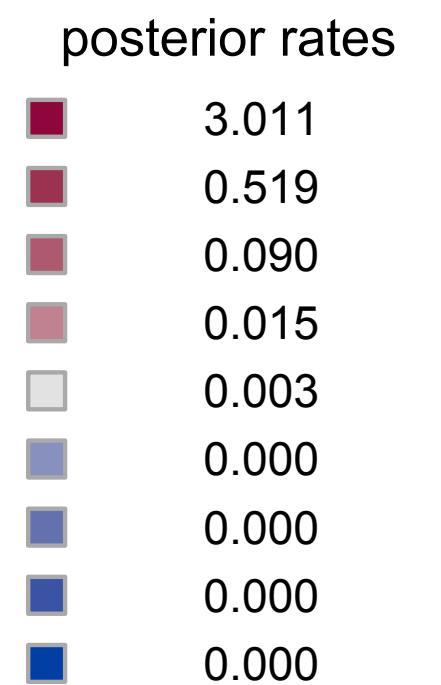


Character evolution





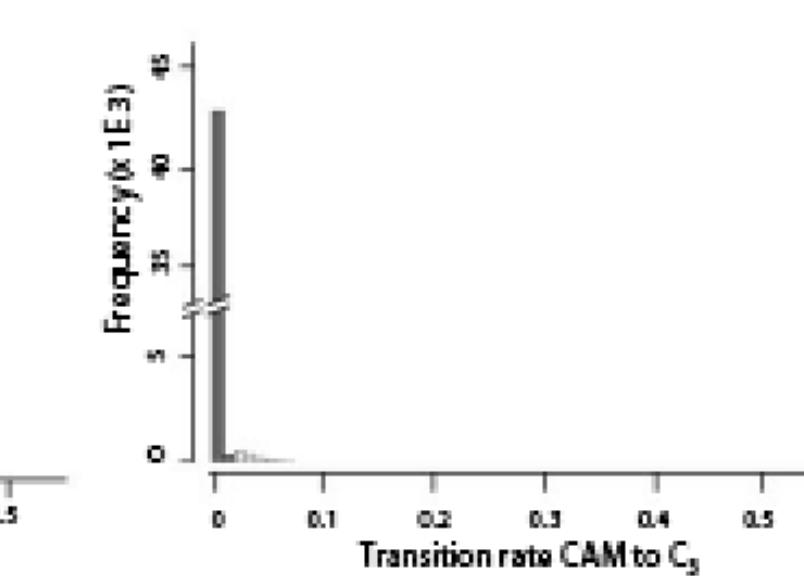
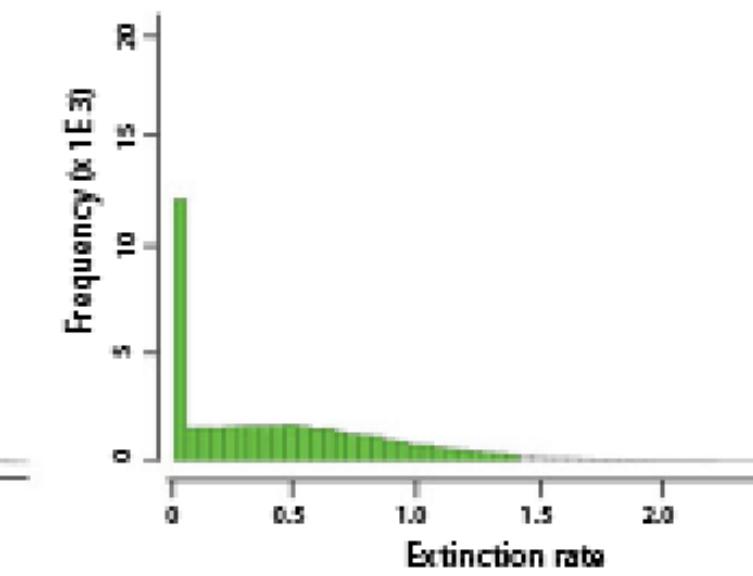
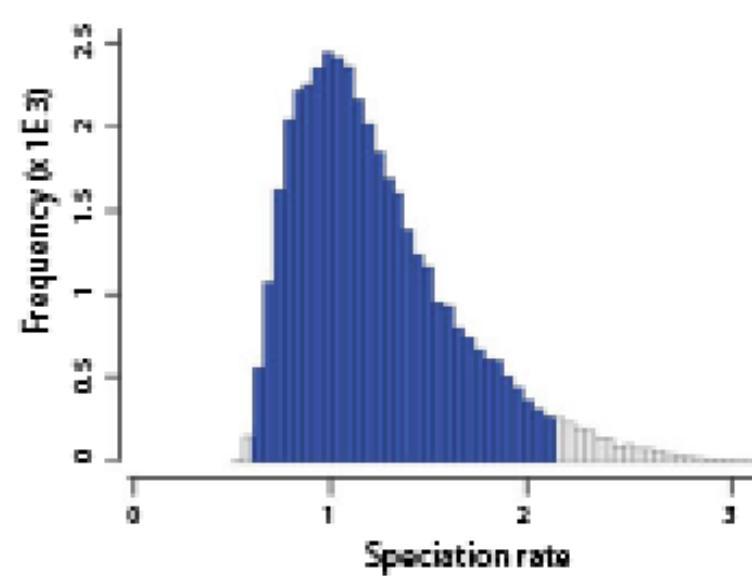
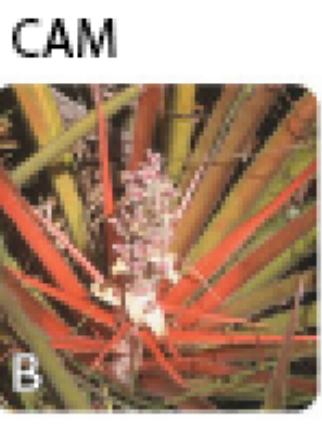
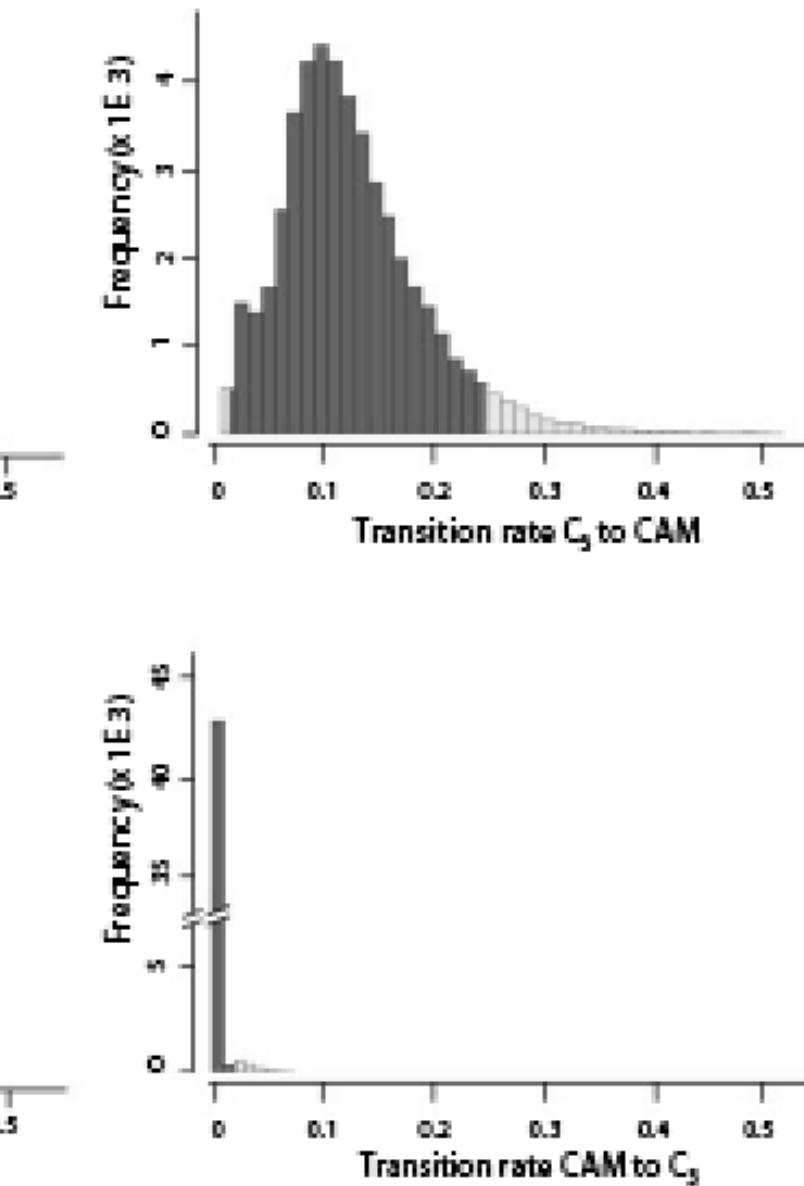
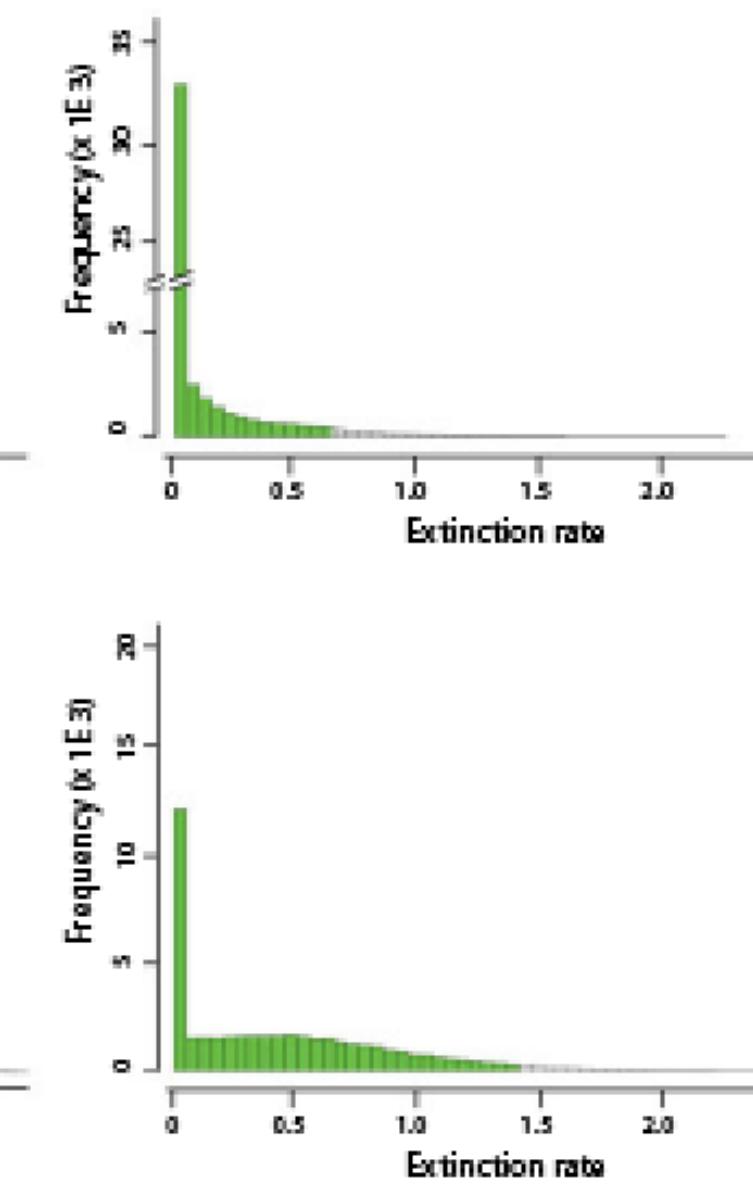
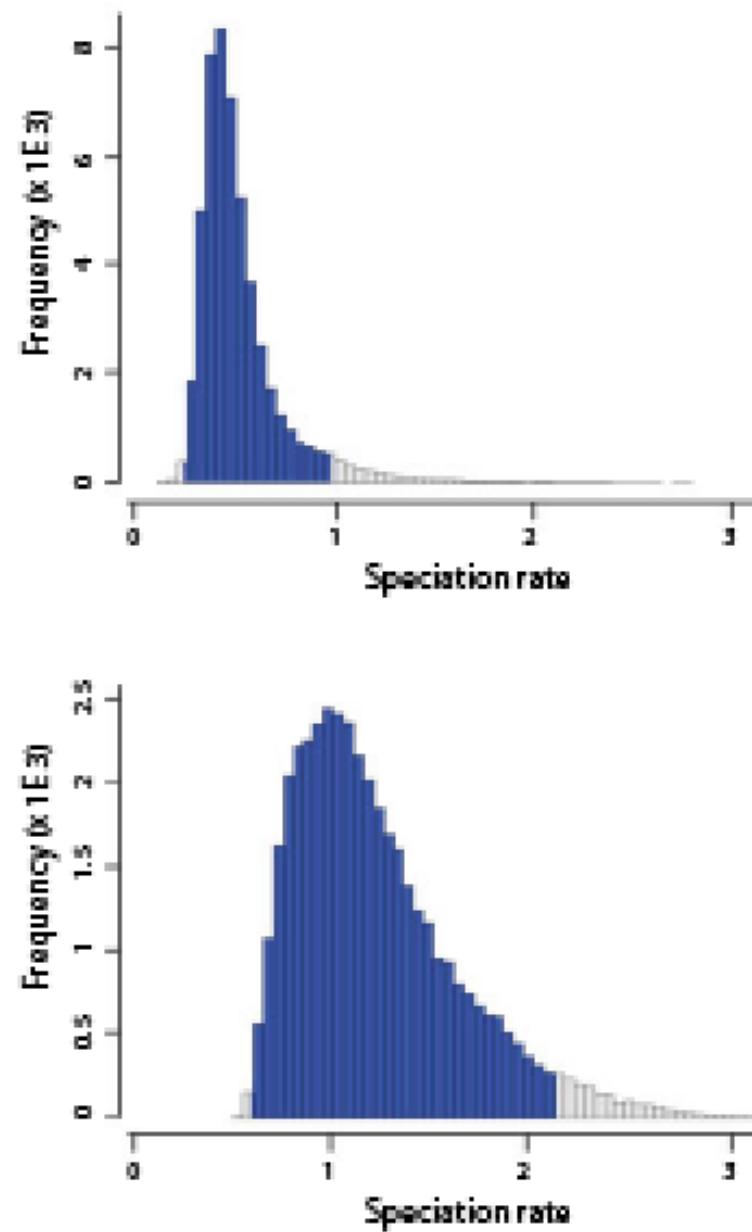
Bolitoglossinae



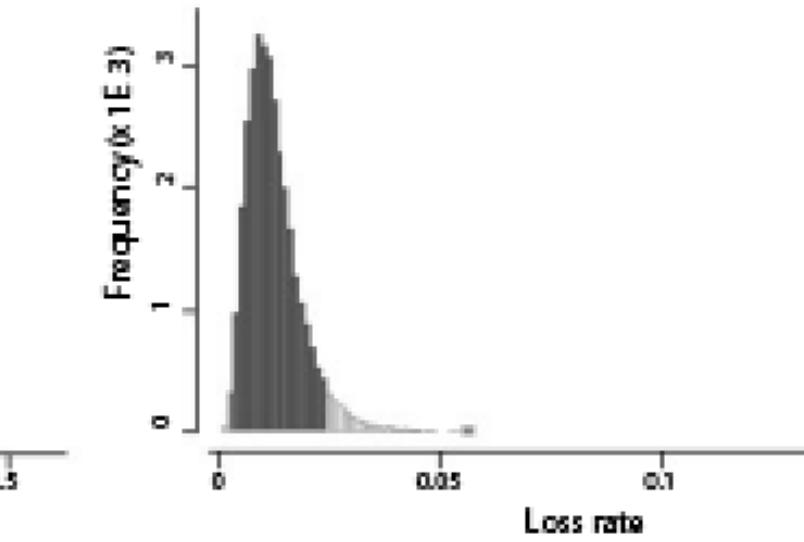
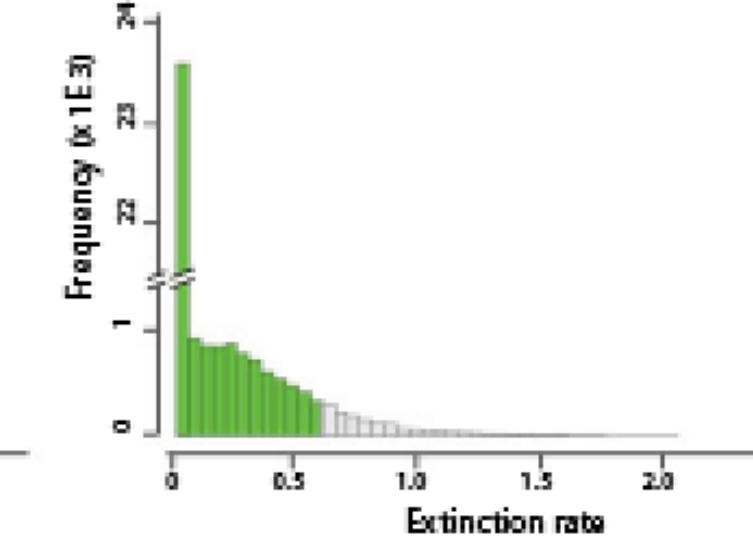
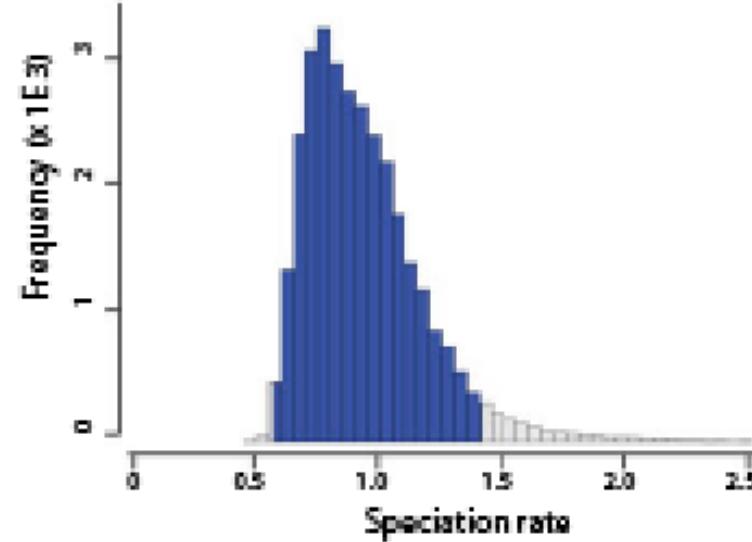
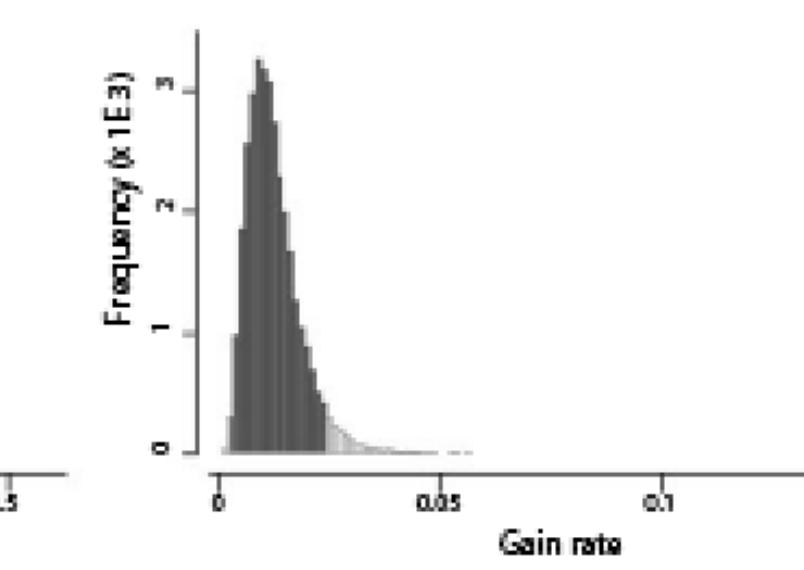
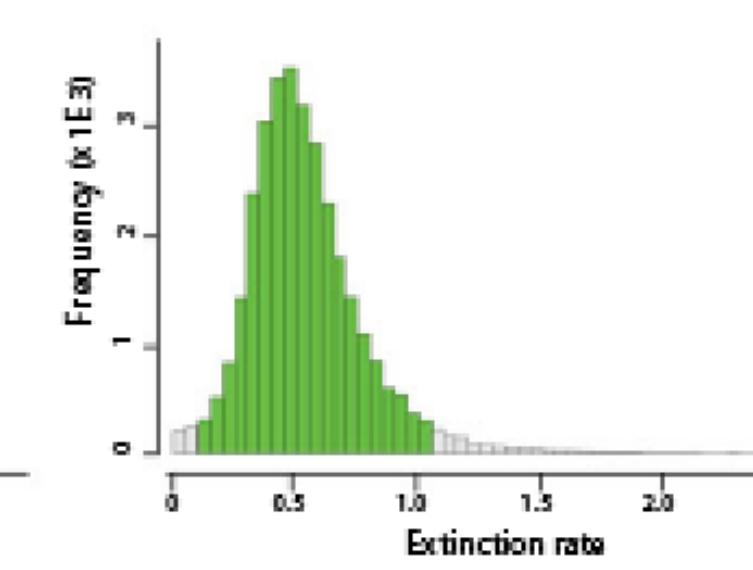
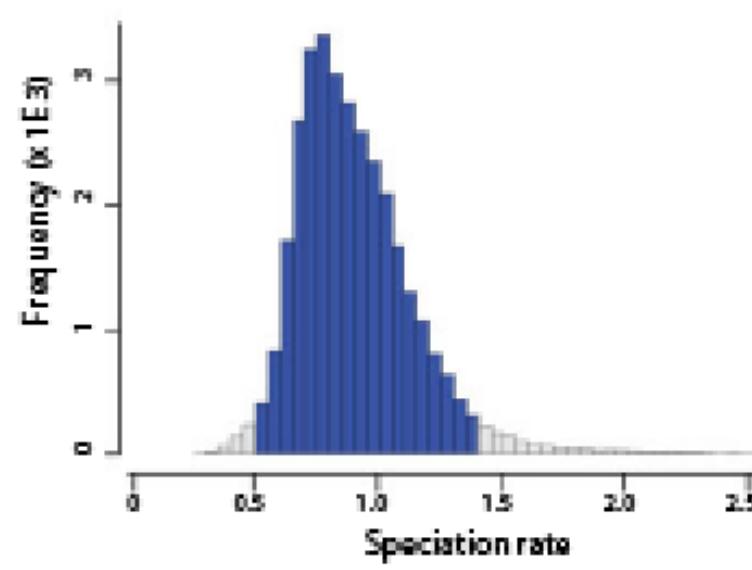
photos from wiki commons

Characters and diversification

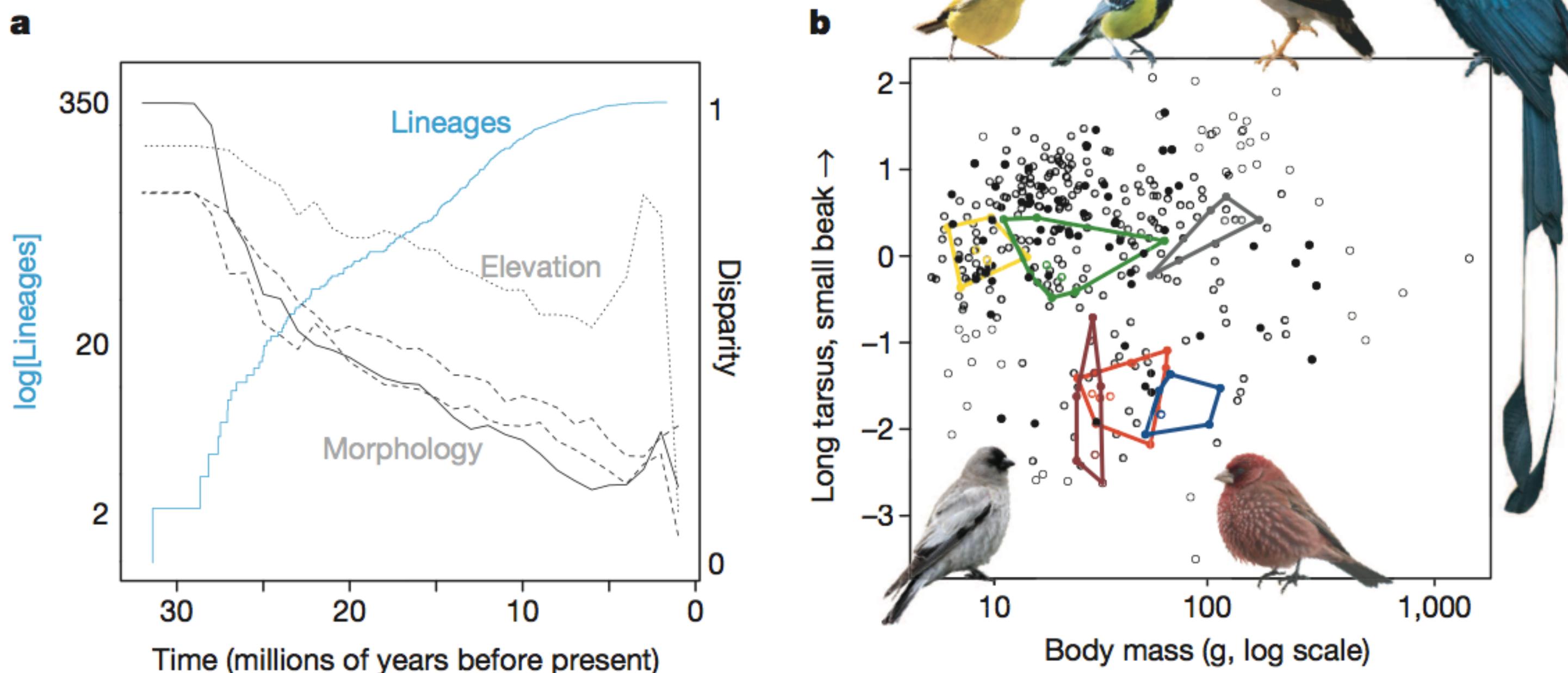
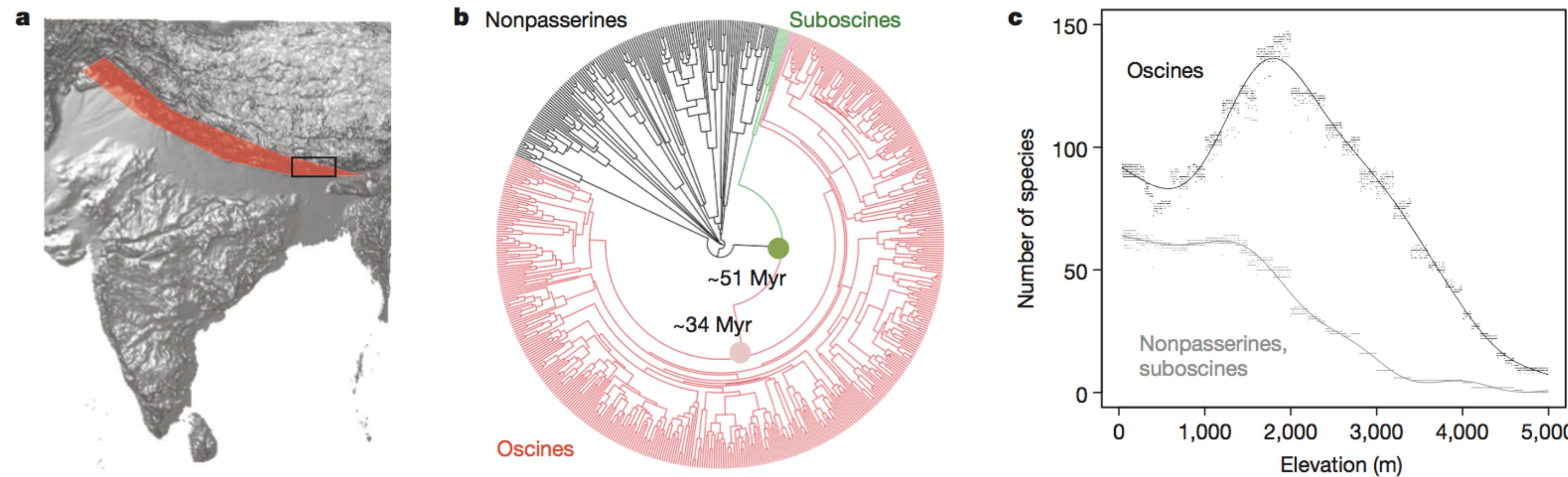
Photosynthetic pathway



Tank habit



Testing Complex Evolutionary Models







@lukejharmon



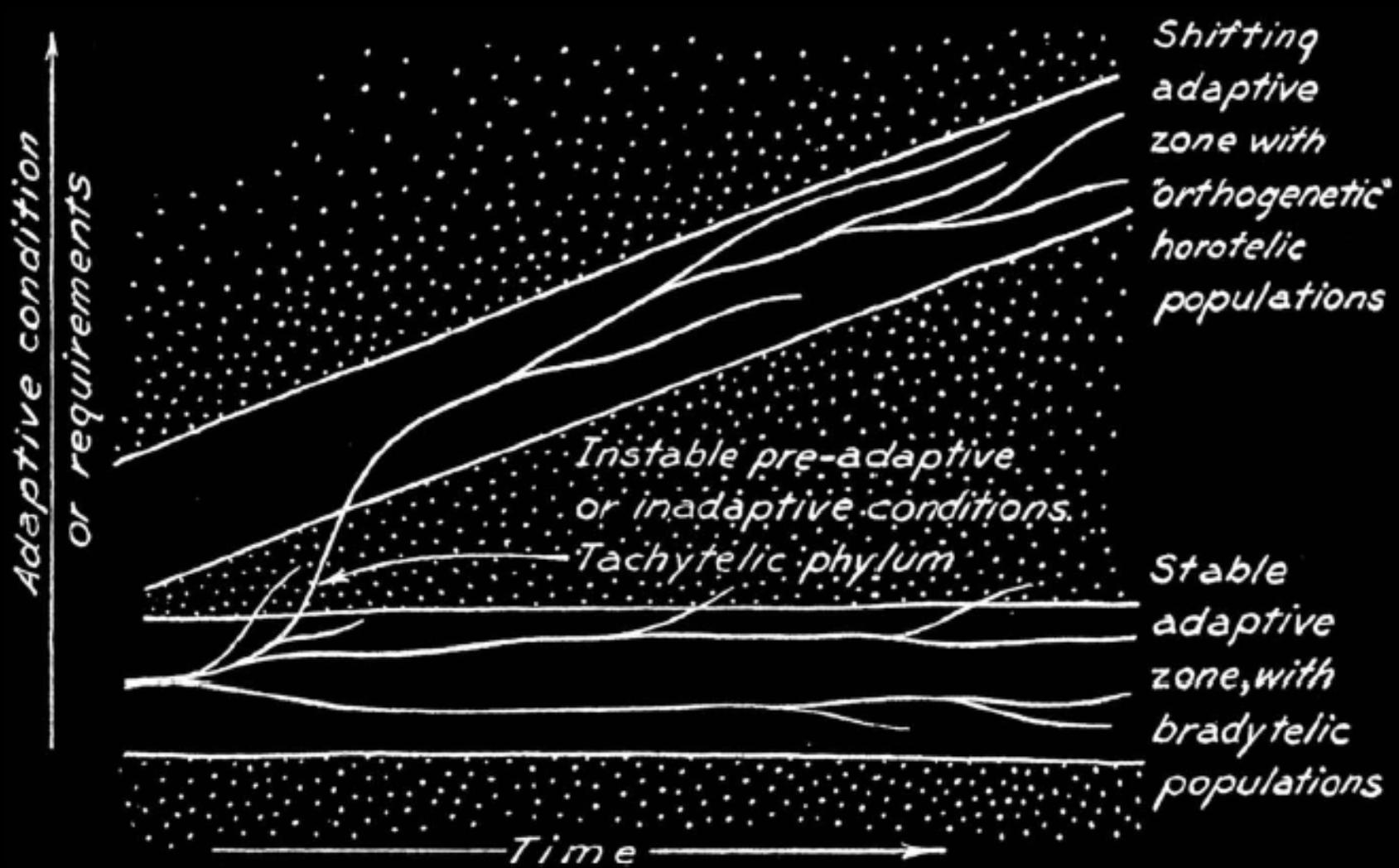
“Tell us a story from before we can remember”

--- from *The Tree of Life* (2011)

Arbor

- Arbor: big picture
- Main features
- Next-generation comparative biology

Adaptive Radiation



Simpson 1953

Arbor: big picture

Comparative
methods through
visual workflows

Comparative
methods through
visual workflows

Girder user management

Comparative
methods through
visual workflows

Girder user management

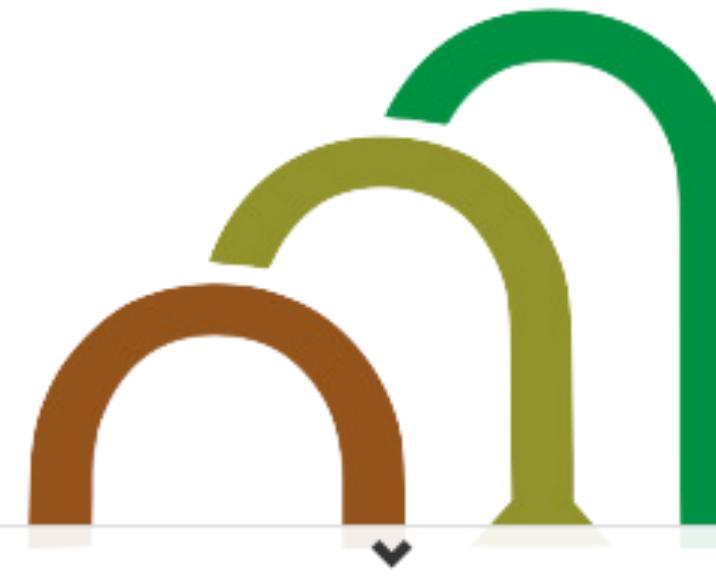
Romanesco workflow engine

Arbor

Luke

<https://arbor.kitware.com/#>

Apps Bookmarks SBB: Switzerland's b journals msOnline cnn Facebook Luke Harmon - Goog Cheap Blu-ray Movie Greatest Books Ever Other Bookmarks



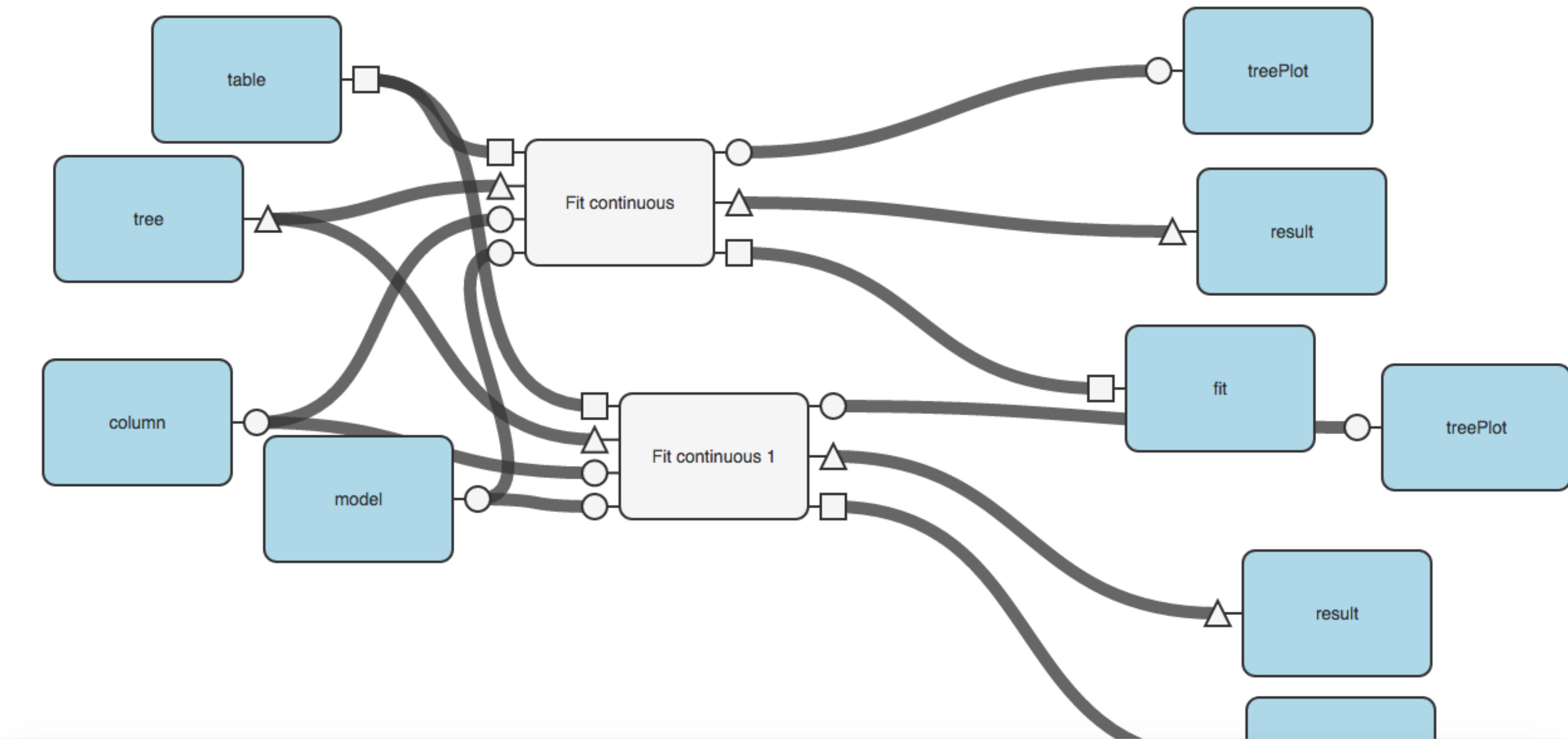
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Data Management Analysis Visualization

Browse or drop files

Use the panel below to visualize, analyze, or manage your data

- Arbor
- base
- Biosphere2
- catfish-media
- chelHack
- Costus



Comparative
methods through
visual workflows

Comparative
methods through
visual workflows

Data exchange
via
web services

Open Tree of
Life

Phenomics

Dryad

GBIF / BISON

Open Tree of
Life

Phenomics

Dryad

GBIF / BISON



Open Tree of
Life

Phenomics



Dryad

GBIF / BISON

MongoDB database

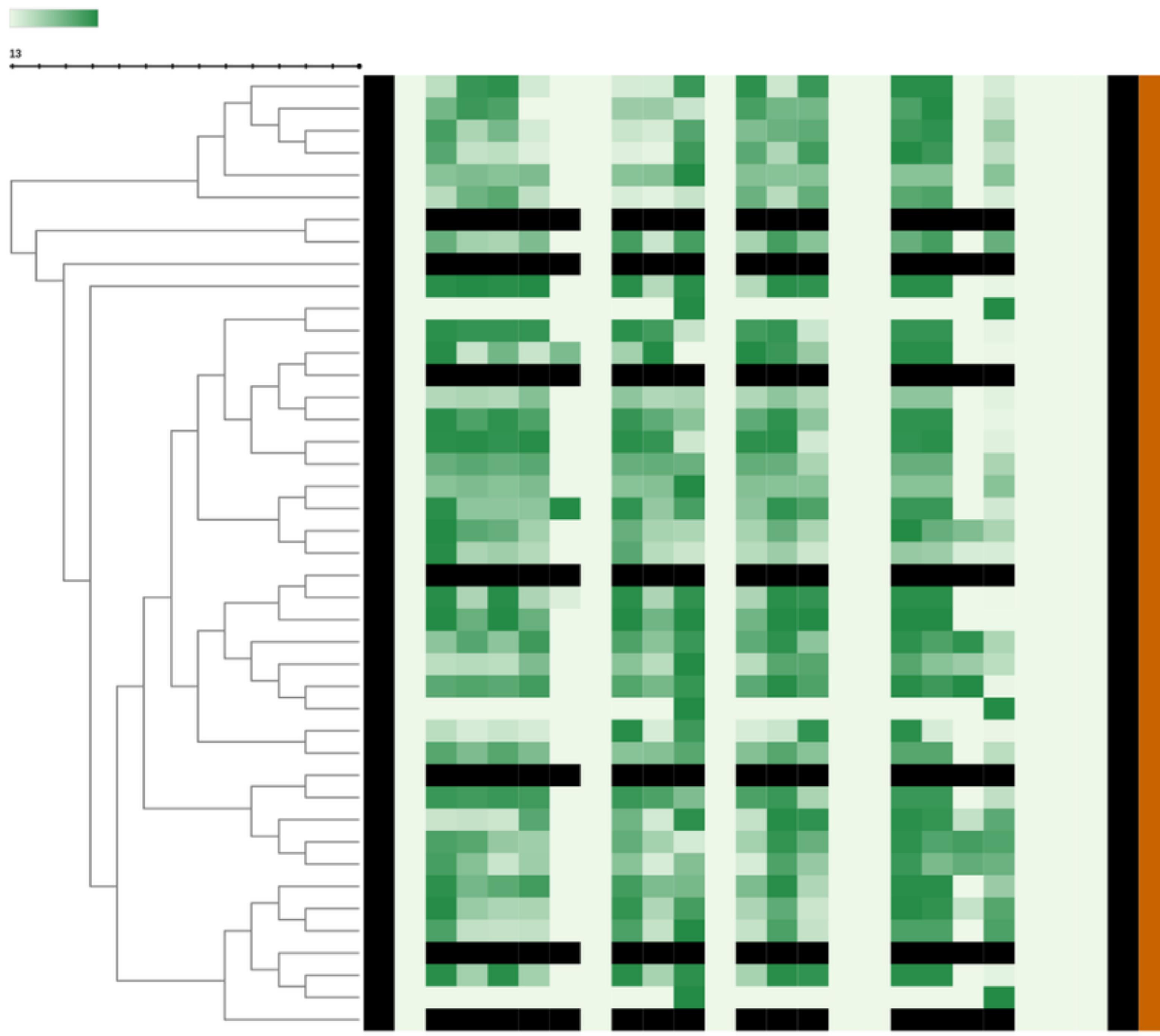
Comparative
methods through
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Data exchange
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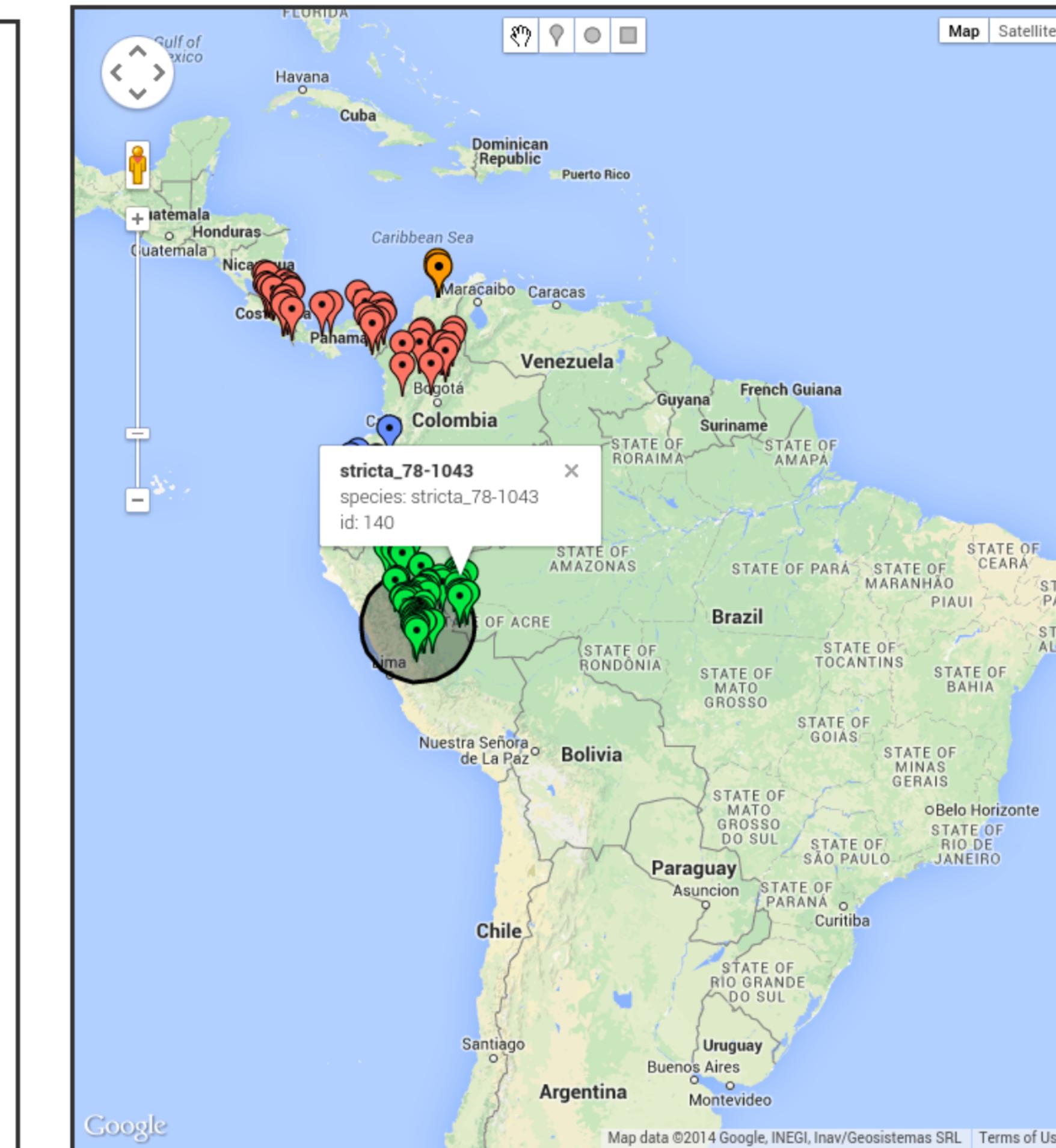
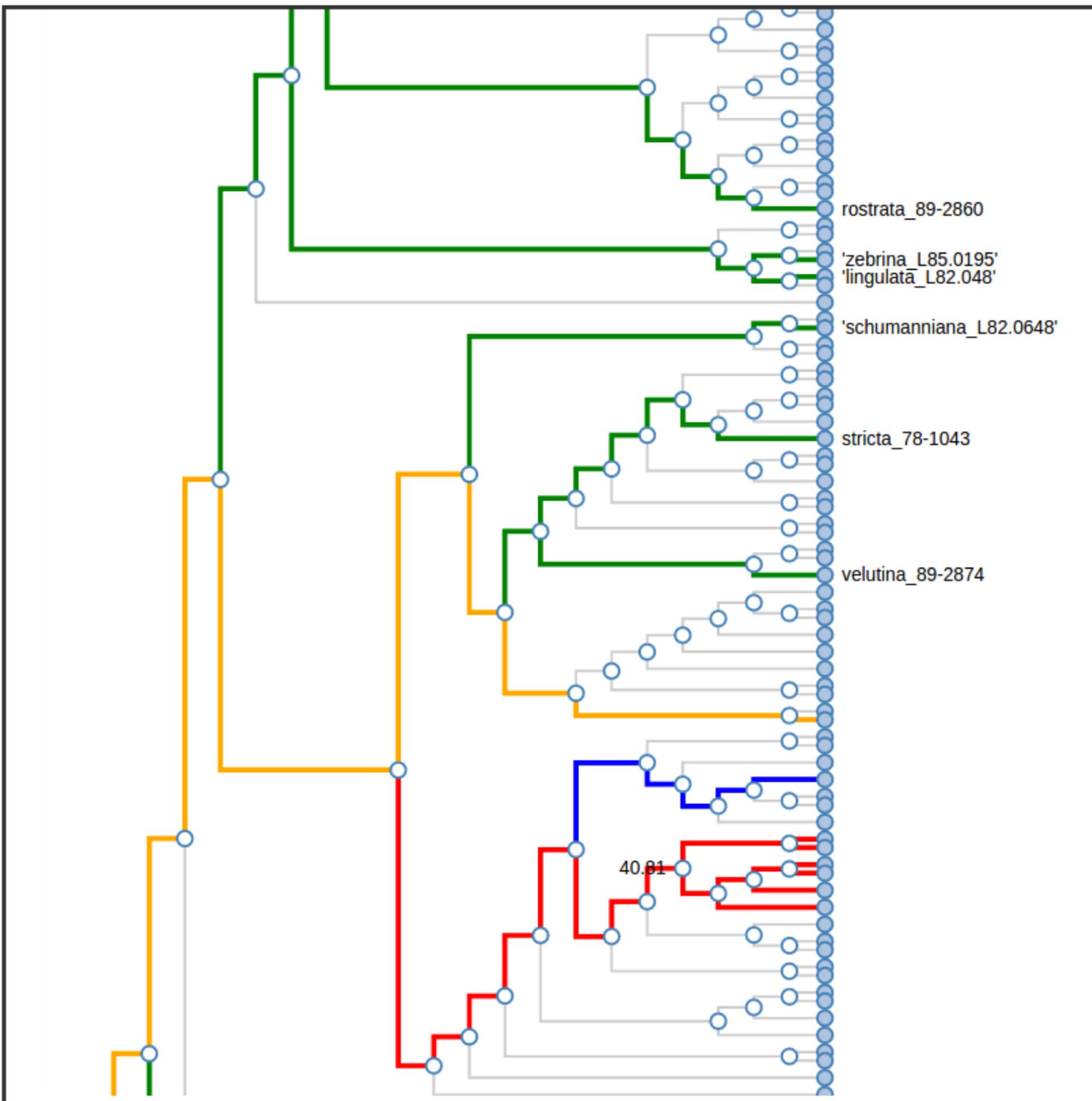
Comparative
methods through
visual workflows

Data exchange
via
web services

Implement novel
analysis workflows



Arbor Collection: Default ▾ Dataset fullHeliconia-loc-ids.nested.json ▾

[Empty Tree](#) [Full Tree](#) Show Names Enable Clade Selection [Increase Depth](#) [Decrease Depth](#) [Increase Height](#) [Decrease Height](#) [Clear Highlights](#) [Clear Map Markers](#)

Comparative
methods through
visual workflows

Data exchange
via
web services

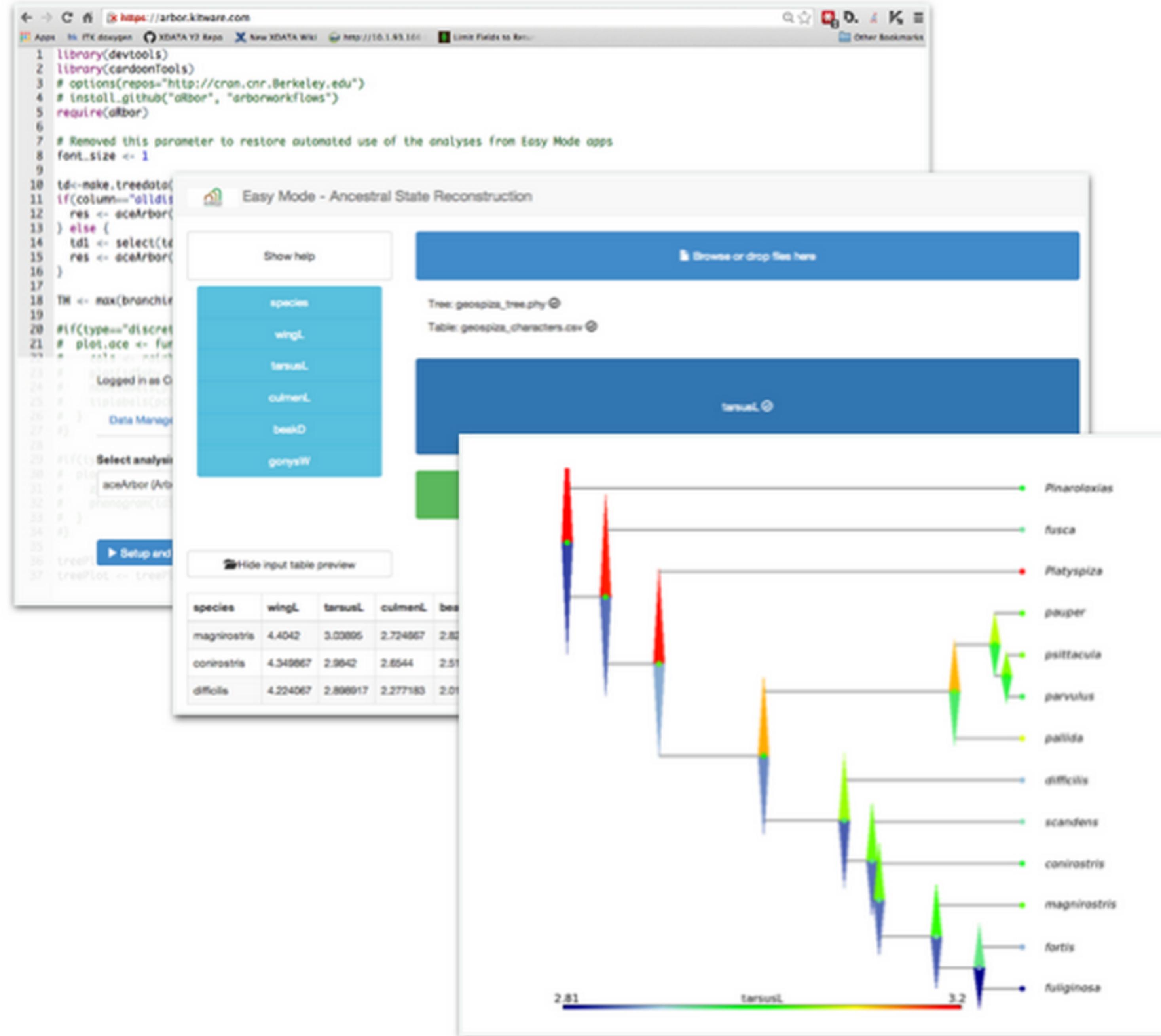
Implement novel
analysis workflows

Comparative
methods through
visual workflows

Data exchange
via
web services

Implement novel
analysis workflows

Arbor
Apps



```

1 library(devtools)
2 library(cardoonTools)
3 # options(repos="http://cran.cnr.Berkeley.edu")
4 # install.github("arbor", "arborworkflows")
5 require(arbor)
6
7 # Removed this parameter to restore automated use of the analyses from Easy Mode apps
8 font.size <- 1
9
10 td<-make.treedata(
11   if(column=="allids"
12     res <- aceArbor(
13   ) else {
14     tdi <- select(tdi,
15     res <- aceArbor(
16   )
17
18 TM <- max(branchtip)
19
20 #if(type=="discret
21 #  plot.ace <- futu
22 #
23 #
24 # Logged in as O
25 # EQUATION LOGO
26 # ]
27 # Data Manager
28 #
29 #if(choose=="treeplot"
30 #  treeplot <- tre
31 #  treeplot <- tre
32 #  treeplot <- tre
33 #  treeplot <- tre
34 #
35 treeplot <- tre
36 treeplot <- tre
37 treeplot <- tre

```



<https://www.arborworkflows.com>