

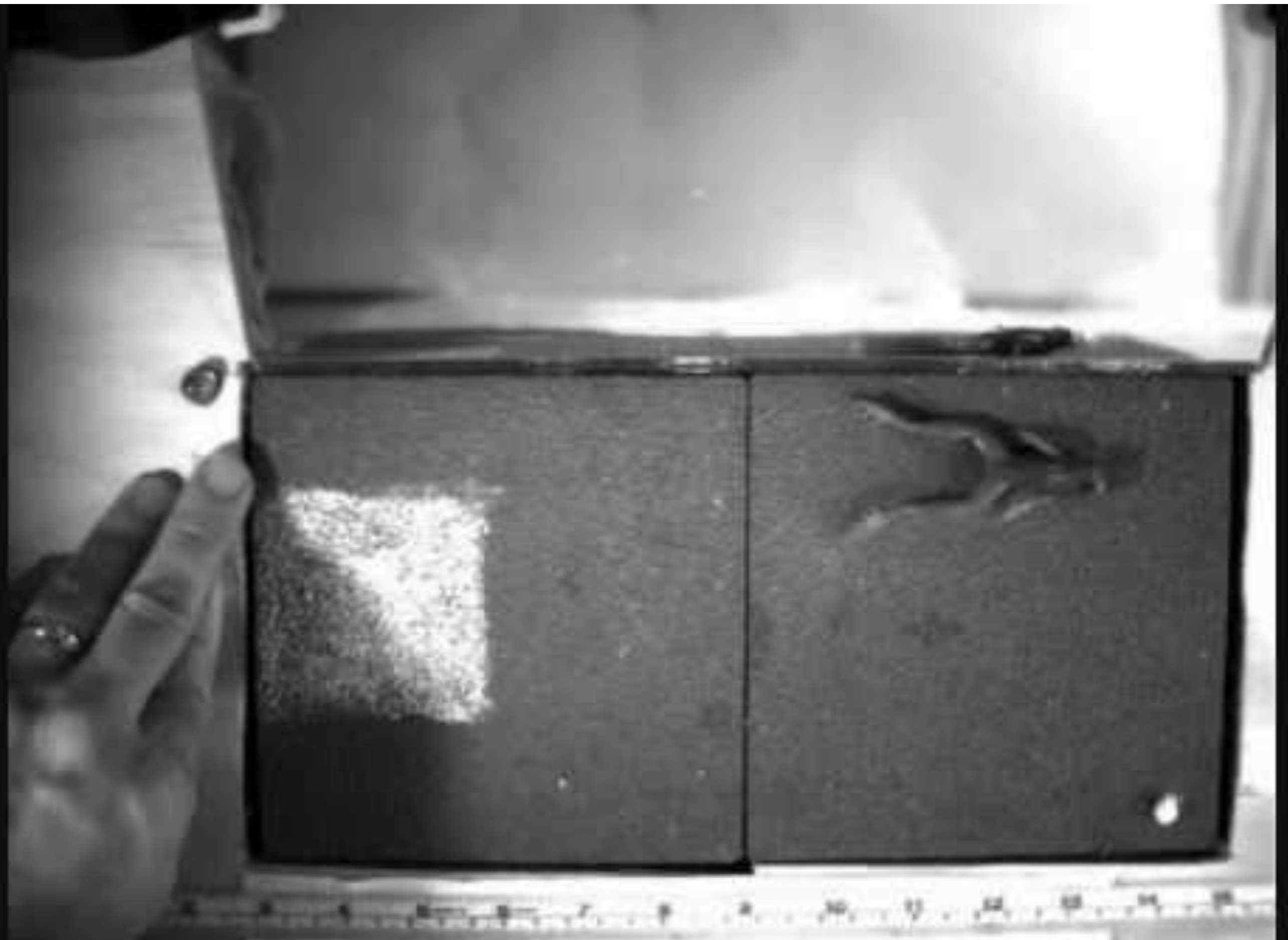
# What can we learn from a tree?



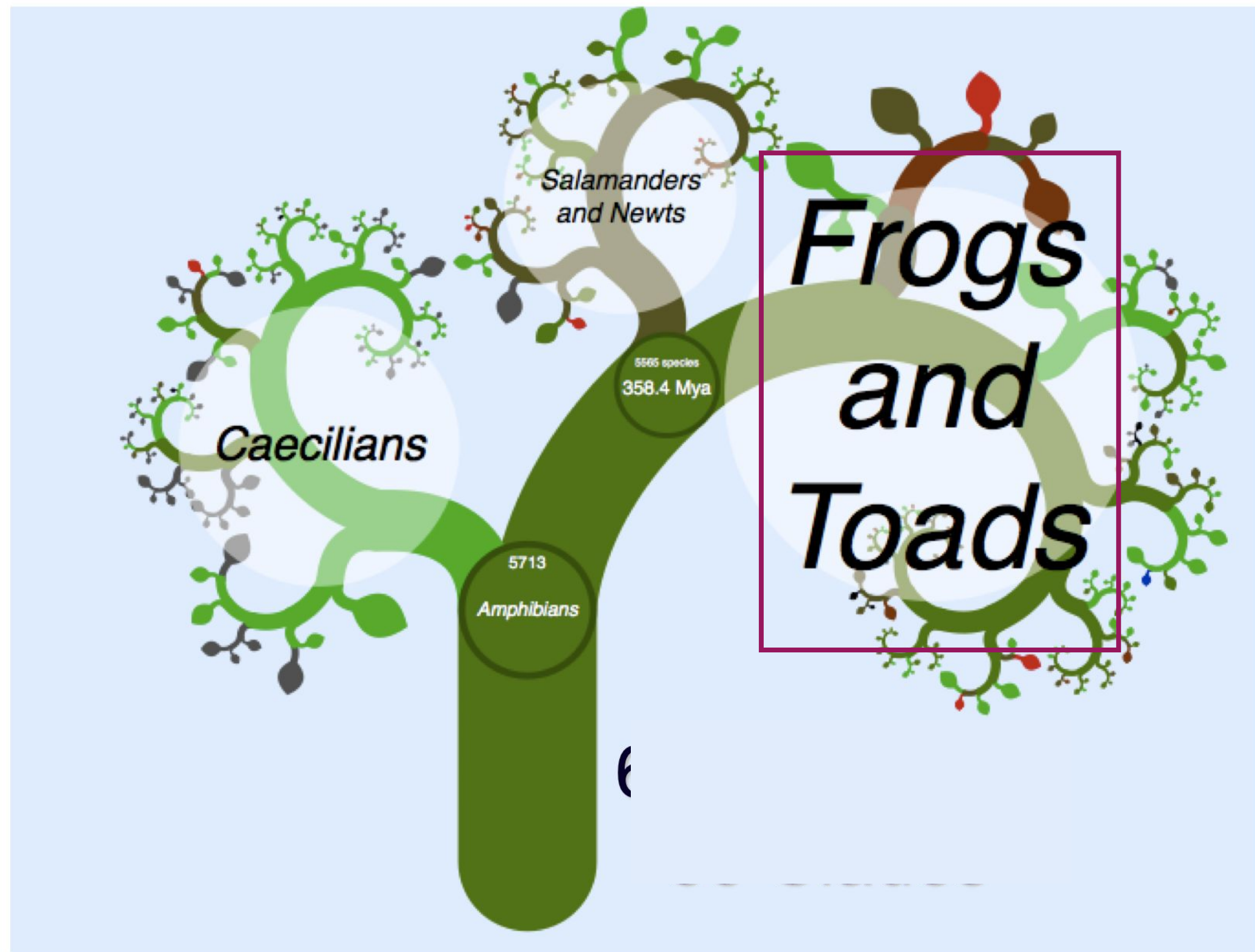




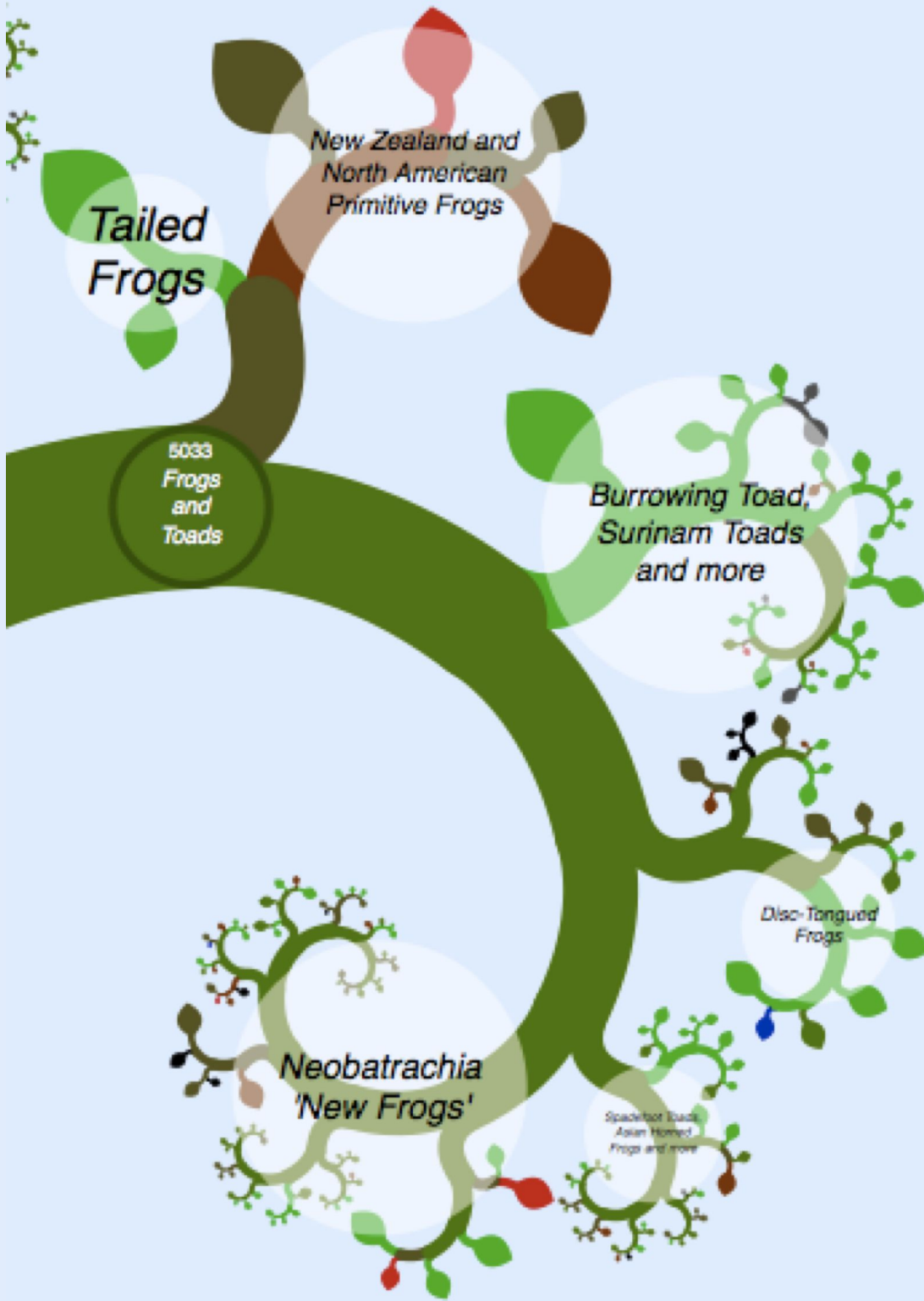


























The answer: in some times and places, new species form very rapidly...

... and other times very slowly.



The pace of evolution varies dramatically  
depending on time, place, and taxonomic group





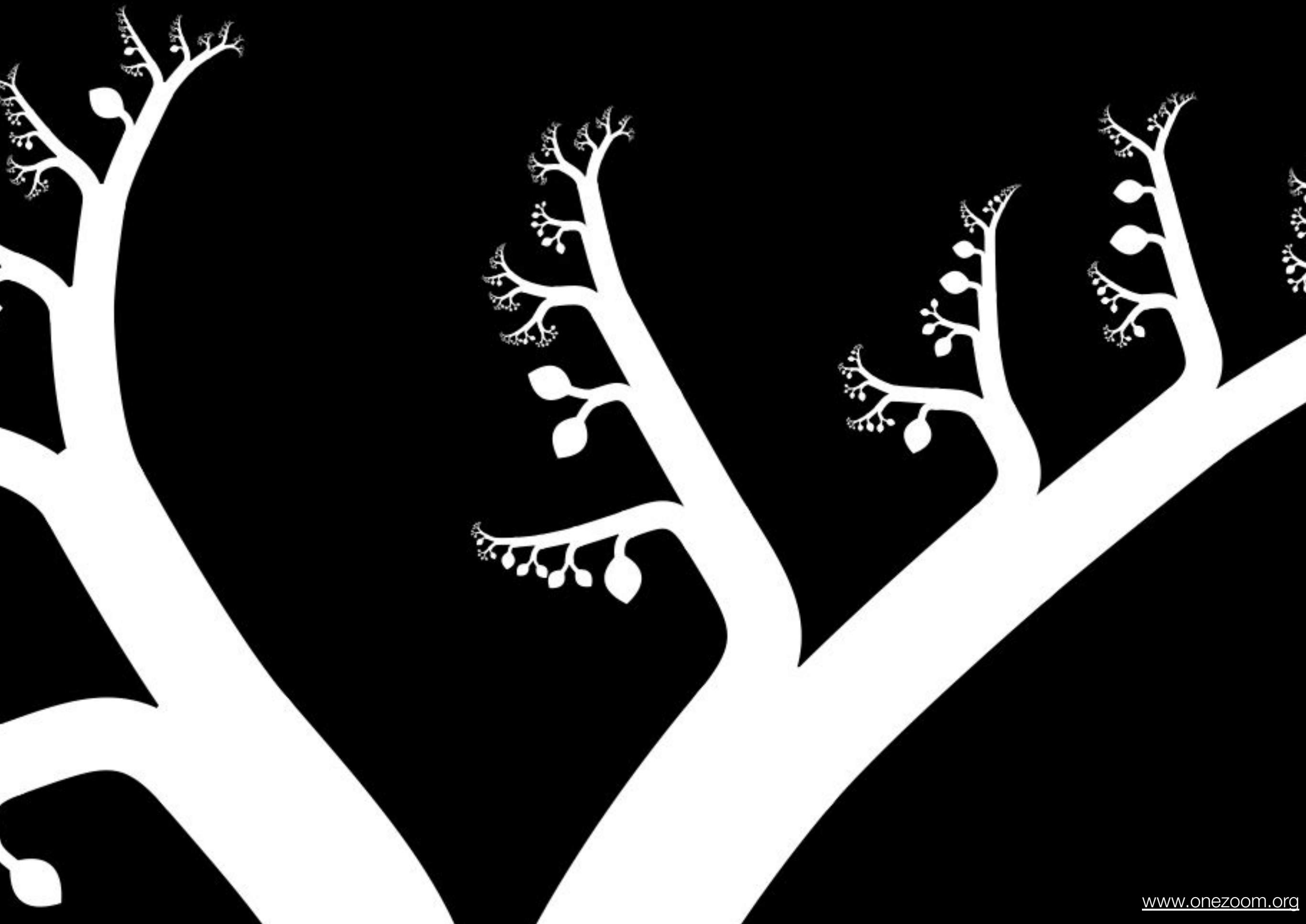








NGC 2818





Learning about Deep  
Time

from the

Tree of Life

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

And is any of this  
**predictable**?



# Phylogenetic comparative methods

population genetics

quantitative genetics

comparative  
methods

paleobiology

phylogenetics





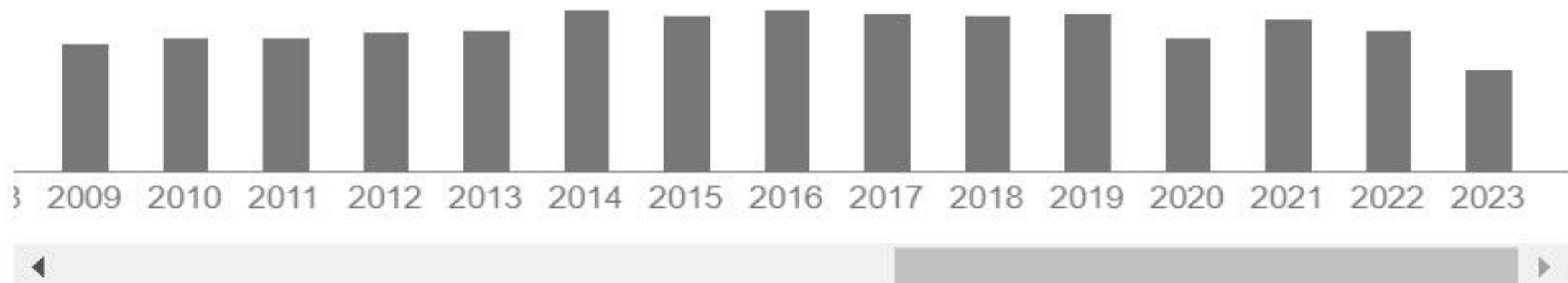
Joe Felsenstein

## 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 10396





[Liam J. Revell](#)

## phytools: an R package for phylogenetic comparative biology (and other things)

[PDF] from google.com

Uploaded 2021/3/24

[Full View](#)

Authors Liam J Revell

Publication date 2012

Journal Methods in Ecology and Evolution

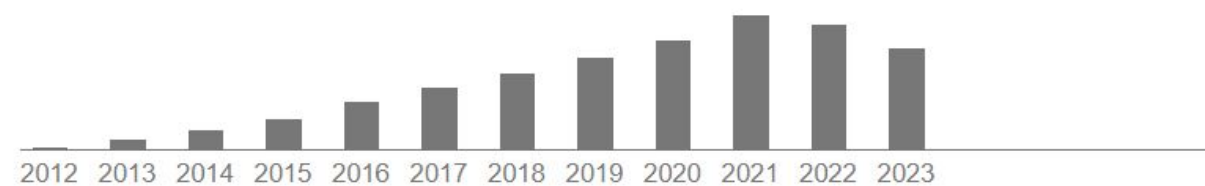
Volume 3

Pages 217-223

Publisher Blackwell Publishing Ltd

Description 1. Here, I present a new, multifunctional phylogenetics package, phytools, for the R statistical computing environment.

Total citations [Cited by 7525](#)



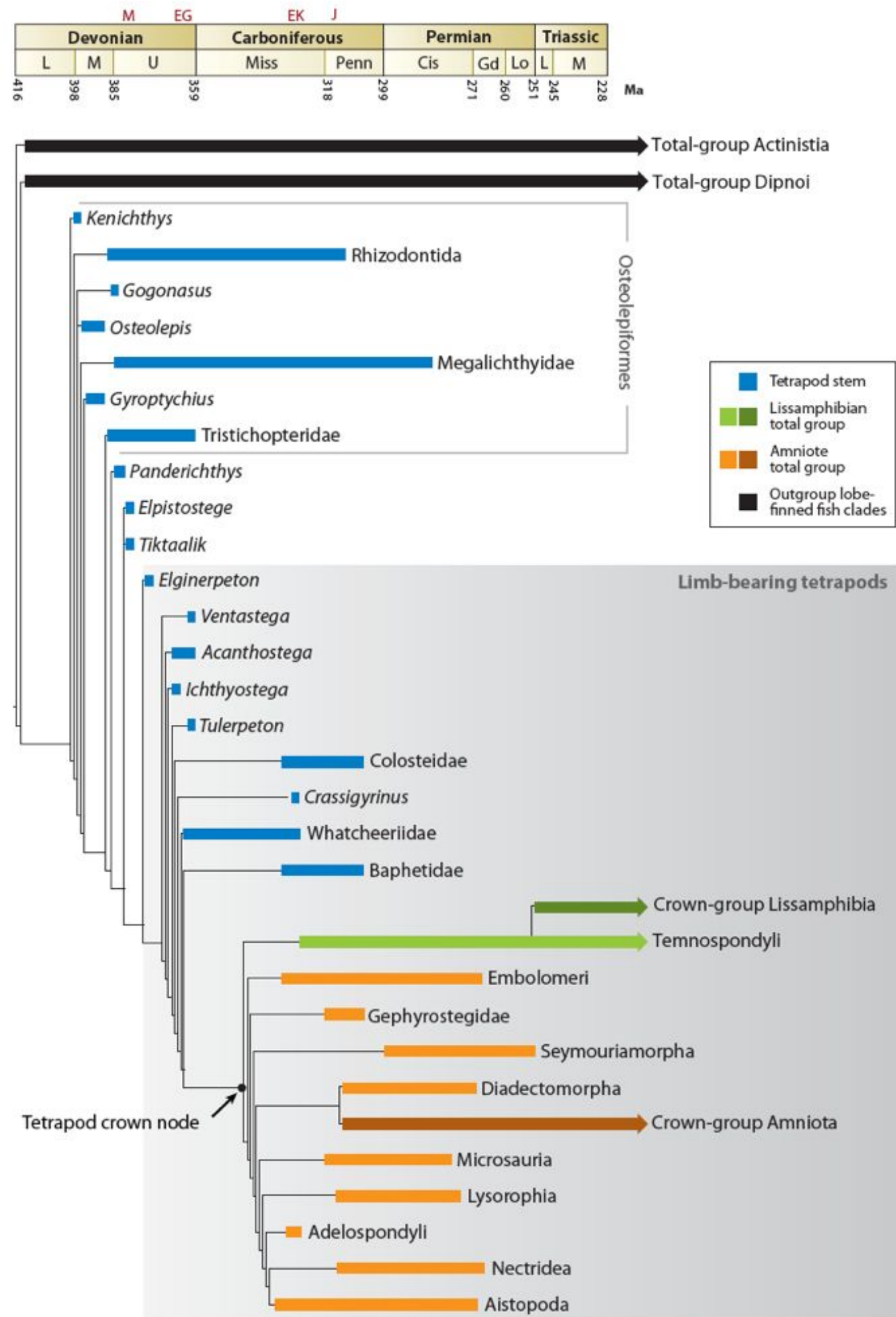


Phylogenetic trees are **difficult** to reconstruct...

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





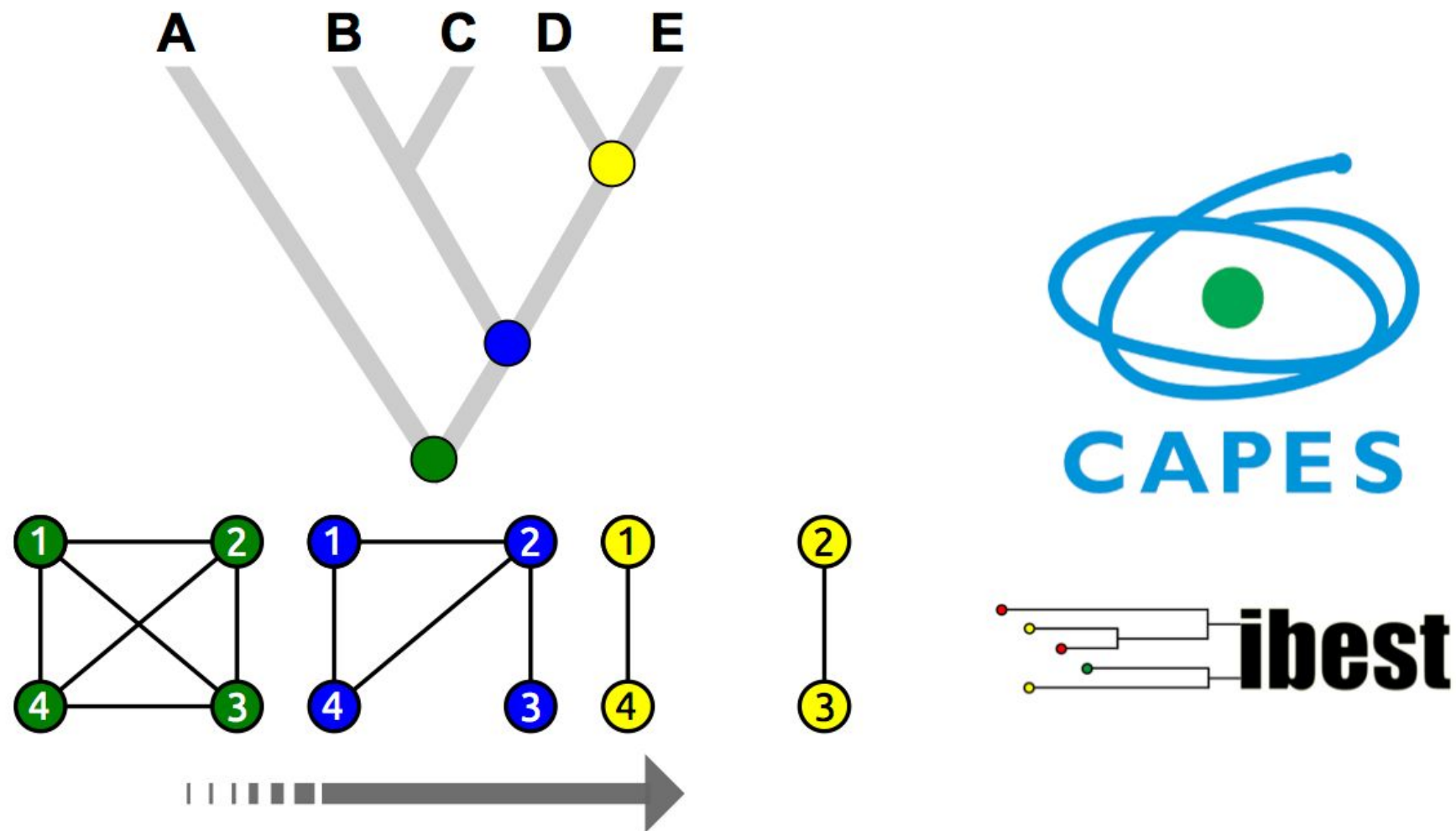




Daniel Caetano



# Estimating correlated rates of trait evolution from phylogenies with uncertainty



Daniel S. Caetano and Luke J. Harmon

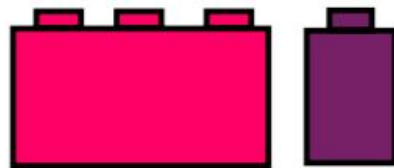
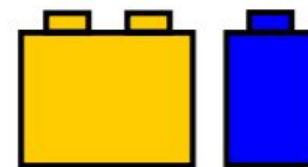
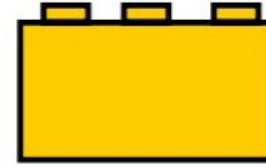
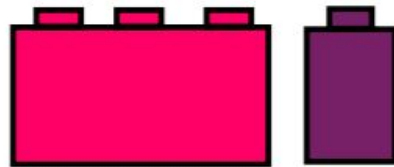
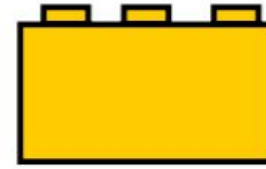
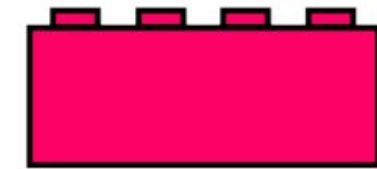


Slingjaw wrasse  
*Epibulus*  
*insidiator*

Video from Peter  
Wainwright

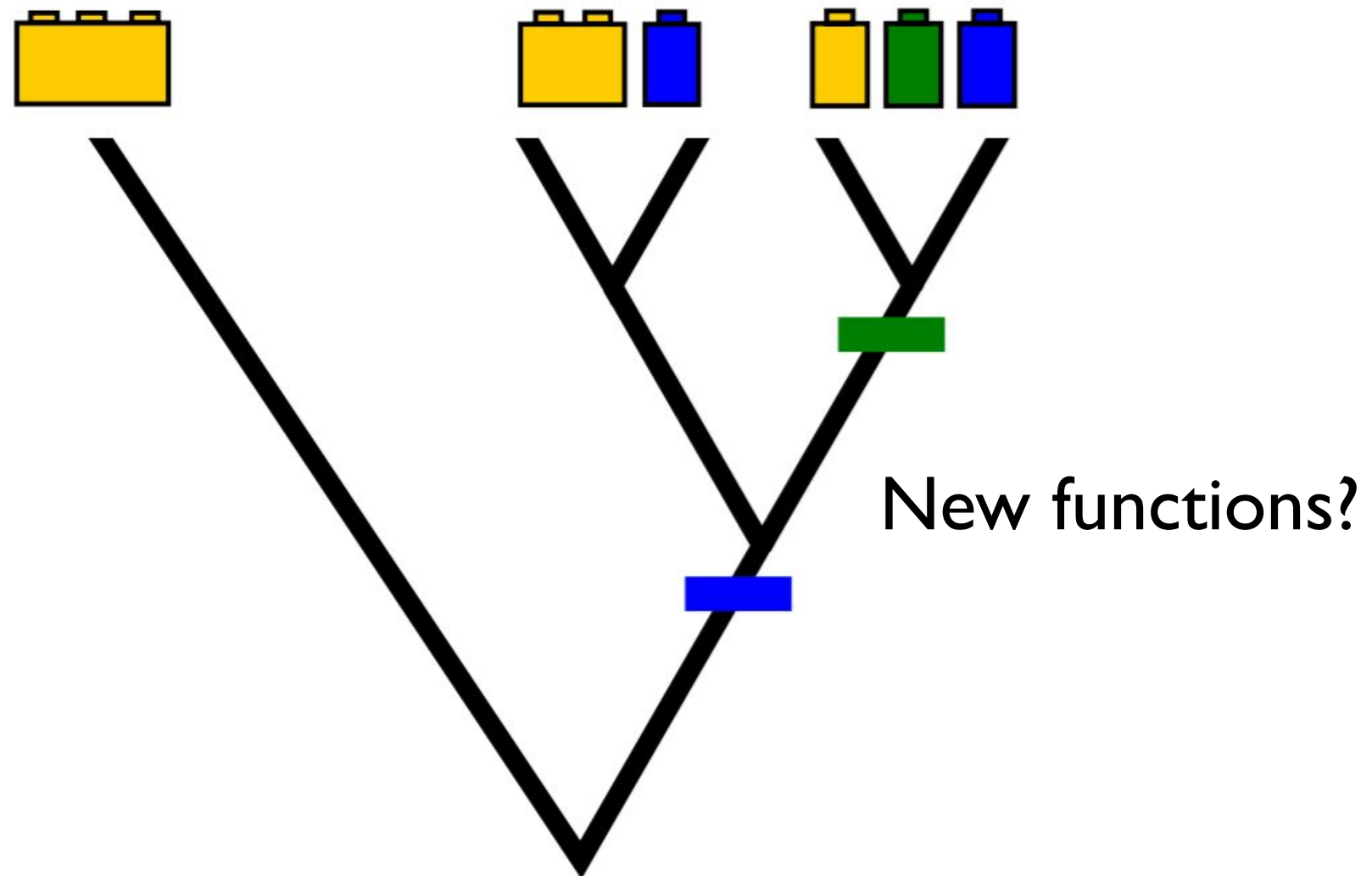


integration

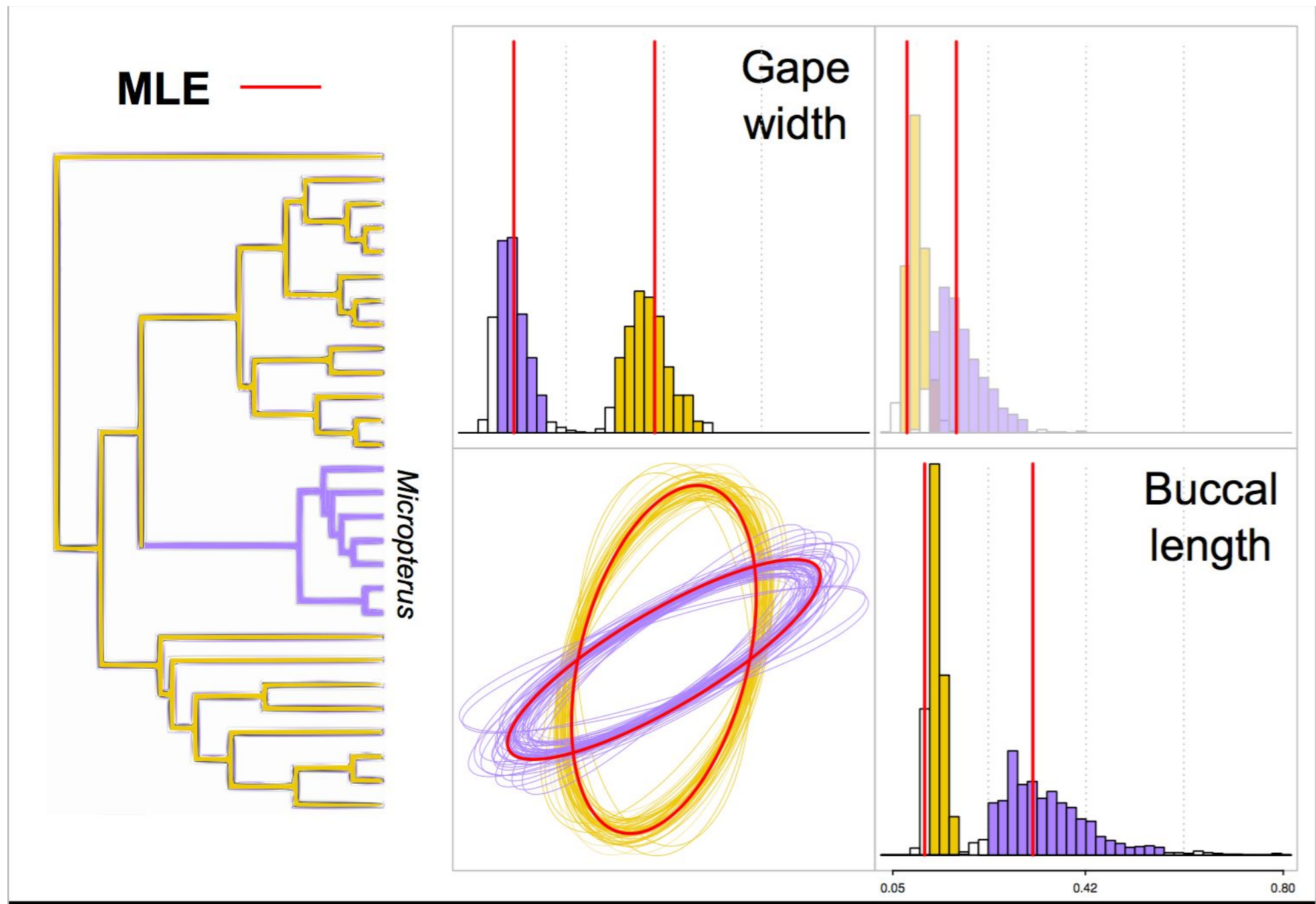


modularity









Data from Revell and Collar  
2009

APPLICATION |  Free Access |

## ratematrix: An R package for studying evolutionary integration among several traits on phylogenetic trees

Daniel S. Caetano , Luke J. Harmon

First published: 30 May 2017 | <https://doi.org/10.1111/2041-210X.12826>

## Estimating Correlated Rates of Trait Evolution with Uncertainty

D S Caetano , L J Harmon

*Systematic Biology*, Volume 68, Issue 3, May 2019, Pages 412–429,

<https://doi.org/10.1093/sysbio/syy067>

**Published:** 17 October 2018    **Article history** ▼

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### Abstract

Correlated evolution among traits, which can happen due to genetic constraints, ontogeny, and selection, can have an important impact on the



# Course structure

Lectures

Exercises

Challenge problems

