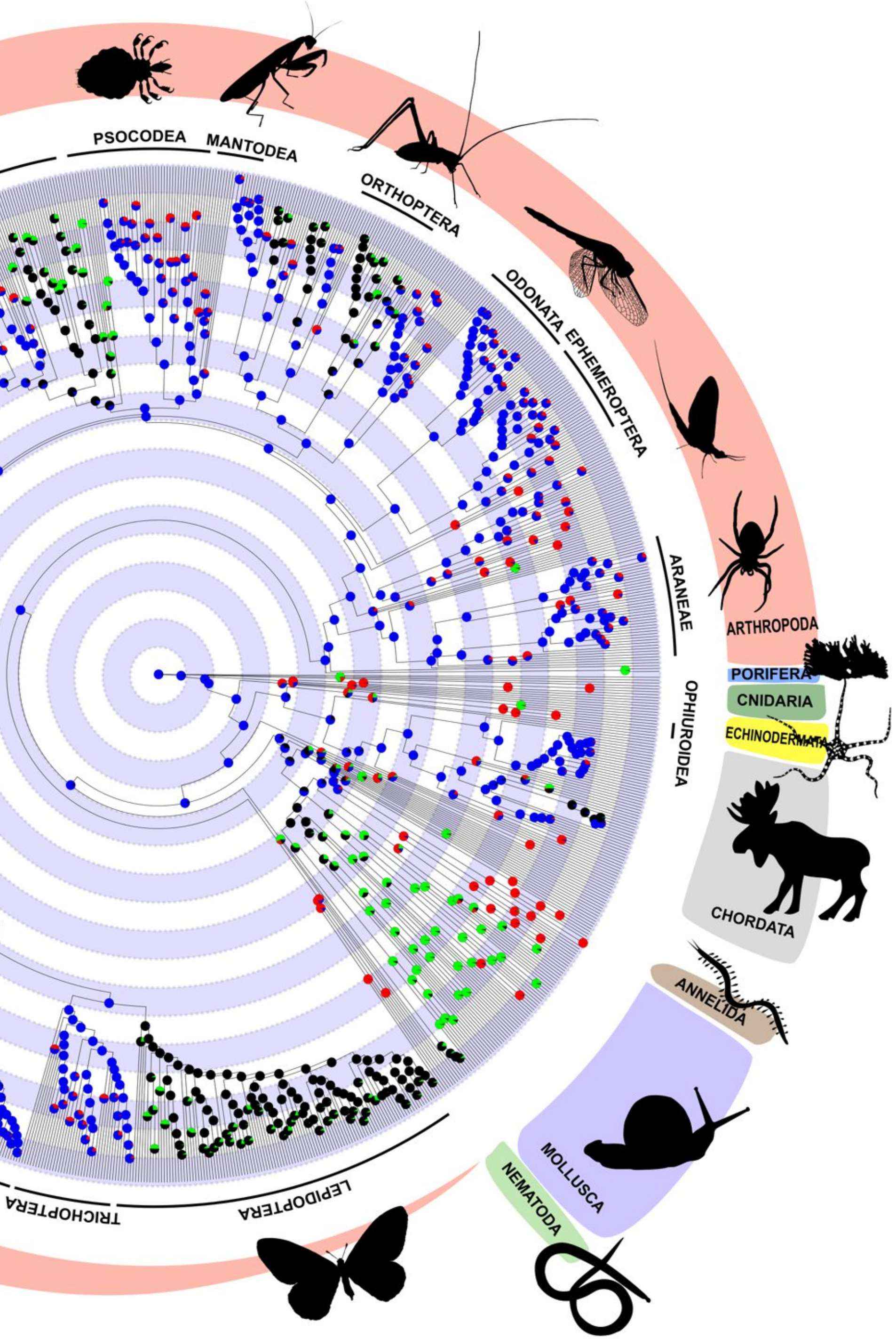

# Phylogenetic ecology

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The University of Arizona

Data Diversity Lab

August 11, 2025
ESA, 2025

# The goal of this talk….

1. Outline key uses of phylogenetic comparative methods to answer questions of particular ecological relevance

2. Summarize current methodological approaches in the intersection between phylogenetics and ecology

# Outline

01

Overview
Ecological patterns and evolutionary relationships

02

Phylogenies
Building, finding, and handling phylogenies

03

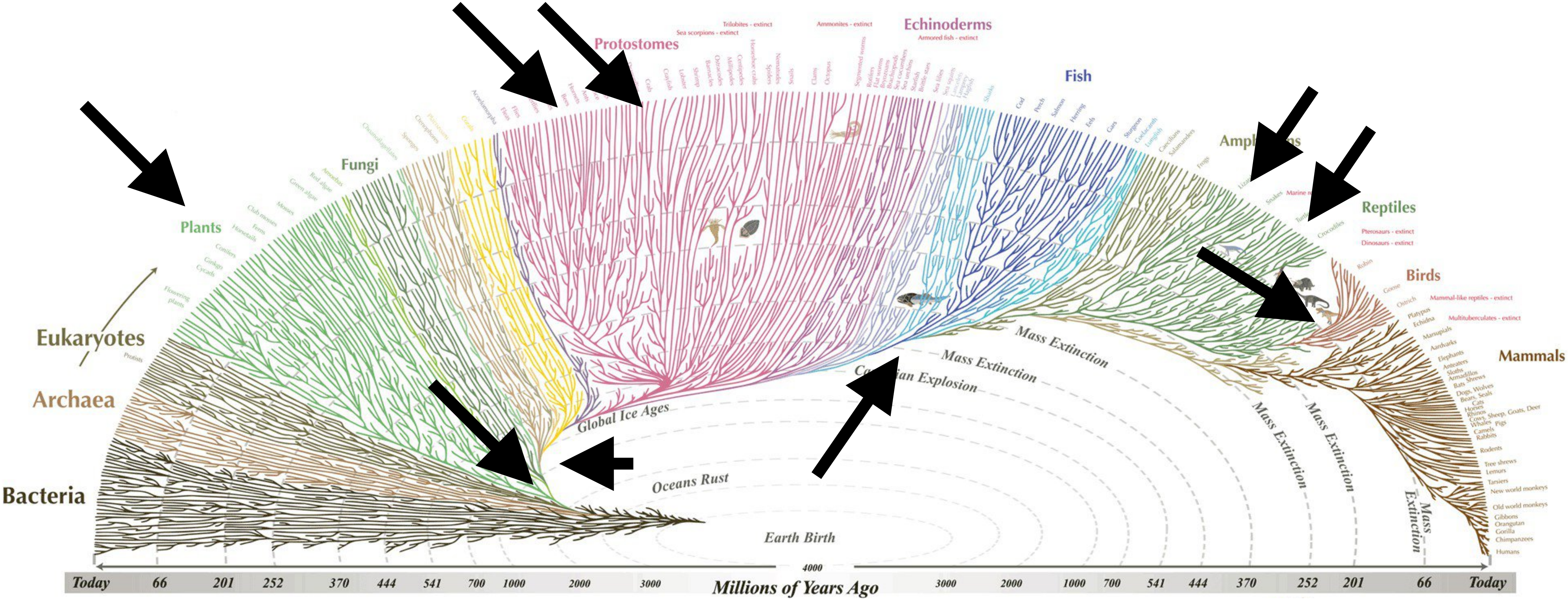
Phylogenetic diversity
How to measure and the effect of spatial scales

04

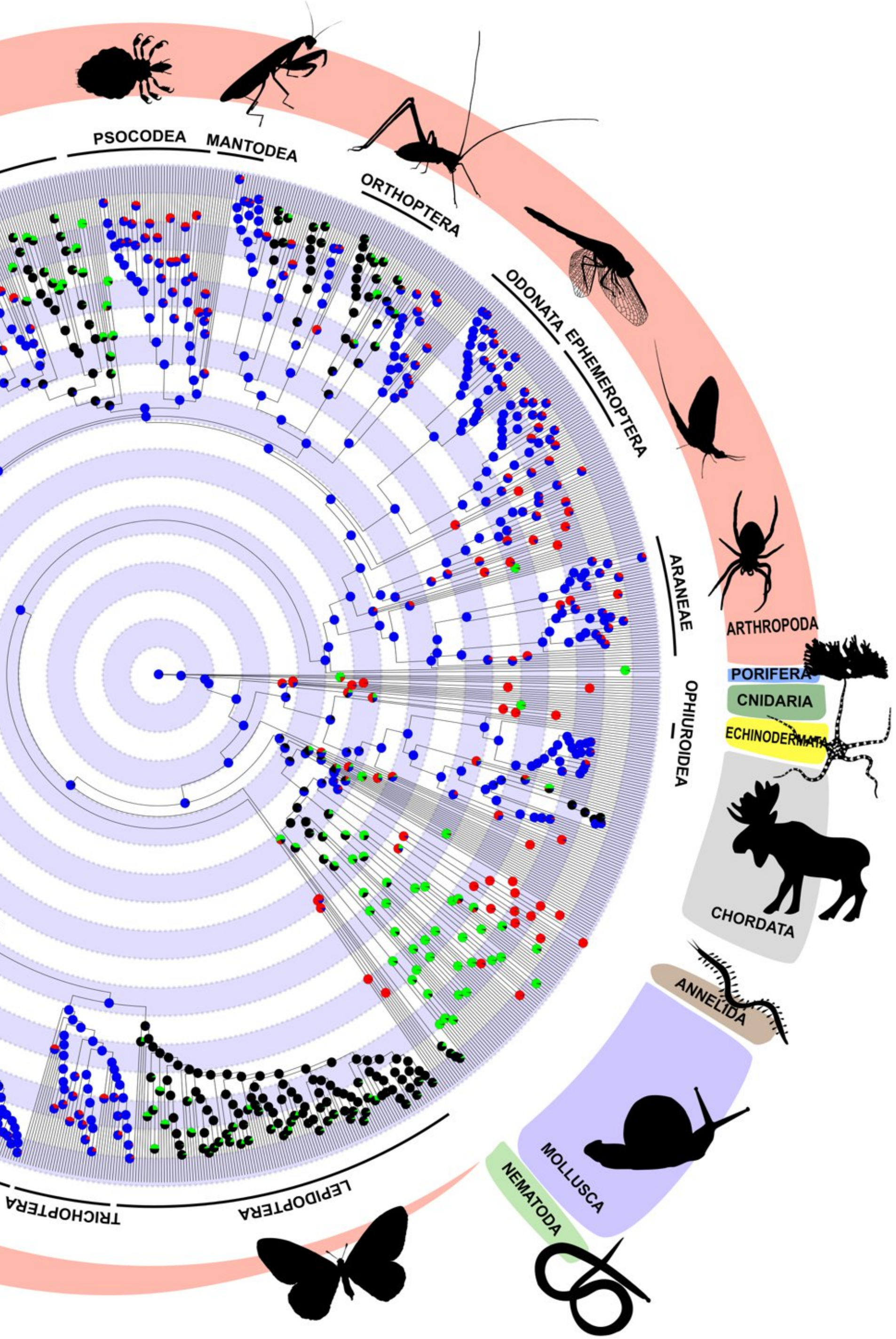
Patterns of trait evolution
Phylogenetic signal, trait evolution, and ancestral states

05

Macroevolution
Speciation, extinction, diversification



Leonard Eisenberg, 2017



# 01

# Overview

Ecological patterns and evolutionary relationships

# Ecological patterns and evolutionary relationships

- Availability of molecular sequences and phylogenetic trees
- Growing interest on this intersectionality
    - Mechanisms of community assembly and coexistence (Webb 2000)
    - Niche conservatism (Holt 1996; Wiens and Graham 2005)
- Non-independence – Phylogenetic corrections in ecology
    - Needed: integrated through methods that account for species covariance in multispecies comparisons
    - Not needed: Phylogenetic correction might erroneously weaken statistical relationships (e.g., importance of a trait in different habitats). Experiments as alternatives.

**Phylogenetic comparative analyses provide a statistical framework to account for phylogenetic information not to "correct"**

# “Correcting” ecological comparisons

*Accounting for phylogenetic information...*

Román-Palacios, C., & Wiens, J. J. (2018). The Tortoise and the Finch: Testing for island effects on diversification using two iconic Galápagos radiations. Journal of biogeography, 45(8), 1701-1712.

# Testing for island effects on diversification

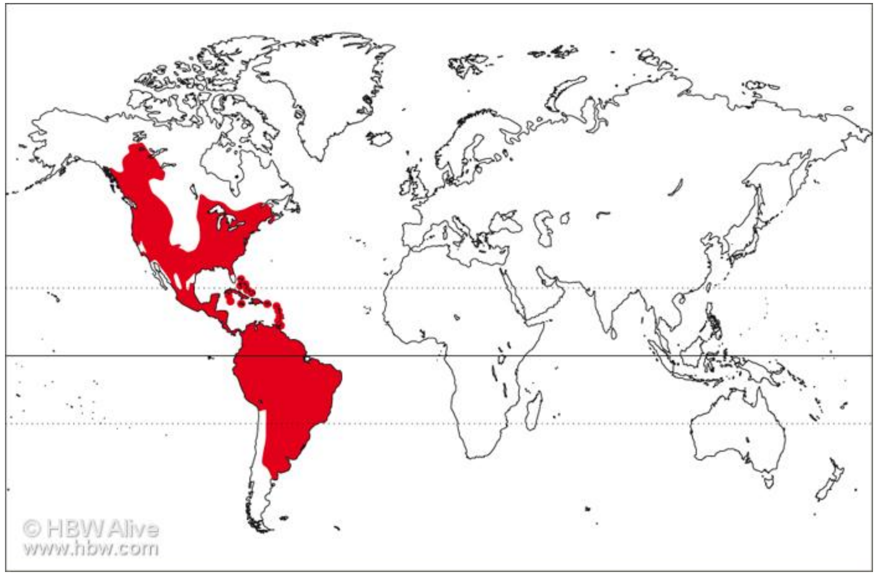
**Questions**

- Do lineages on islands have increased diversification rates relative to mainland lineages?

- Does the same geographical context (e.g., same archipelago) have similar effects on diversification in unrelated groups?

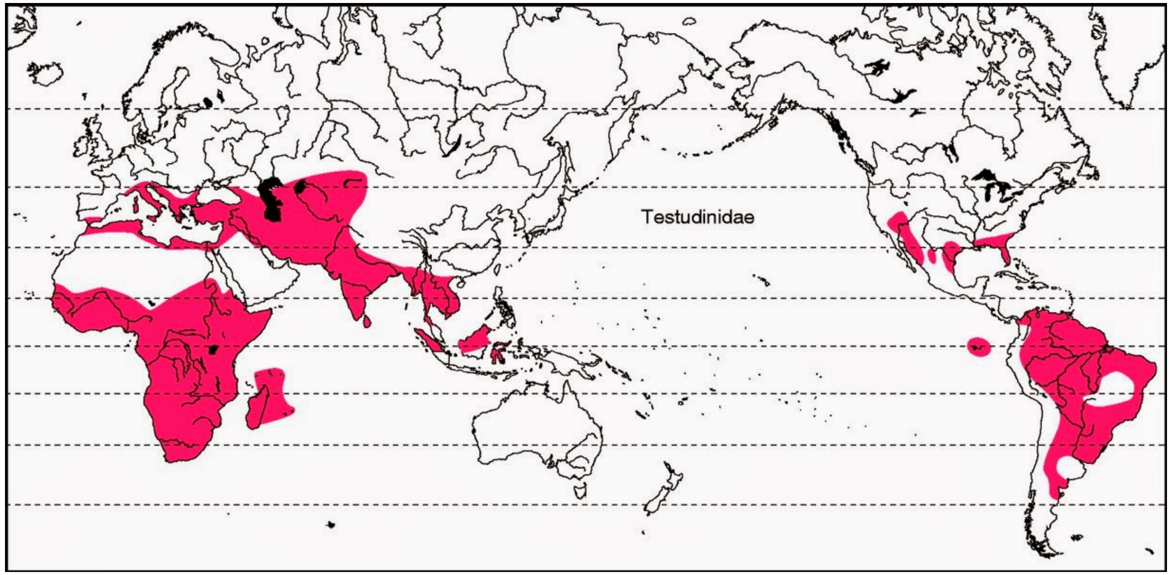
# Testing for island effects on diversification

**Tanagers (Thraupidae)**



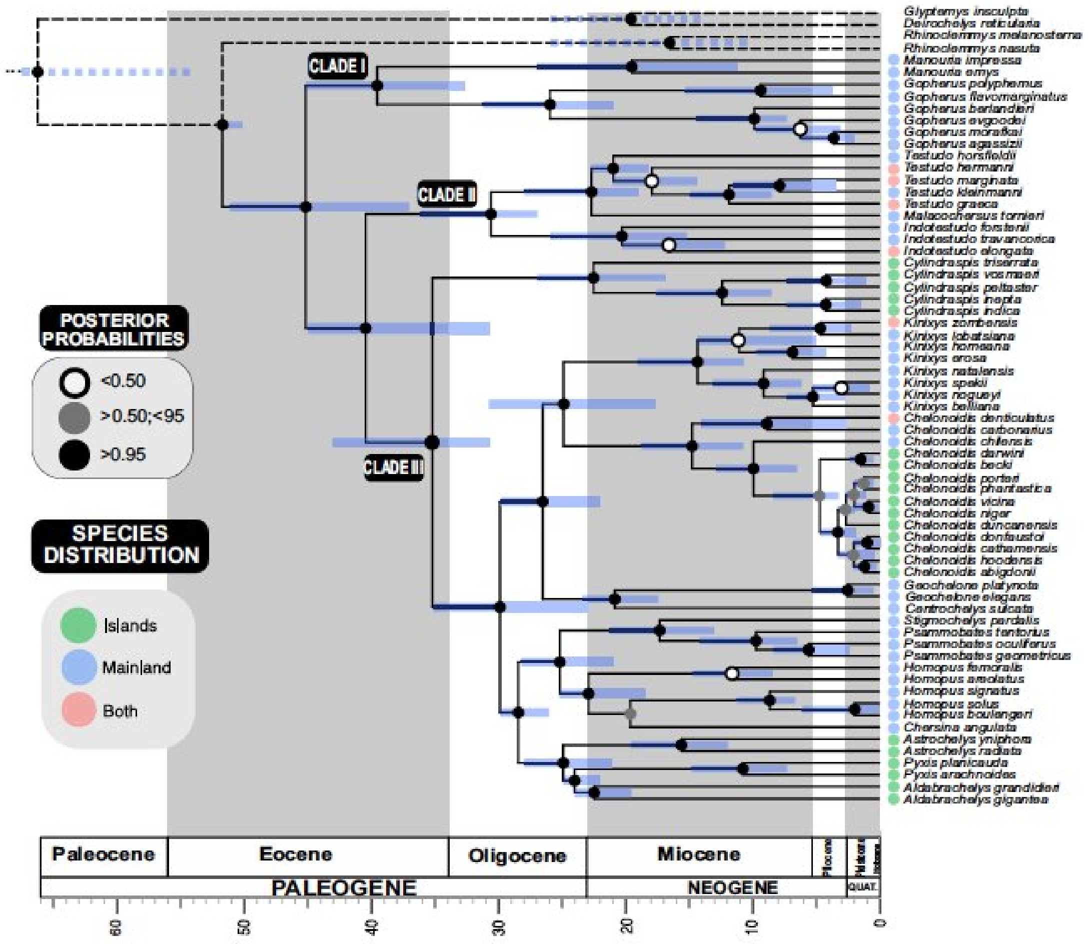
~386 species
Insular species: 31 (Caribbean, Galápagos islands, Tristão da Cunha)

**Tortoises (Testudinidae)**

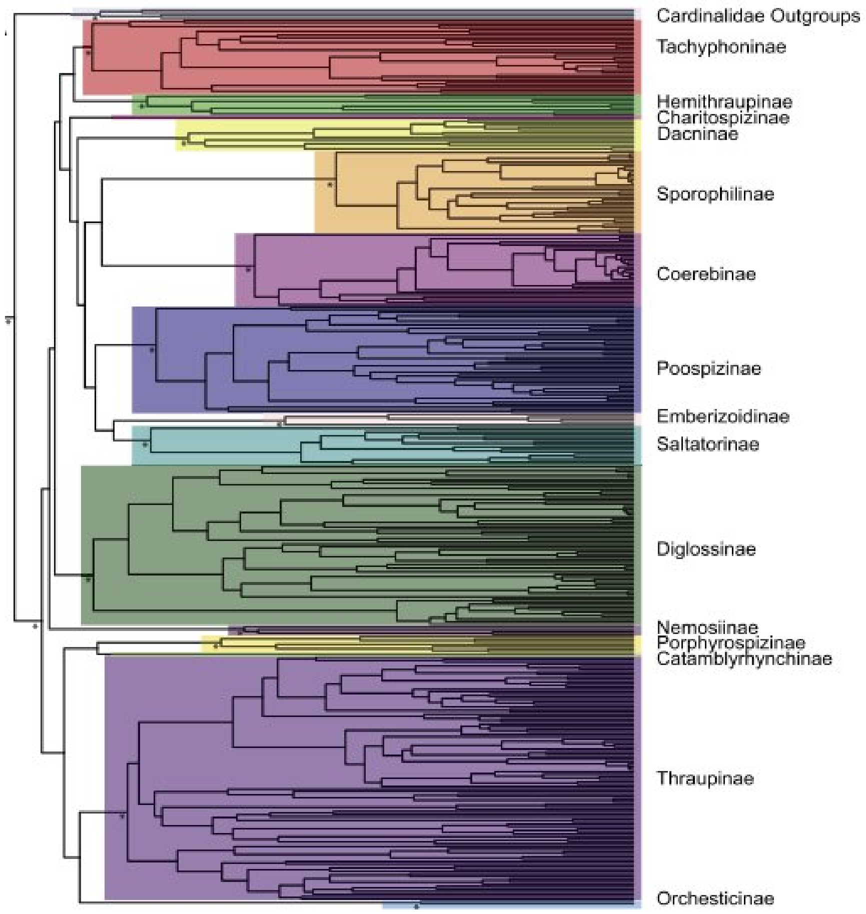


~59 species
Insular species: 19 (Caribbean, Galápagos islands, Madagascar, the Seychelles, Mascarene)

# Testing for island effects on diversification



Tortoise phylogeny (98% of extant taxa + 6 recently extinct lineages; Román-Palacios & Wiens 2018)



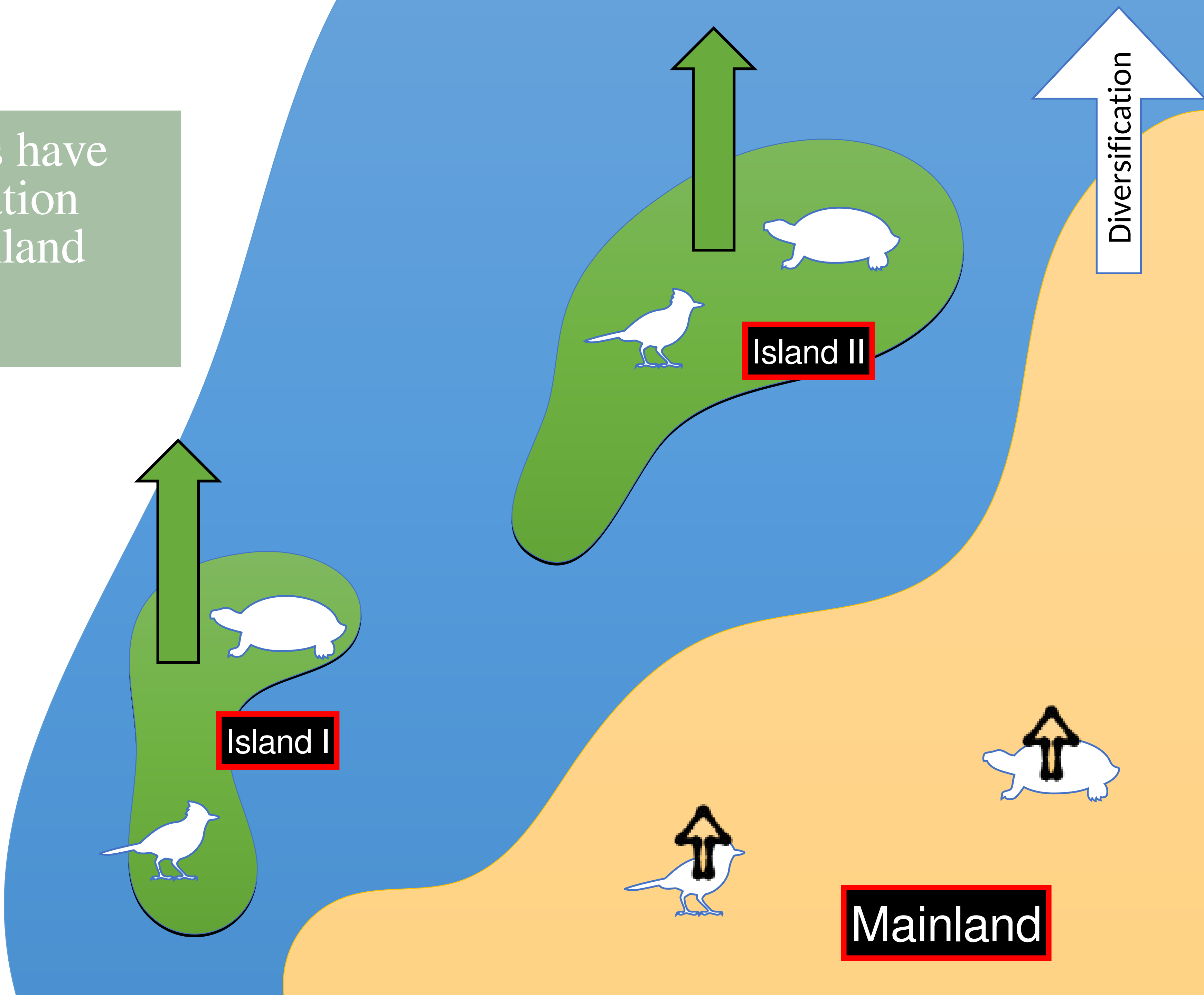
Tanager phylogeny (92% of extant taxa; Barker et al. 2015)

# Do lineages on islands have increased diversification rates relative to mainland lineages?

Phylogenetic regressions between the occurrence on islands and net rates of diversification

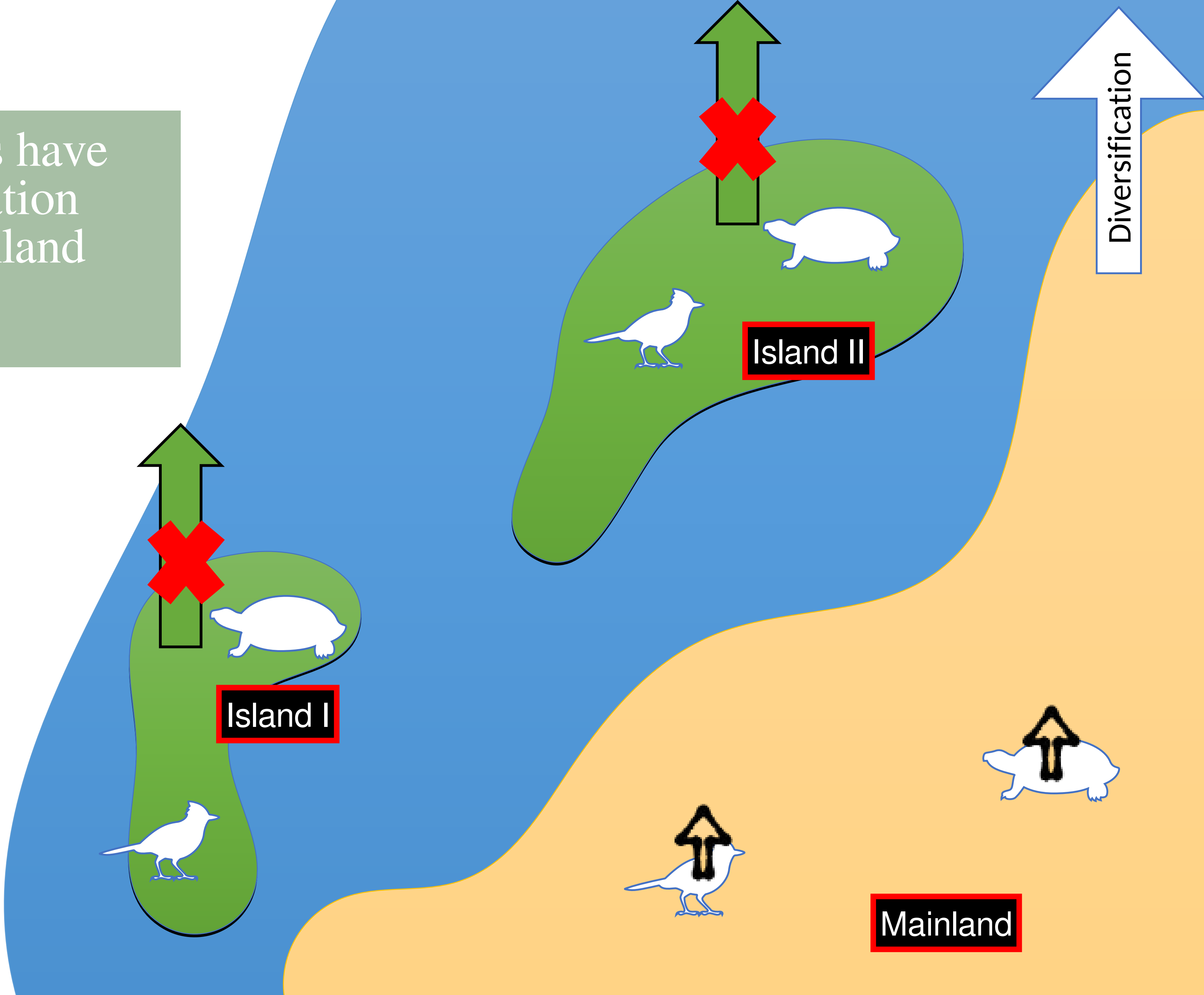
Tortoises: $R^2<0.02$, $P>0.05$

Tanagers: $R^2<0.04$, $P>0.05$

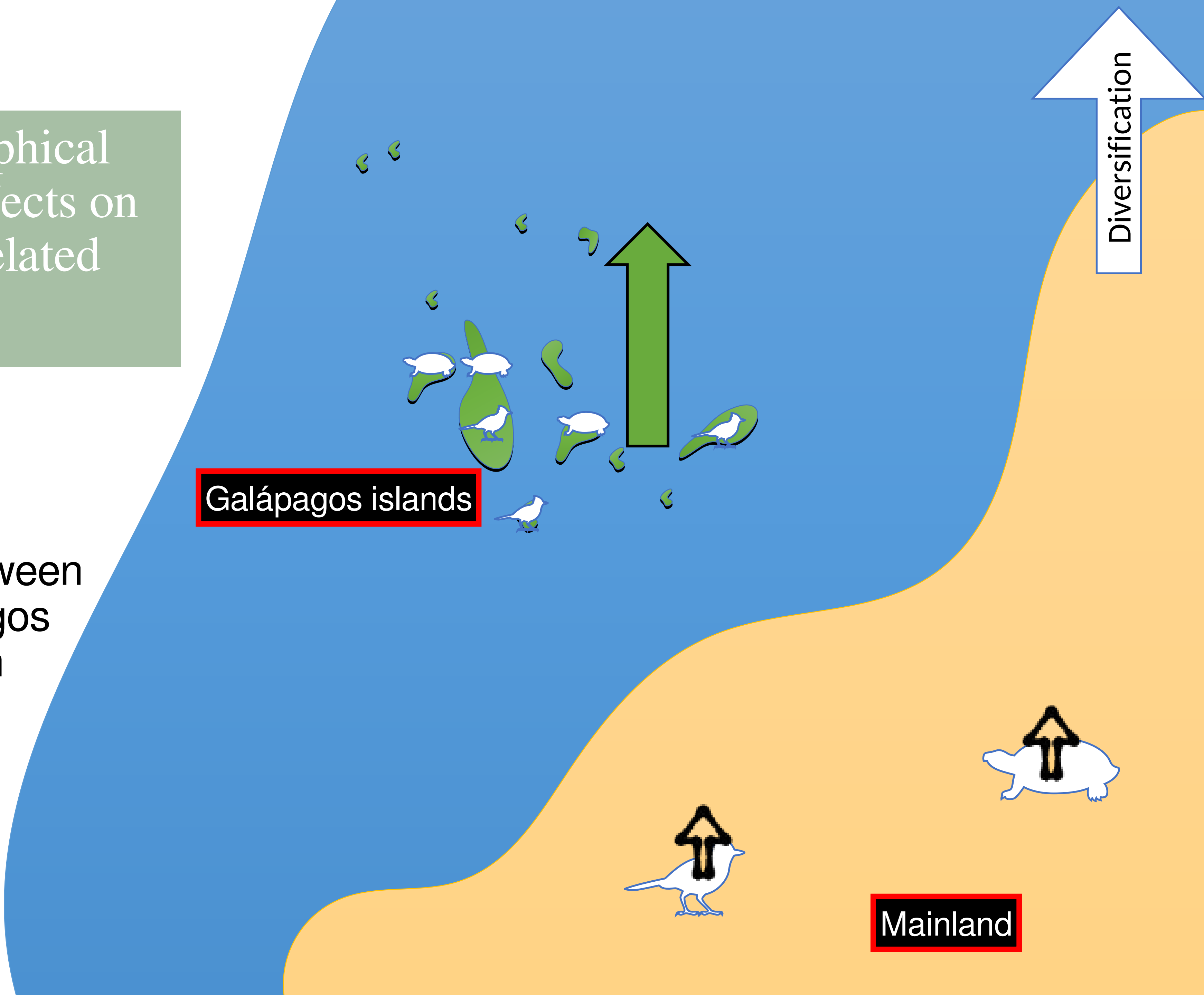


# Do lineages on islands have increased diversification rates relative to mainland lineages?

No – Occurring on islands in general did not increase diversification rates in these clades



# Does the same geographical context have similar effects on diversification in unrelated groups?



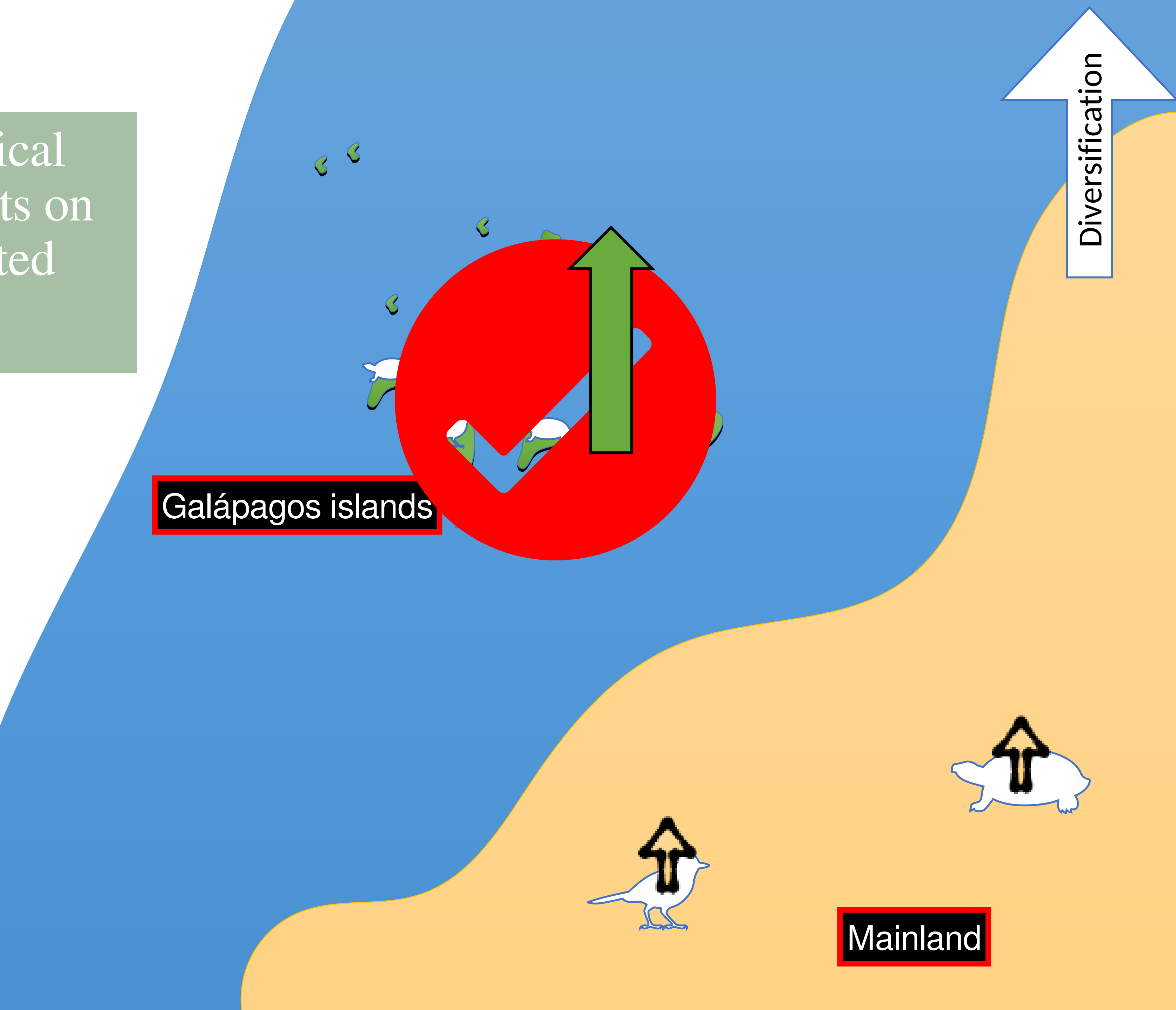
Phylogenetic regressions between the occurrence in the Galápagos and net rates of diversification

Tortoises: $R^2 > 0.4$, $P < 0.01$

Tanagers: $R^2 > 0.2$, $P < 0.01$

# Does the same geographical context have similar effects on diversification in unrelated groups?

Yes – The Galápagos Islands in particular have strongly accelerated diversification rates in both tanagers and tortoises

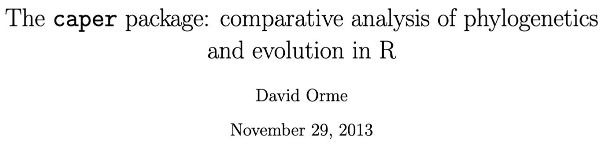


# Testing for island effects on diversification

## Phylogenetic regressions

Lineages are not independent–They share an evolutionary history

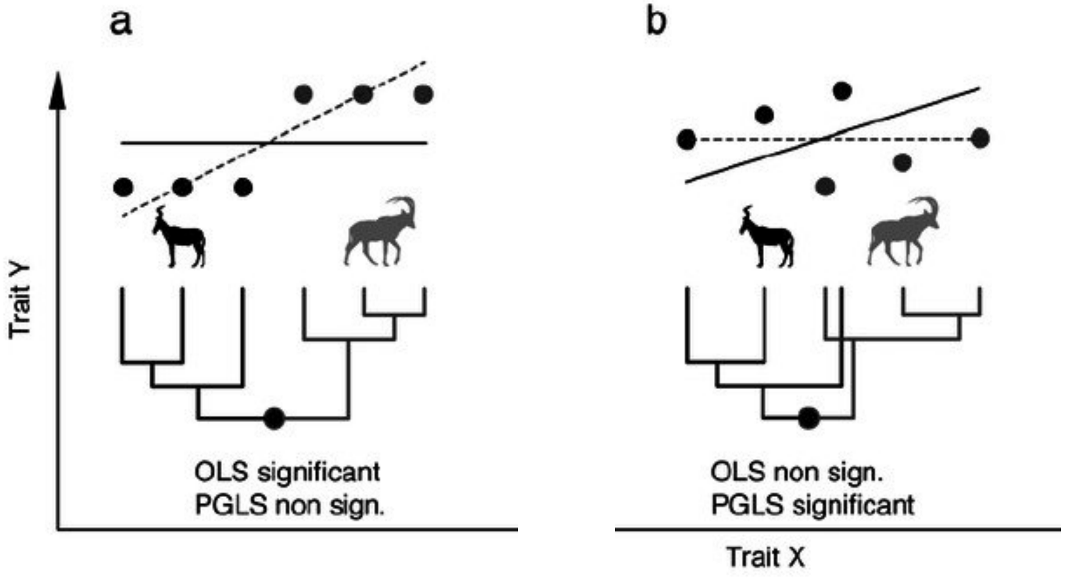
PGLS (“Phylogenetic regressions”) vs OLS (“Ordinary least squares regressions”)


The caper package: comparative analysis of phylogenetics and evolution in R

David Orme

November 29, 2013

*Are the relationships between variables explained by the phylogeny?*



Within clades: similar
Among clades: different

Within clades: different
Among clades: similar

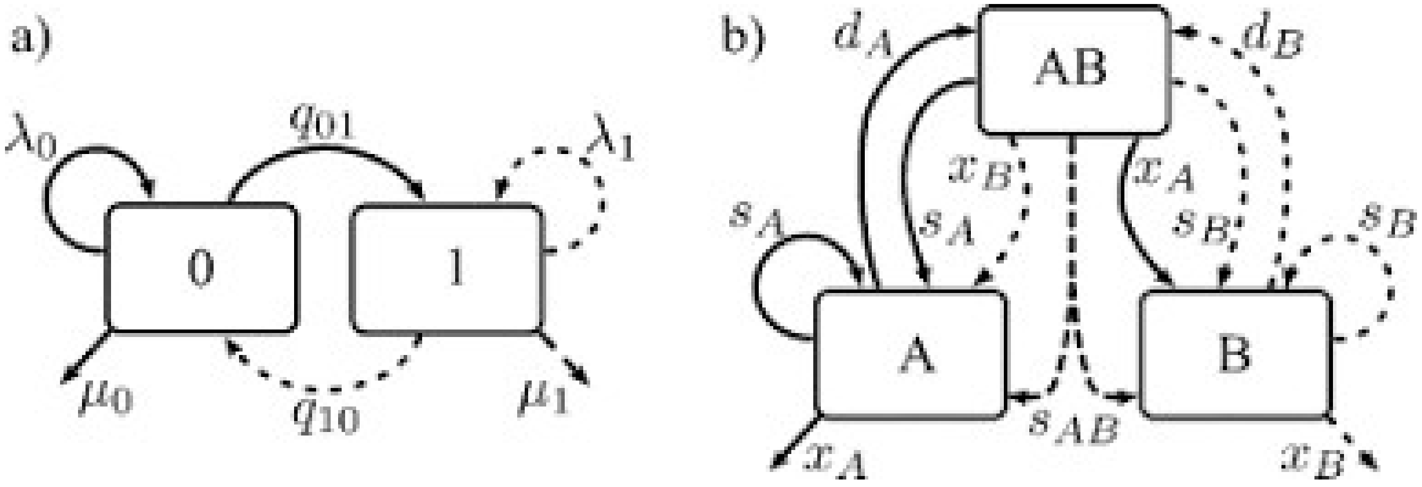
Cantalapiedra et al. (2014)

# Testing for island effects on diversification

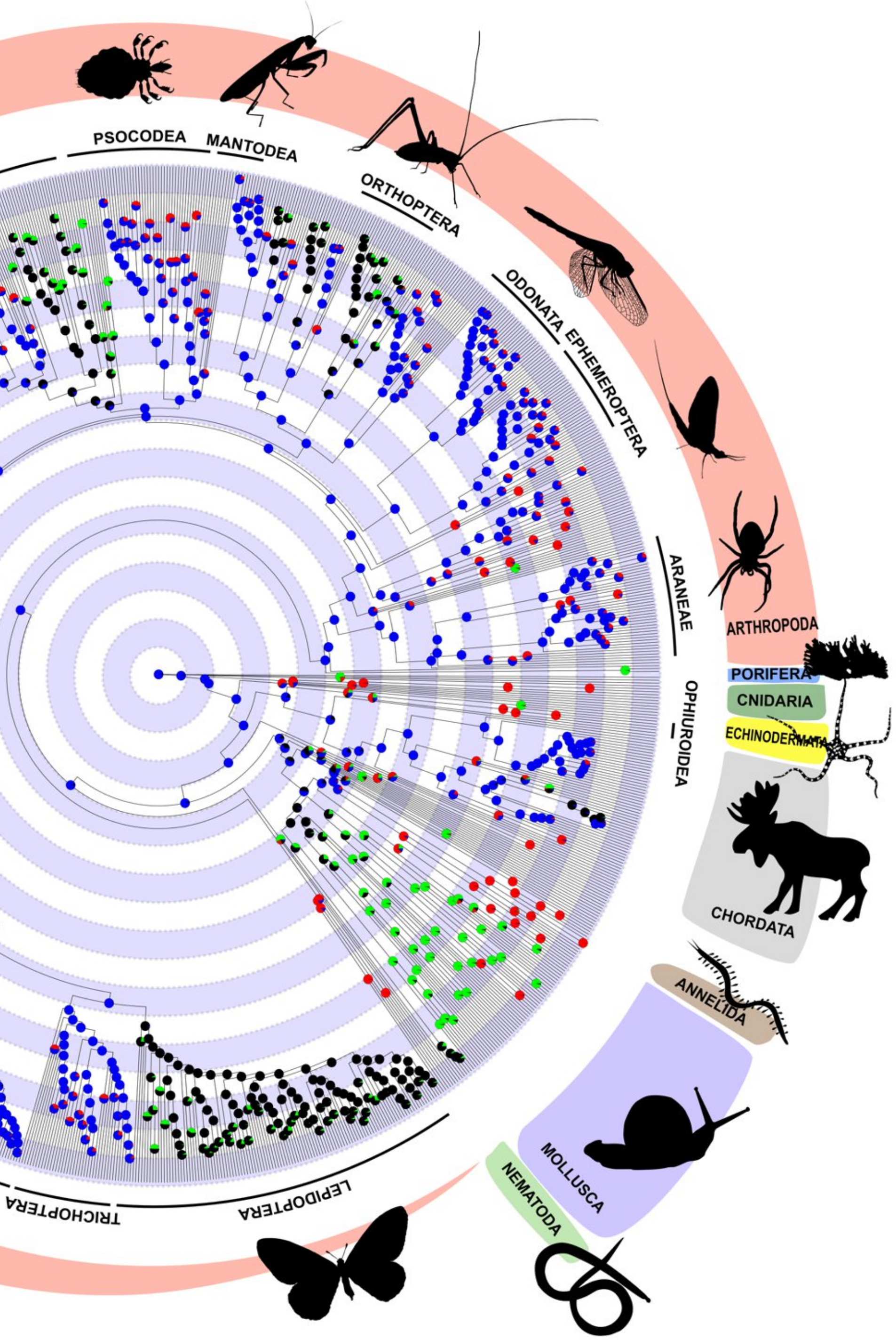
## Binary Speciation and Extinction (BiSSE)
## Geographic Speciation and Extinction (GeoSSE)

Used to test for an association between traits and diversification rates.

*Traits (e.g., BiSSE)*
*Geography (e.g. GeoSSE)*



Goldberg et al. (2011)



# 02

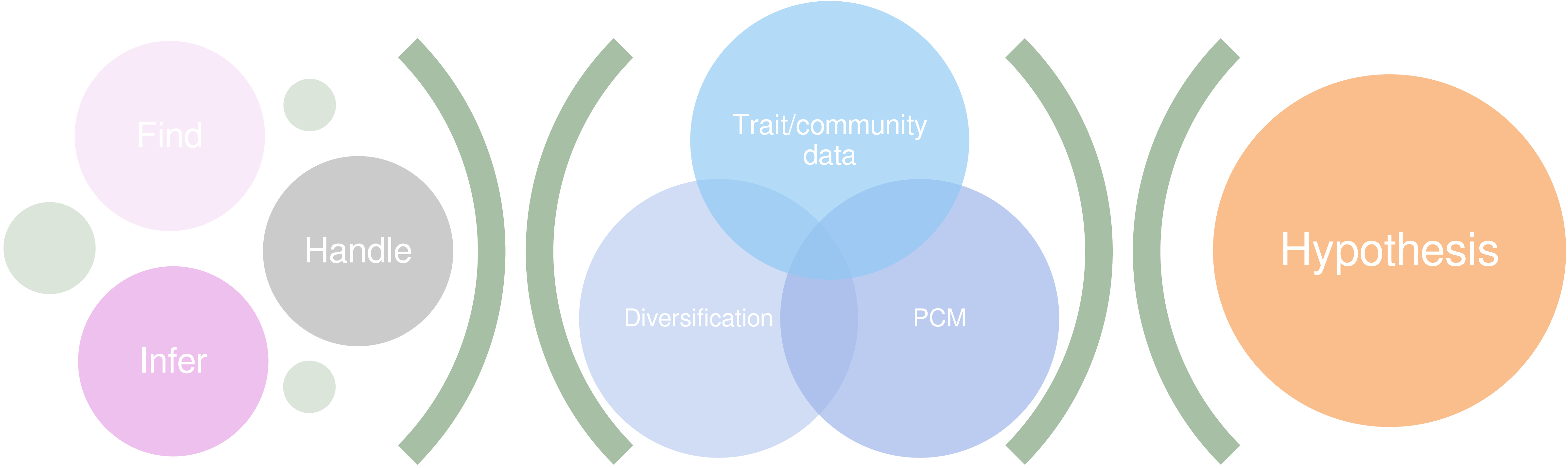
# Phylogenies

Building, finding, and handling phylogenies

# Phylogenies

- Phylogenetic trees provide a new framework for analyzing ecological data
- Trees summarize species inter-relatedness
    - Recent ancestry
    - Clades
    - Distances (time, genetic, character)
- Unlikely to find a tree with exactly the species that are needed
- Finding, building, and handling existing trees is critical to integrate phylogenetics and ecologicy

# The pipeline in short...



Find

Handle

Infer

Trait/community data

Diversification

PCM

Hypothesis

**Phylogeny**

Time-calibrated

**Method/data**

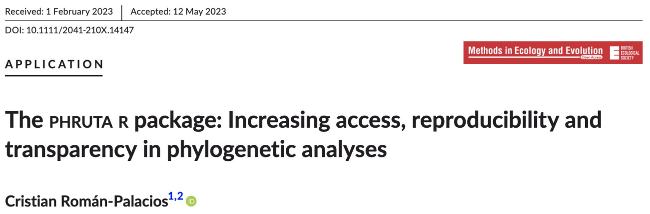
**Question**

# Building phylogenies

# Building phylogenetic trees

*Use existing pipelines optimized for this task and that help increase the reproducibility of your analyses*

**phruta (R)**

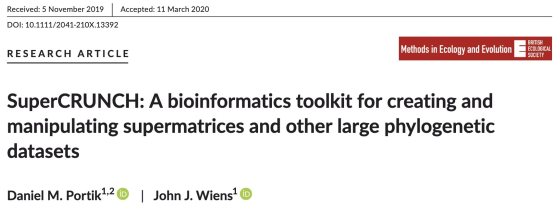

Received: 1 February 2023 | Accepted: 12 May 2023
DOI: 10.1111/2041-210X.14147

Methods in Ecology and Evolution

APPLICATION

The PHRUTA R package: Increasing access, reproducibility and transparency in phylogenetic analyses

Cristian Román-Palacios[1,2]


Received: 5 November 2019 | Accepted: 11 March 2020
DOI: 10.1111/2041-210X.13392

RESEARCH ARTICLE

Methods in Ecology and Evolution

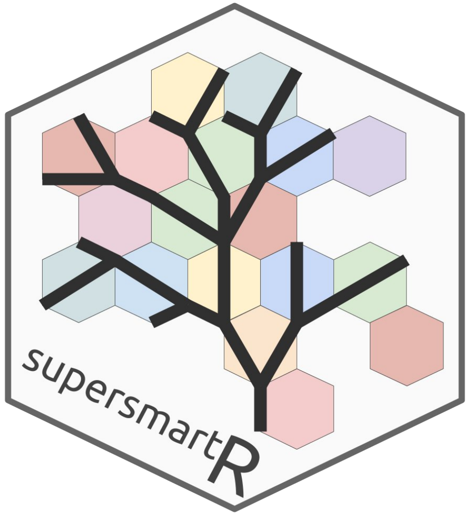
SuperCRUNCH: A bioinformatics toolkit for creating and manipulating supermatrices and other large phylogenetic datasets

Daniel M. Portik[1,2] | John J. Wiens[1]

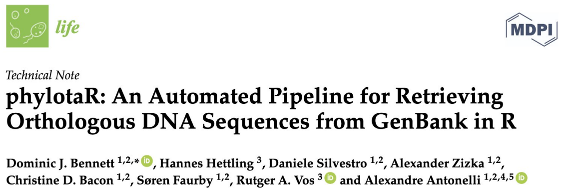
SuperCRUNCH

for phylogenetic datasets

**SuperCRUNCH (CLI)**



**supersmartR (R)**


life

MDPI

*Technical Note*

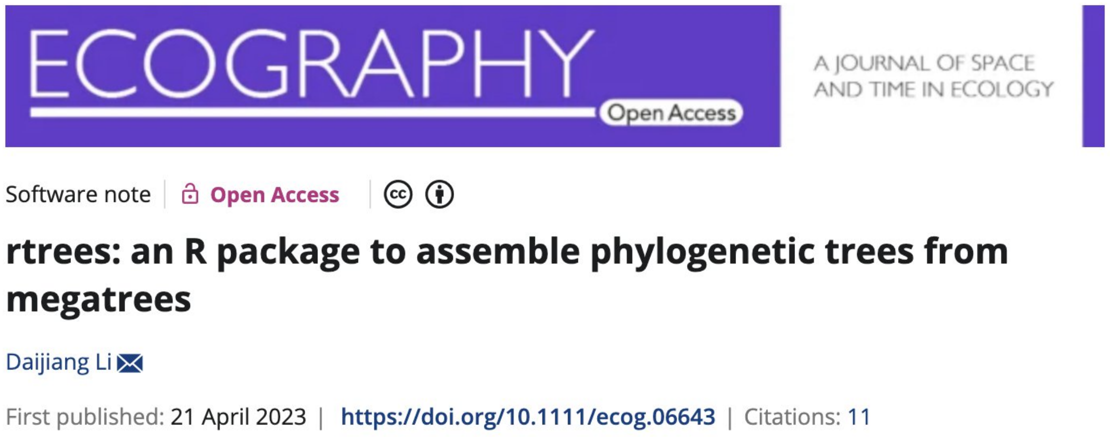
phylotaR: An Automated Pipeline for Retrieving Orthologous DNA Sequences from GenBank in R

Dominic J. Bennett [1,2,*], Hannes Hettling [3], Daniele Silvestro [1,2], Alexander Zizka [1,2], Christine D. Bacon [1,2], Søren Faurby [1,2], Rutger A. Vos [3] and Alexandre Antonelli [1,2,4,5]

# Finding trees

# Finding trees

I



ECOGRAPHY Open Access

A JOURNAL OF SPACE AND TIME IN ECOLOGY

Software note | Open Access

**rtrees: an R package to assemble phylogenetic trees from megatrees**

Daijiang Li

First published: 21 April 2023 | https://doi.org/10.1111/ecog.06643 | Citations: 11

II

TIMETREE 5

THE TIMESCALE *of* LIFE

III

BIEN

IV

Google

species filetype:nex
species filetype:tre*

V

TreeBASE *A Database of Phylogenetic Knowledge*

VI

VertLife

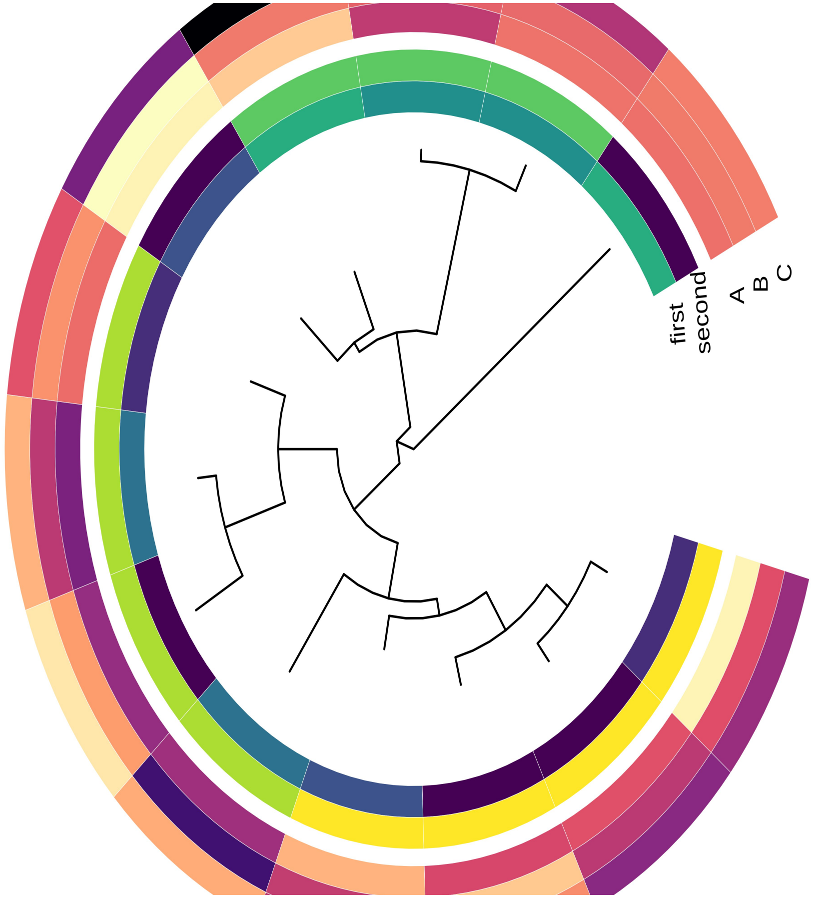
# Handling phylogenetic trees

Using R

# Handling trees (in R)

## Key packages: **ape** and picante

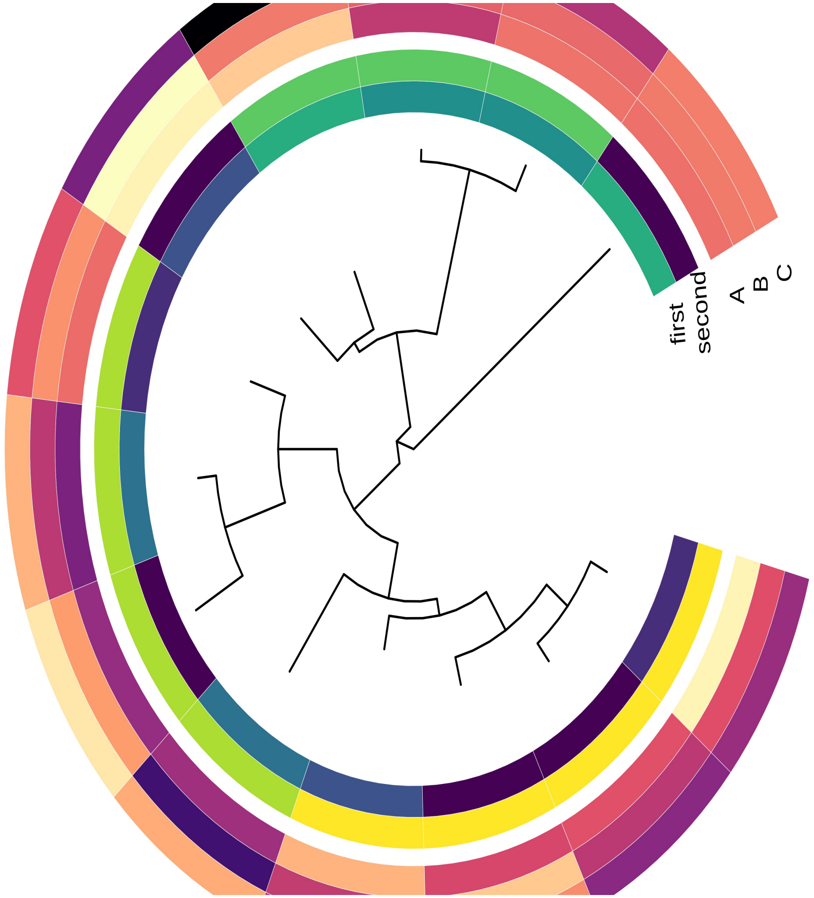
```
> library(ape)
> library(here)
> tree <- read.tree(here(“data”, “tree.tre”))
> tree
Phylogenetic tree with 4 tips and 3 internal nodes.

Tip labels:
[1] “Sp1” “Sp2” “Sp3” “Sp4”

Node labels:
[1] “5” “6” “7”

Rooted; include branch lengths
```



# Handling trees (in R)

## Key packages: **ape** and picante

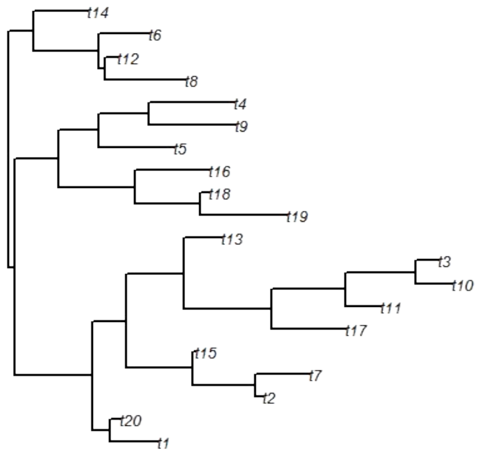
```
> class(tree)
[1] “phylo”

> attributes(tree)
$names
[1] “edge” “Nnode” “tip.label” “edge.lengths”

$class
[1] “phylo”

$order
[1] “cladewise”
```



# Handling trees (in R)

## Key packages: **ape** and picante

```
plot(tree, edge.width=3, label.offset=0.3)
add.scale.bar()
text(1,1.1, “MY”)
```

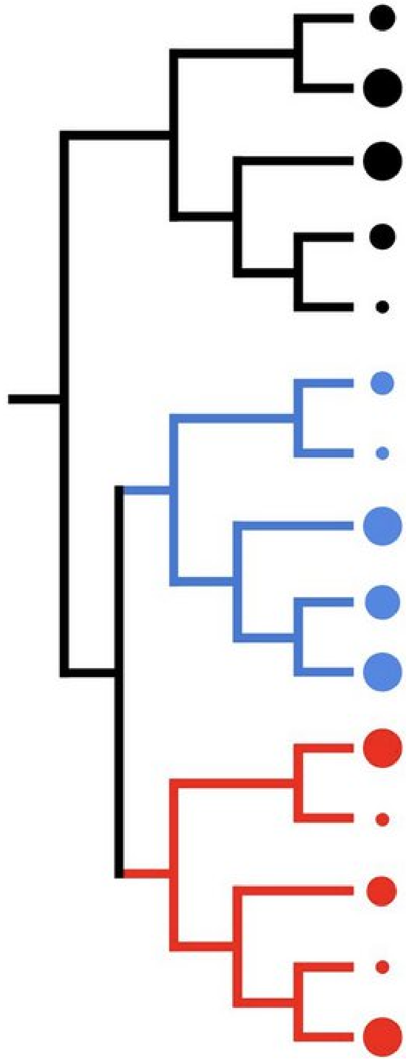


| Function | Description |
|---|---|
| chronos | Rate smoothing to create an ultrametric tree |
| cophenetic | All pairwise distances between species |
| drop.tip | Creates new tree without tips that are to be excluded |
| mrca | Matrix of ancestral nodes for all pairs of tips |
| multi2di | Resolves polytomies |
| pic | Estimates phylogenetic independent contrasts |
| vcv | Variance-covariance matrix – species relatedness |

# Handling trees (in R)

## Key packages: ape and **picante**

```
> library(picante)
> data(phylocom)
> attributes(phylocom)
$names
[1] “phylo” “sample” “traits”

#Some functions will need a tree and a community matrix

> pd(comm, phy)
          PD    SR
clump1    16     8
clump2a   17     8
```



# Handling trees (in R)

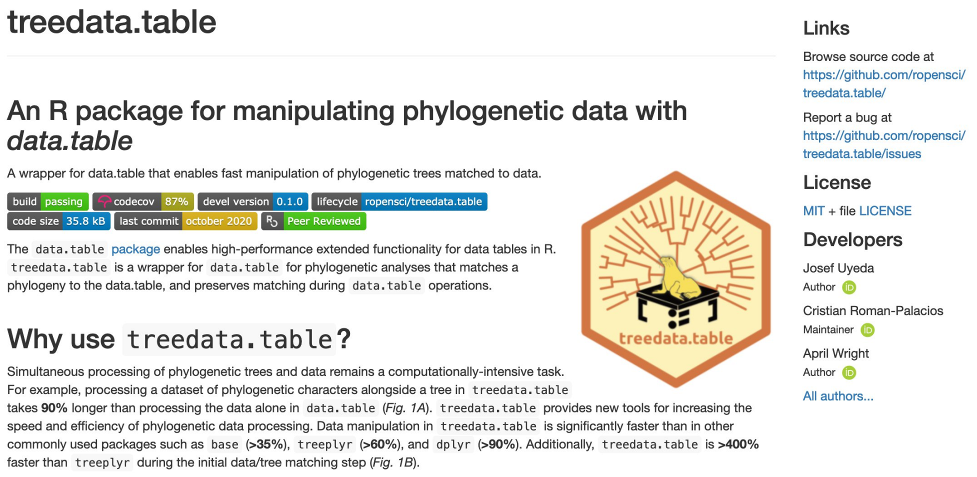
## Key packages: ape and **picante**

```
>mpd(comm, cophenetic(phy))
>cophenetic(phy)
```

$$A = \begin{bmatrix} 0 & d_{12}^2 & d_{13}^2 & \dots & d_{1n}^2 \\ d_{21}^2 & 0 & d_{23}^2 & \dots & d_{2n}^2 \\ d_{31}^2 & d_{32}^2 & 0 & \dots & d_{3n}^2 \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ d_{n1}^2 & d_{n2}^2 & d_{n3}^2 & \dots & 0 \end{bmatrix}$$

| **Function** | **Description** |
|---|---|
| comdist, comdistnt | Average pairwise distances between community pairs |
| evol.distinct | Measure of species evolutionary distinctiveness |
| mpd, mntd | Mean pairwise or nearest taxon distances within communities |
| pd | Community phylogenetic diversity values |
| phylosignal | Blomber’s K and PIC values |
| ses.mpd, ses.mnrd | Randomizations for standarized effect sizes and significance of distances (mean pairwise or nearest) |
| ses.pd | Randomizations for standarized effect sizes and significance of community phylo diversity |

# Handling very large trees (in R)



## treedata.table

### An R package for manipulating phylogenetic data with *data.table*

A wrapper for data.table that enables fast manipulation of phylogenetic trees matched to data.

build passing | codecov 87% | devel version 0.1.0 | lifecycle ropensci/treedata.table
code size 35.8 kB | last commit october 2020 | Peer Reviewed

The `data.table` package enables high-performance extended functionality for data tables in R. `treedata.table` is a wrapper for `data.table` for phylogenetic analyses that matches a phylogeny to the data.table, and preserves matching during `data.table` operations.

### Why use `treedata.table`?

Simultaneous processing of phylogenetic trees and data remains a computationally-intensive task. For example, processing a dataset of phylogenetic characters alongside a tree in `treedata.table` takes **90%** longer than processing the data alone in `data.table` (*Fig. 1A*). `treedata.table` provides new tools for increasing the speed and efficiency of phylogenetic data processing. Data manipulation in `treedata.table` is significantly faster than in other commonly used packages such as `base` (**>35%**), `treeplyr` (**>60%**), and `dplyr` (**>90%**). Additionally, `treedata.table` is **>400%** faster than `treeplyr` during the initial data/tree matching step (*Fig. 1B*).

#### Links

Browse source code at
https://github.com/ropensci/treedata.table/

Report a bug at
https://github.com/ropensci/treedata.table/issues

#### License

MIT + file LICENSE

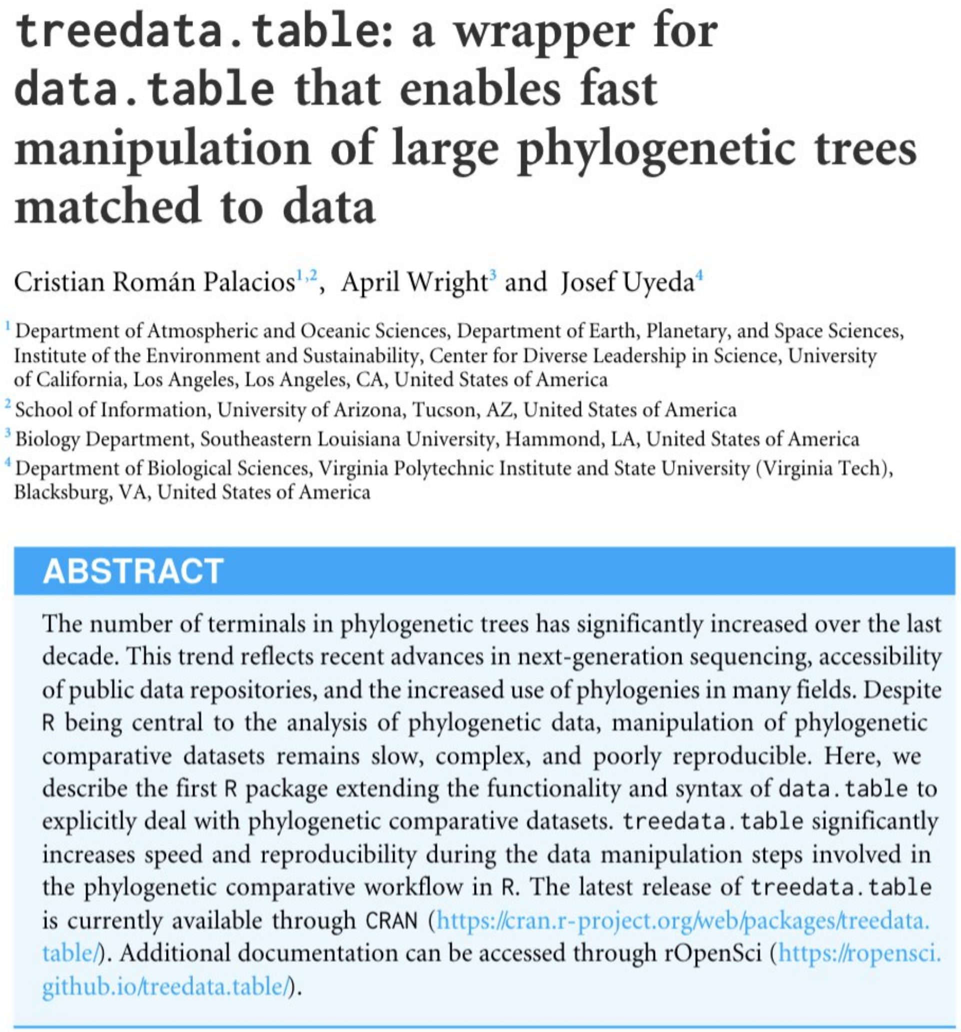
#### Developers

Josef Uyeda
Author

Cristian Roman-Palacios
Maintainer

April Wright
Author

All authors...



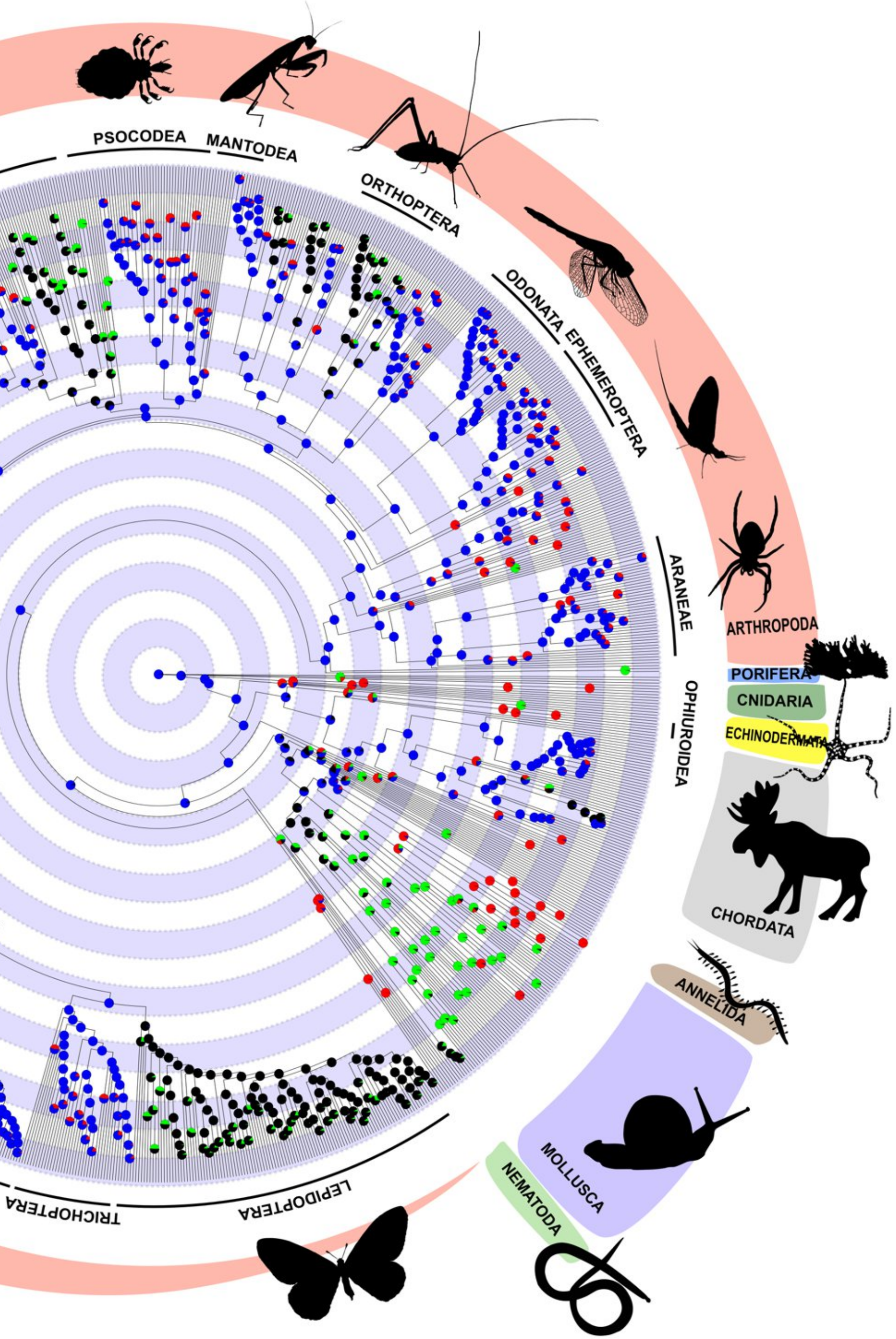
## `treedata.table`: a wrapper for `data.table` that enables fast manipulation of large phylogenetic trees matched to data

Cristian Román Palacios[1,2], April Wright[3] and Josef Uyeda[4]

[1] Department of Atmospheric and Oceanic Sciences, Department of Earth, Planetary, and Space Sciences, Institute of the Environment and Sustainability, Center for Diverse Leadership in Science, University of California, Los Angeles, Los Angeles, CA, United States of America
[2] School of Information, University of Arizona, Tucson, AZ, United States of America
[3] Biology Department, Southeastern Louisiana University, Hammond, LA, United States of America
[4] Department of Biological Sciences, Virginia Polytechnic Institute and State University (Virginia Tech), Blacksburg, VA, United States of America

### ABSTRACT

The number of terminals in phylogenetic trees has significantly increased over the last decade. This trend reflects recent advances in next-generation sequencing, accessibility of public data repositories, and the increased use of phylogenies in many fields. Despite `R` being central to the analysis of phylogenetic data, manipulation of phylogenetic comparative datasets remains slow, complex, and poorly reproducible. Here, we describe the first `R` package extending the functionality and syntax of `data.table` to explicitly deal with phylogenetic comparative datasets. `treedata.table` significantly increases speed and reproducibility during the data manipulation steps involved in the phylogenetic comparative workflow in `R`. The latest release of `treedata.table` is currently available through `CRAN` (https://cran.r-project.org/web/packages/treedata.table/). Additional documentation can be accessed through rOpenSci (https://ropensci.github.io/treedata.table/).



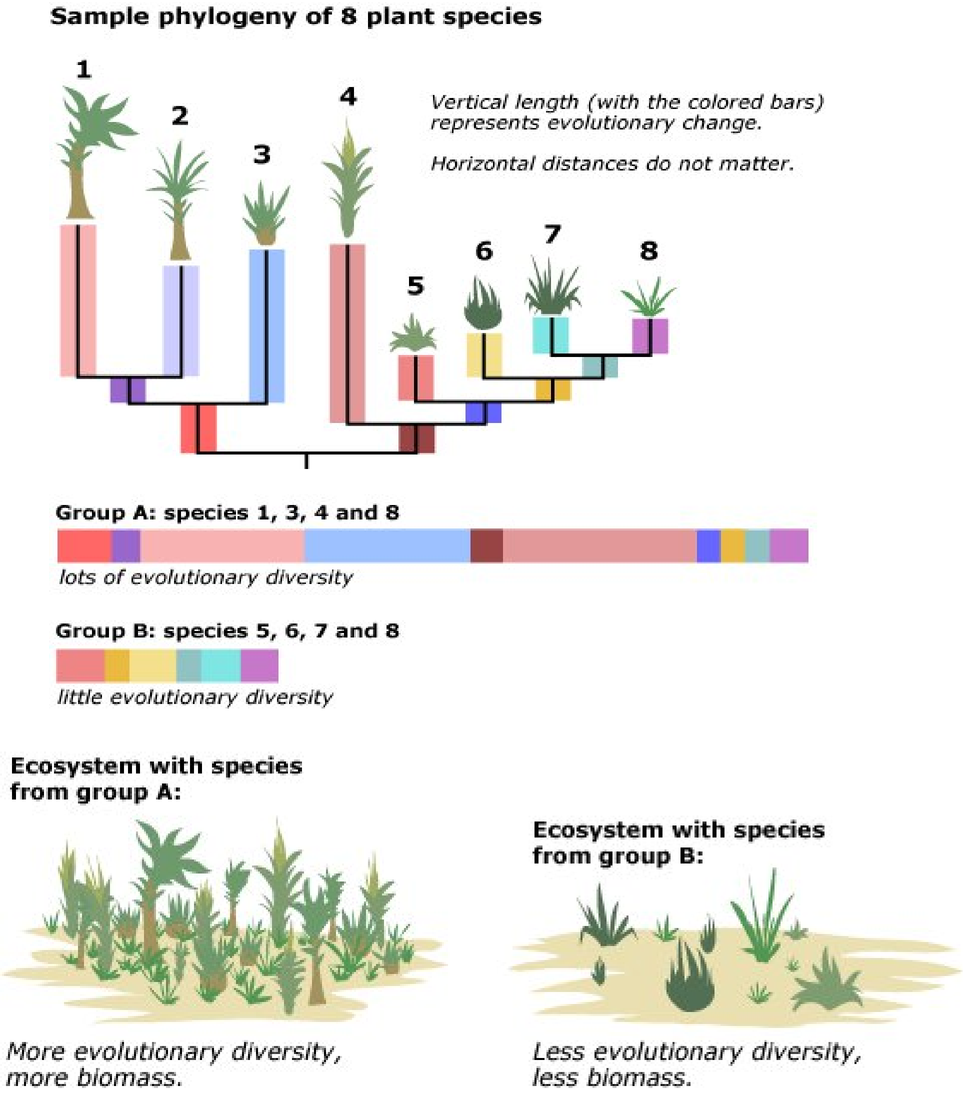
# 03

# Phylogenetic diversity

How to measure and the effect of spatial scales

# Phylogenetic diversity

- Depending the question, species diversity is not very informative
- The same numbers of species might correspond with different amounts of phylogenetic diversity (PD)
- High amounts of PD seem to correspond with large amounts of biomass



Cadotte et al. (2018)

# What explains diversity differences across habitats?

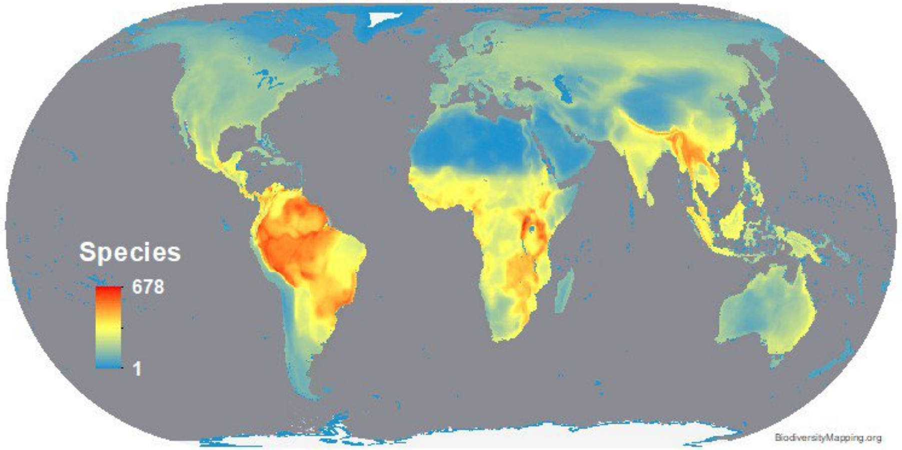
Román-Palacios, C., Moraga-López, D., & Wiens, J. J. (2022). The origins of global biodiversity on land, sea and freshwater. Ecology letters, 25(6), 1376-1386.

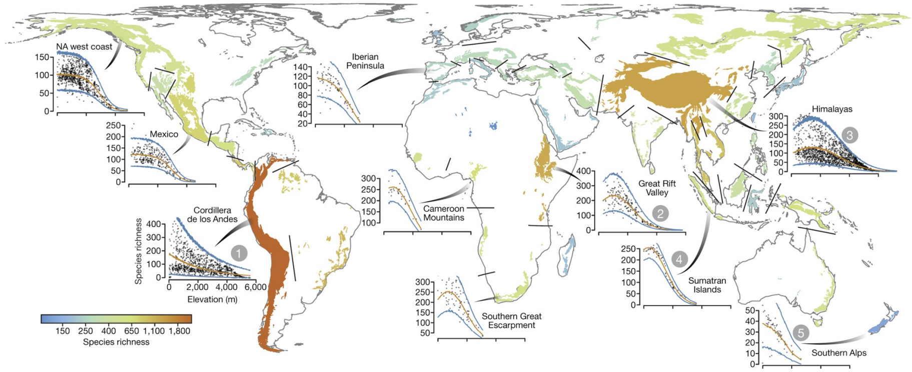
# Global biodiversity patterns

**Some are widely studied:**

Tropics vs temperate zones

Mountain ranges vs lowlands



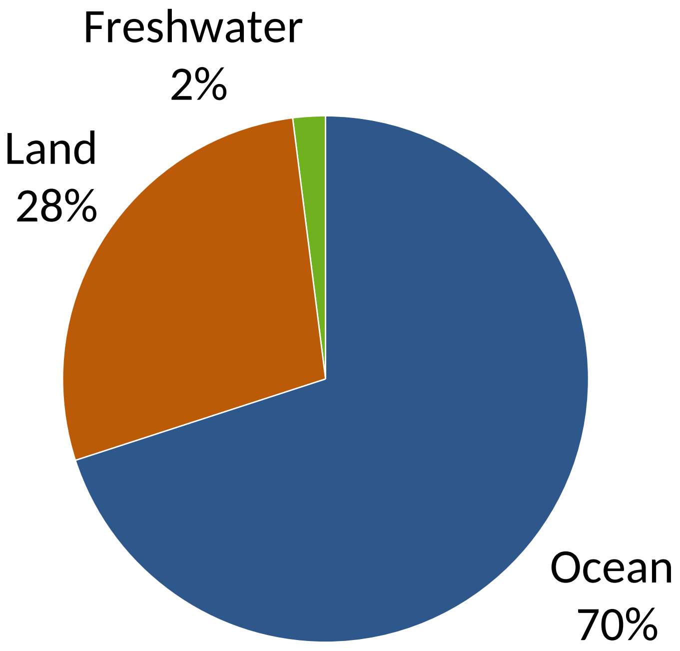


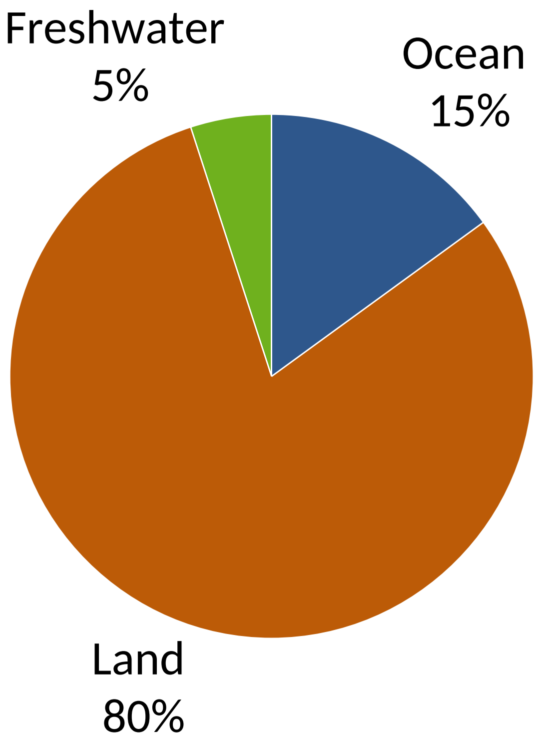
**But others remain poorly discussed...**

Marine, freshwater, and land

Quintero and Jetz (2007)

# Area vs habitat biodiversity





Surface area

Species richness

Grosberg et al. (2012)

# What drives diversity patterns among habitats?

Multiple studies have concluded on:

- Differences in diversification rates
- Differential extinction

**However, no study have included all three major habitats: marine, freshwater, and terrestrial**

Wiens (2015), Miller and Wiens (2017), Carrete-Vega and Wiens (2012)

# Our objectives

**(1) Find the dominant groups in marine, freshwater, and terrestrial habitats**

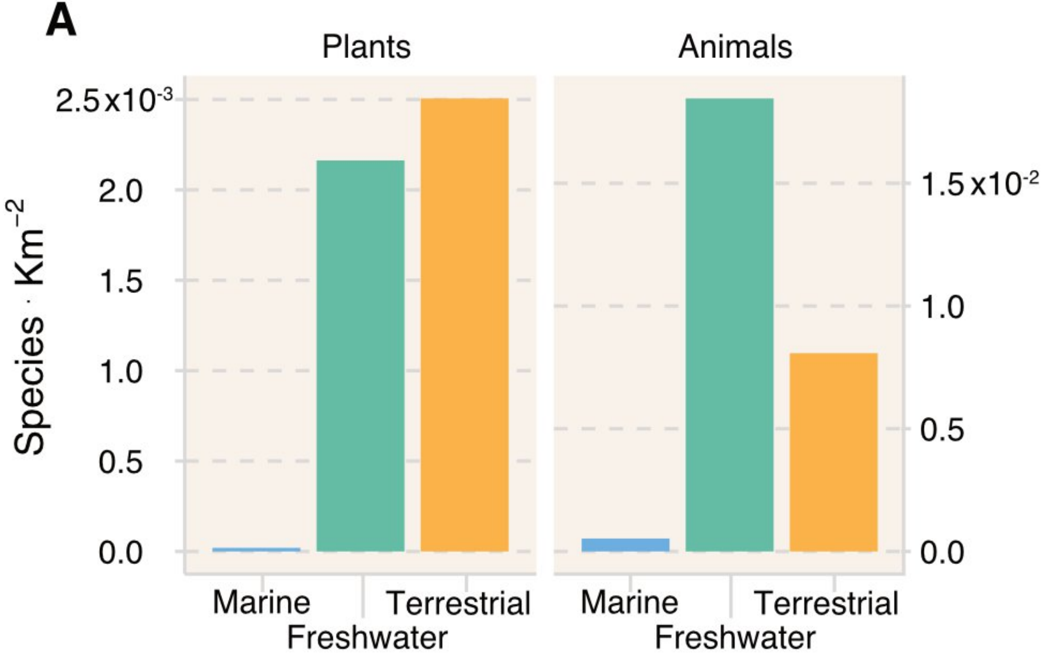
(2) Test for differences in diversification rates among habitats

(3) Examine whether times of first colonization to habitats can help explain diversity patterns

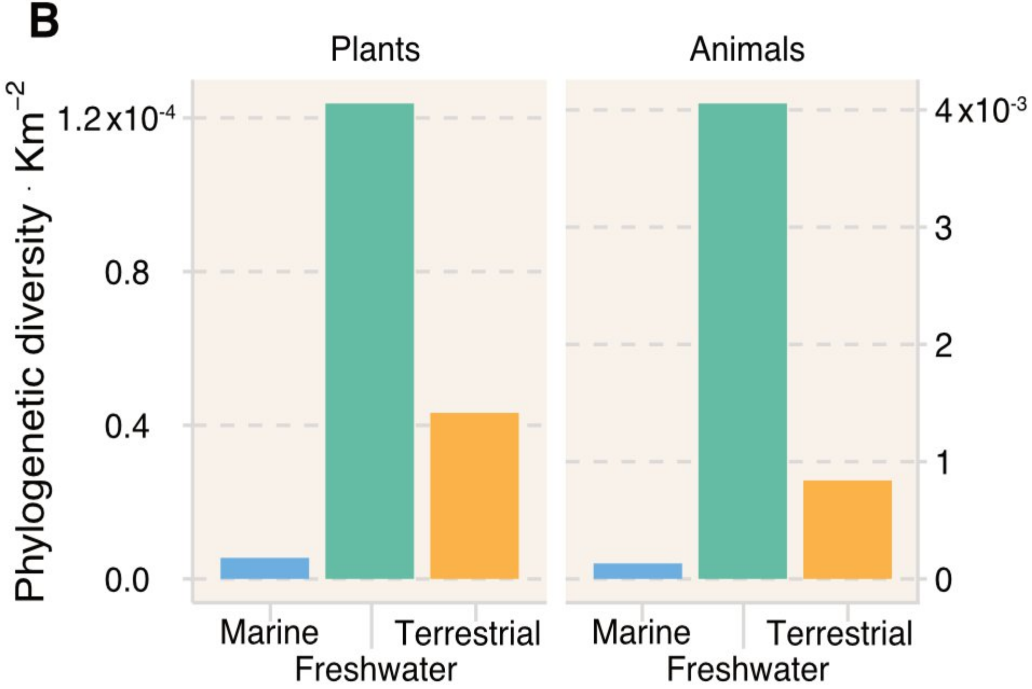
(4) Explore transition patterns and sources of extant biodiversity to each habitat

# Outstanding diversity by unit area in freshwater

Taxonomic and phylogenetic diversity per unit area in freshwater is similar or even higher than on land



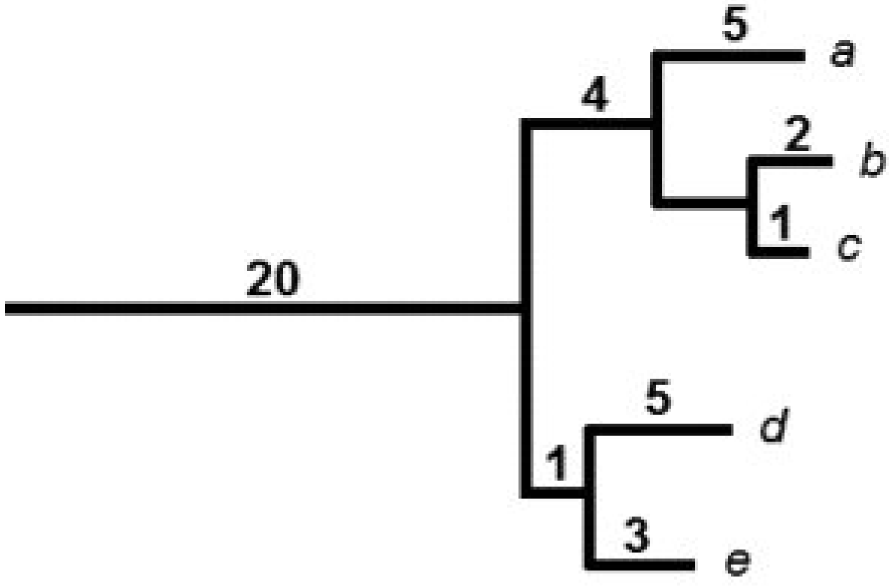
Taxonomic diversity per unit area

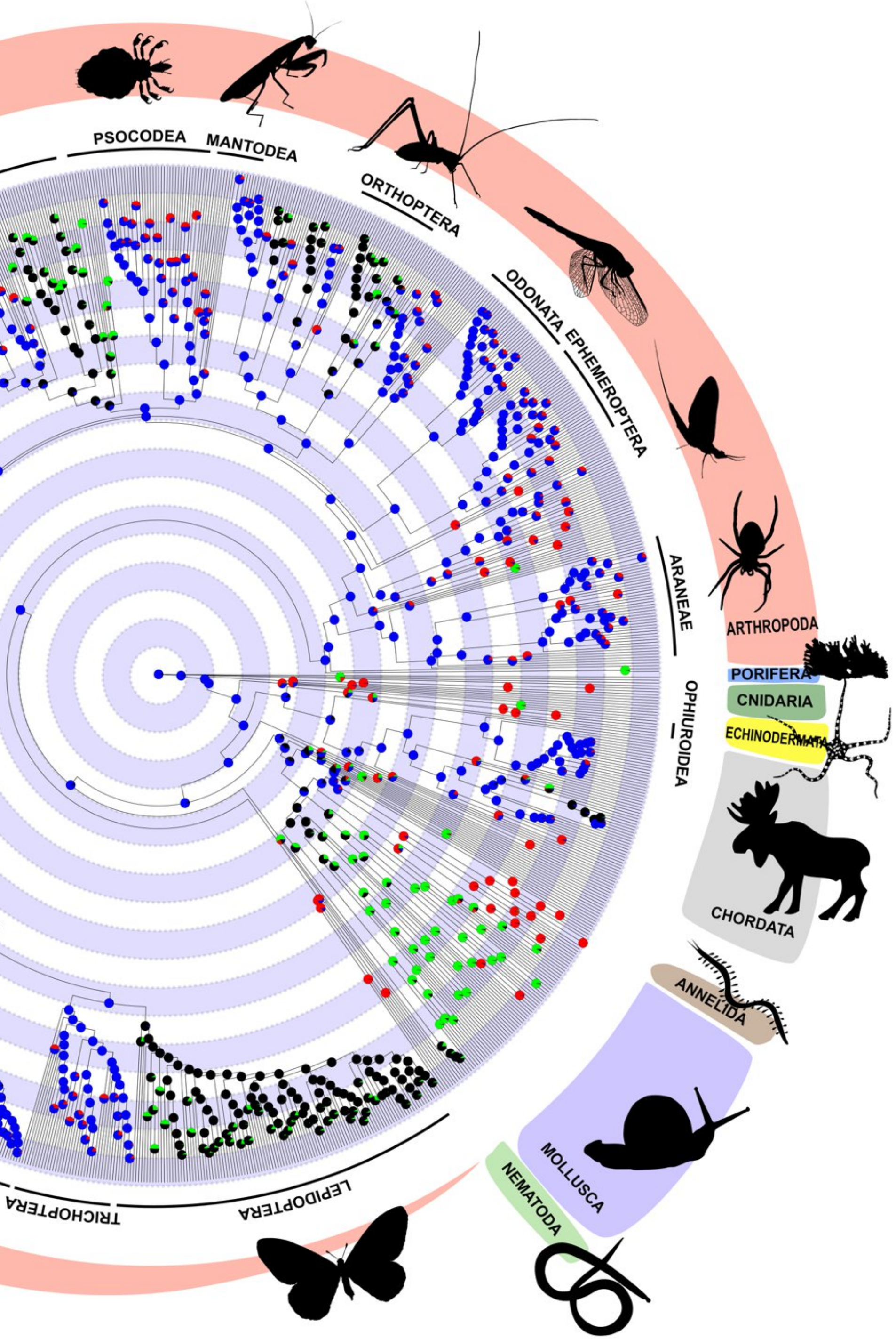


Phylogenetic diversity per unit area

# Phylogenetic diversity

- Faith’s (1992) phylogenetic diversity
- Phylogenetic diversity of a set of species as equal to the sum of the lengths of all those branches on the tree that span the members of the set





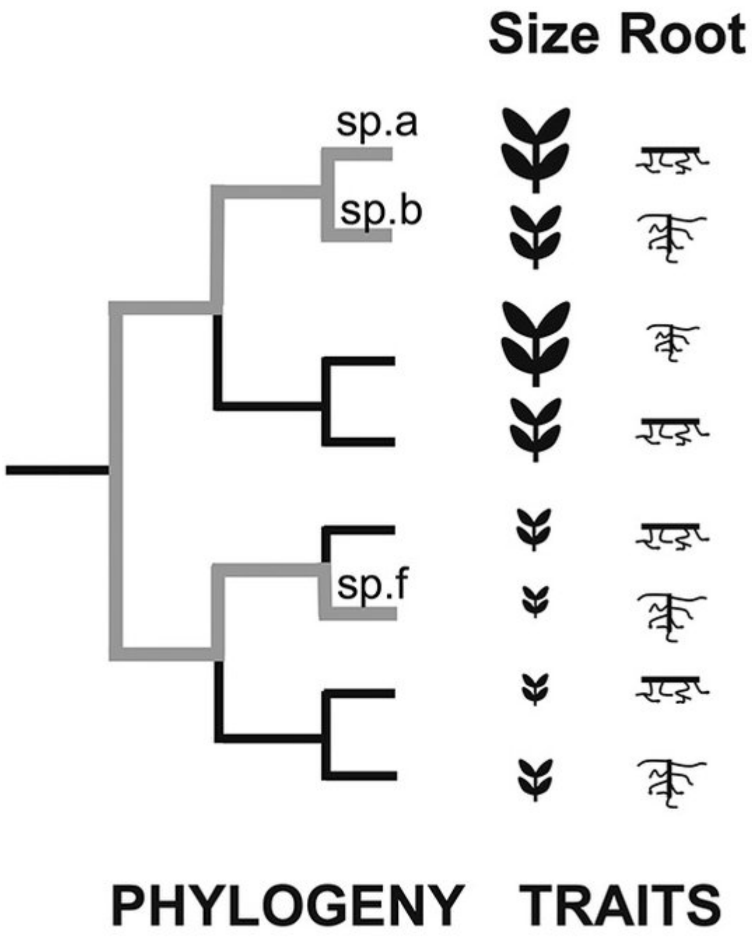
# 04

# Patterns of trait evolution

Phylogenetic signal, trait evolution, and ancestral states

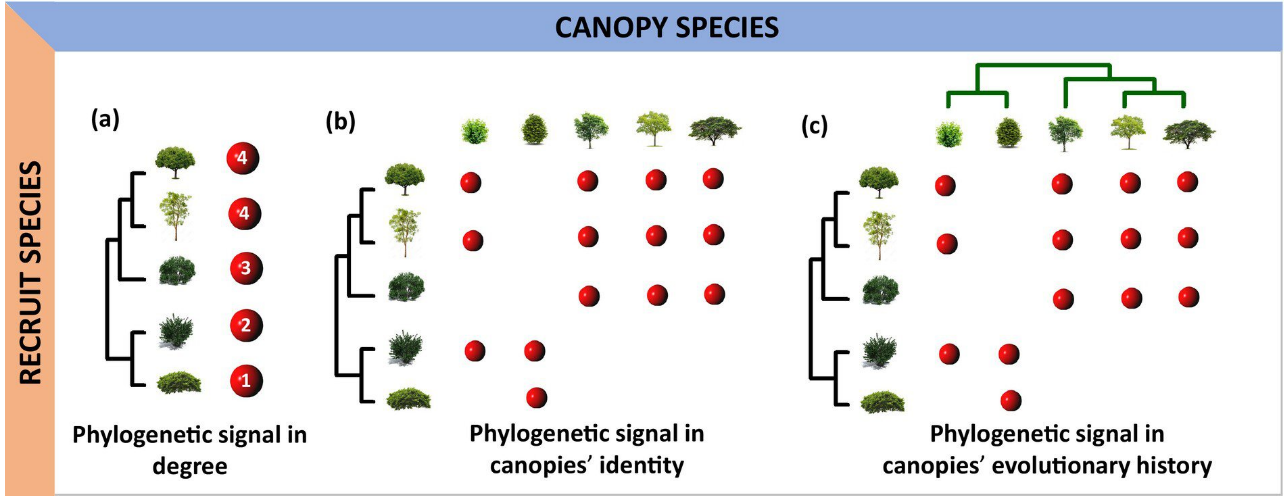
# Patterns of trait evolution

- So far...more closely related species are expected to be more ecologically similar
- There is more complexity, eg mode of evolution of the character
  - Neutral evolution of a trait, but with constrains
  - Trait lability
- Important to estimate conservatism before attempting to infer ecological processes structuring communities from their phylogenetic interactions



# Phylogenetic signal

- Strength of the covariation in the differences in measured traits among taxa with the phylogenetic distances separating them
- Strong signal = close relatives share similar traits (or trait values for continuous characters), while more distant relatives are less similar to each other
- Phylogenetic conservatism (eg climatic niche) might arise via inheritance of genetically conserved environmental tolerances or via phylogenetic conservatism in species geography
- Weak conservatism when environmentally determined or strong directional selection on phenotypes



Phylogenetic signal in degree

Phylogenetic signal in canopies' identity

Phylogenetic signal in canopies' evolutionary history

Gleiser et al. 2025

# Ancestral states

- Apparent limited use in ecological contexts due the relevance of current traits, not ancestral
- Current traits are still the product of ancestral ones
- Yet...multiple key hypotheses in the field have found ancestral traits to be relevant to explain current patterns: Ghost of competition past

# Ancestral states

# Background

- *Hemibrycon:* characterized by the presence of more than four teeth on the maxilla (in adults) (Eigenmann 1927, Román-Valencia et al. 2013).
- *H. brevispini* is endemic to La Venada and La Negra Creeks, tributaries of the Quindío River, in the upper Cauca River drainage (Colombia).
- ~30-60 mins from home.

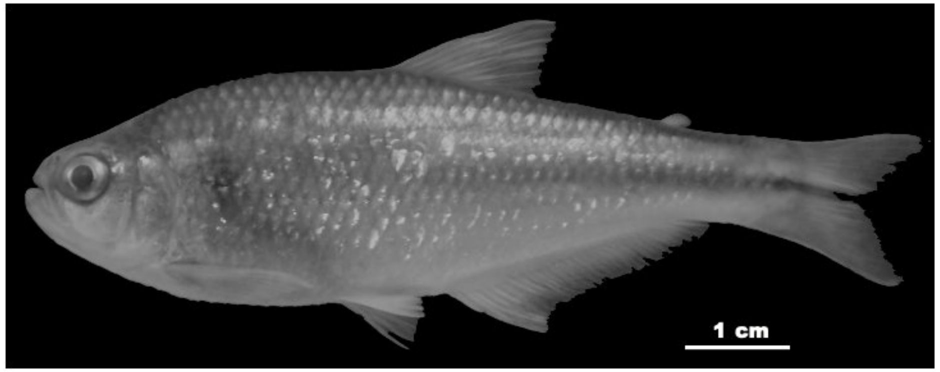


Fig. 1. *Hemibrycon brevispini* n. sp. Holotype IUQ 2008, Colombia, Quindío, Calarcá, Alto Cauca, Quindio River system, La Venada Creek.

*Fig. 1.* Hemibrycon brevispini *sp. n. Holotipo IUQ 2008, Colombia, Quindío, Calarcá, Alto Cauca, sistema fluvial del Quindío, arroyo La Venada.*

Román-Valencia, C., & Arcila-Mesa, D. K. (2009). Two new species of *Hemibrycon* (Characiformes, Characidae) from the Magdalena River, Colombia. *Animal Biodiversity and Conservation*, *32*(2), 77-87.

# Objective

This species was described back in 2009. Up to this point, only morphological information was available for this species.

- We...
  - ...describe basic aspects of *H. brevispini*‘s diet, reproduction and habitat.
  - ...provide baseline information useful for conservation and management efforts.

# *H. brevispinni* diet

Feeding is diurnal, with prey ingestion occurring shortly before capture.

41 total prey categories...

1. Diptera
2. Hymenoptera: Formicidae
3. Ephemeroptera: Baetidae

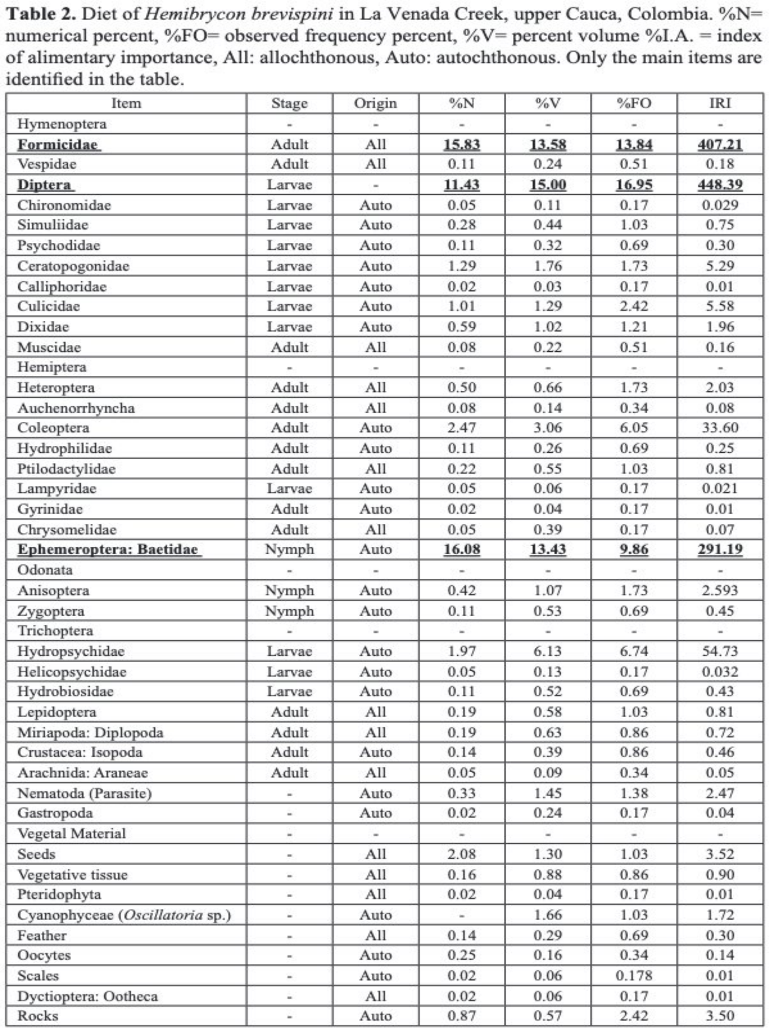


**Table 2.** Diet of *Hemibrycon brevispini* in La Venada Creek, upper Cauca, Colombia. %N= numerical percent, %FO= observed frequency percent, %V= percent volume %I.A. = index of alimentary importance, All: allochthonous, Auto: autochthonous. Only the main items are identified in the table.

| Item | Stage | Origin | %N | %V | %FO | IRI |
|---|---|---|---|---|---|---|
| Hymenoptera | - | - | - | - | - | - |
| **Formicidae** | Adult | All | **15.83** | **13.58** | **13.84** | **407.21** |
| Vespidae | Adult | All | 0.11 | 0.24 | 0.51 | 0.18 |
| **Diptera** | Larvae | - | **11.43** | **15.00** | **16.95** | **448.39** |
| Chironomidae | Larvae | Auto | 0.05 | 0.11 | 0.17 | 0.029 |
| Simuliidae | Larvae | Auto | 0.28 | 0.44 | 1.03 | 0.75 |
| Psychodidae | Larvae | Auto | 0.11 | 0.32 | 0.69 | 0.30 |
| Ceratopogonidae | Larvae | Auto | 1.29 | 1.76 | 1.73 | 5.29 |
| Calliphoridae | Larvae | Auto | 0.02 | 0.03 | 0.17 | 0.01 |
| Culicidae | Larvae | Auto | 1.01 | 1.29 | 2.42 | 5.58 |
| Dixidae | Larvae | Auto | 0.59 | 1.02 | 1.21 | 1.96 |
| Muscidae | Adult | All | 0.08 | 0.22 | 0.51 | 0.16 |
| Hemiptera | - | - | - | - | - | - |
| Heteroptera | Adult | All | 0.50 | 0.66 | 1.73 | 2.03 |
| Auchenorrhyncha | Adult | All | 0.08 | 0.14 | 0.34 | 0.08 |
| Coleoptera | Adult | Auto | 2.47 | 3.06 | 6.05 | 33.60 |
| Hydrophilidae | Adult | Auto | 0.11 | 0.26 | 0.69 | 0.25 |
| Ptilodactylidae | Adult | All | 0.22 | 0.55 | 1.03 | 0.81 |
| Lampyridae | Larvae | Auto | 0.05 | 0.06 | 0.17 | 0.021 |
| Gyrinidae | Adult | Auto | 0.02 | 0.04 | 0.17 | 0.01 |
| Chrysomelidae | Adult | All | 0.05 | 0.39 | 0.17 | 0.07 |
| **Ephemeroptera: Baetidae** | Nymph | Auto | **16.08** | **13.43** | **9.86** | **291.19** |
| Odonata | - | - | - | - | - | - |
| Anisoptera | Nymph | Auto | 0.42 | 1.07 | 1.73 | 2.593 |
| Zygoptera | Nymph | Auto | 0.11 | 0.53 | 0.69 | 0.45 |
| Trichoptera | - | - | - | - | - | - |
| Hydropsychidae | Larvae | Auto | 1.97 | 6.13 | 6.74 | 54.73 |
| Helicopsychidae | Larvae | Auto | 0.05 | 0.13 | 0.17 | 0.032 |
| Hydrobiosidae | Larvae | Auto | 0.11 | 0.52 | 0.69 | 0.43 |
| Lepidoptera | Adult | All | 0.19 | 0.58 | 1.03 | 0.81 |
| Miriapoda: Diplopoda | Adult | All | 0.19 | 0.63 | 0.86 | 0.72 |
| Crustacea: Isopoda | Adult | Auto | 0.14 | 0.39 | 0.86 | 0.46 |
| Arachnida: Araneae | Adult | All | 0.05 | 0.09 | 0.34 | 0.05 |
| Nematoda (Parasite) | - | Auto | 0.33 | 1.45 | 1.38 | 2.47 |
| Gastropoda | - | Auto | 0.02 | 0.24 | 0.17 | 0.04 |
| Vegetal Material | - | - | - | - | - | - |
| Seeds | - | All | 2.08 | 1.30 | 1.03 | 3.52 |
| Vegetative tissue | - | All | 0.16 | 0.88 | 0.86 | 0.90 |
| Pteridophyta | - | All | 0.02 | 0.04 | 0.17 | 0.01 |
| Cyanophyceae (*Oscillatoria* sp.) | - | Auto | - | 1.66 | 1.03 | 1.72 |
| Feather | - | All | 0.14 | 0.29 | 0.69 | 0.30 |
| Oocytes | - | Auto | 0.25 | 0.16 | 0.34 | 0.14 |
| Scales | - | Auto | 0.02 | 0.06 | 0.178 | 0.01 |
| Dyctioptera: Ootheca | - | All | 0.02 | 0.06 | 0.17 | 0.01 |
| Rocks | - | Auto | 0.87 | 0.57 | 2.42 | 3.50 |

# Principal Component Analysis of diet

- A centered principal component analysis was made using stomach contents abundances (%N)
- In short: Broad trophic niche and relatively low between-individual variation in diets
- No association between the first axis scores (% PCA1) and fish size (r=0.12, p=0.615)

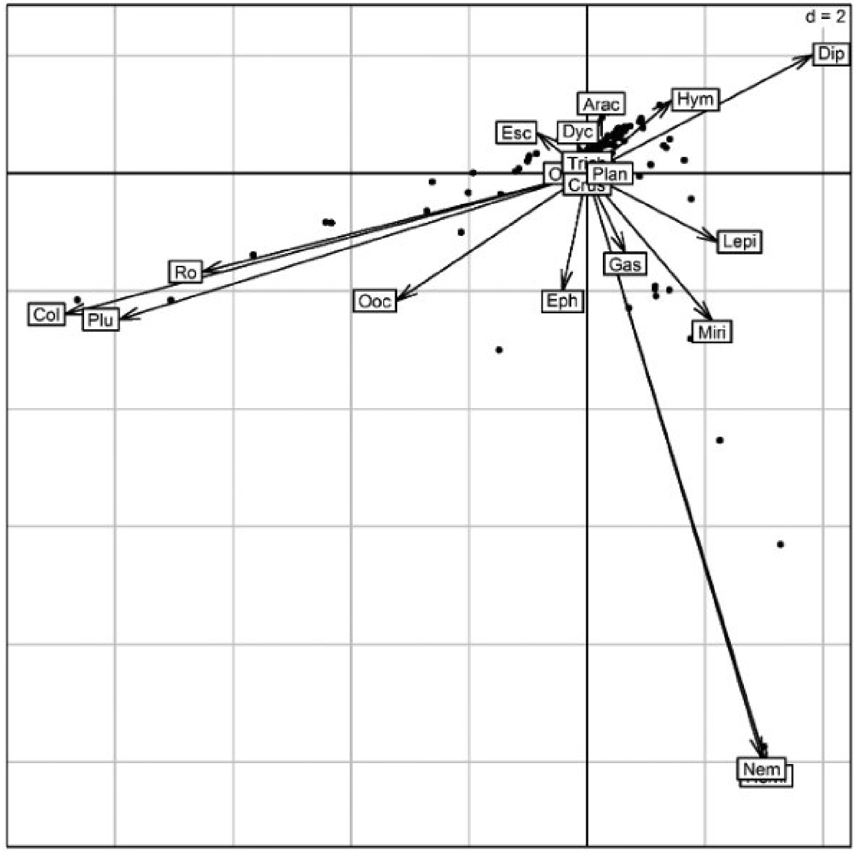
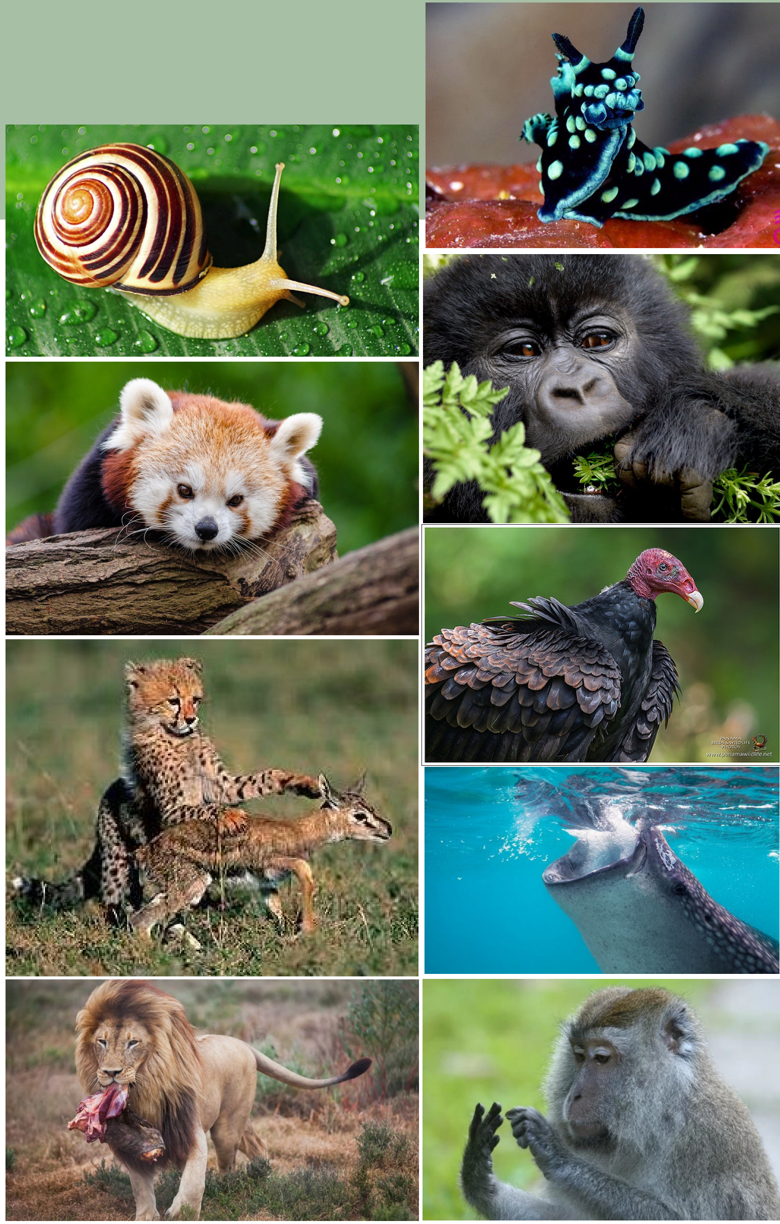


**Figure 2.** Biplot of prey and stomachs obtained from a Centered Principal Component Analysis (first factorial plane) for *Hemibrycon brevispini*, in La Venada Creek, Quindío River. Dots represent stomachs. Where, Hym: Hymenoptera, Dip: Diptera, Hemi: Hemiptera, Col: Coleoptera, Eph: Ephemeroptera, Odo: Odonata, Trich: Trichoptera, Lepi: Lepidoptera, Miri: Miriapoda, Crus: Crustacea, Arac: Aracnae, Nem: Nematoda, Gas: Gastropoda. Plan: Plantae, Plu: Feather, Ooc: Oocyte, Esc: Escale, Dyc: Dyctioptera, Ro: Rocks.

# What was the big picture…?

Roman-Palacios, C., Scholl, J. P., & Wiens, J. J. (2019). Evolution of diet across the animal tree of life. Evolution letters, 3(4), 339-347.

# Trophic diversity in animals



Remarkable diversity of diets and associated lifestyles:

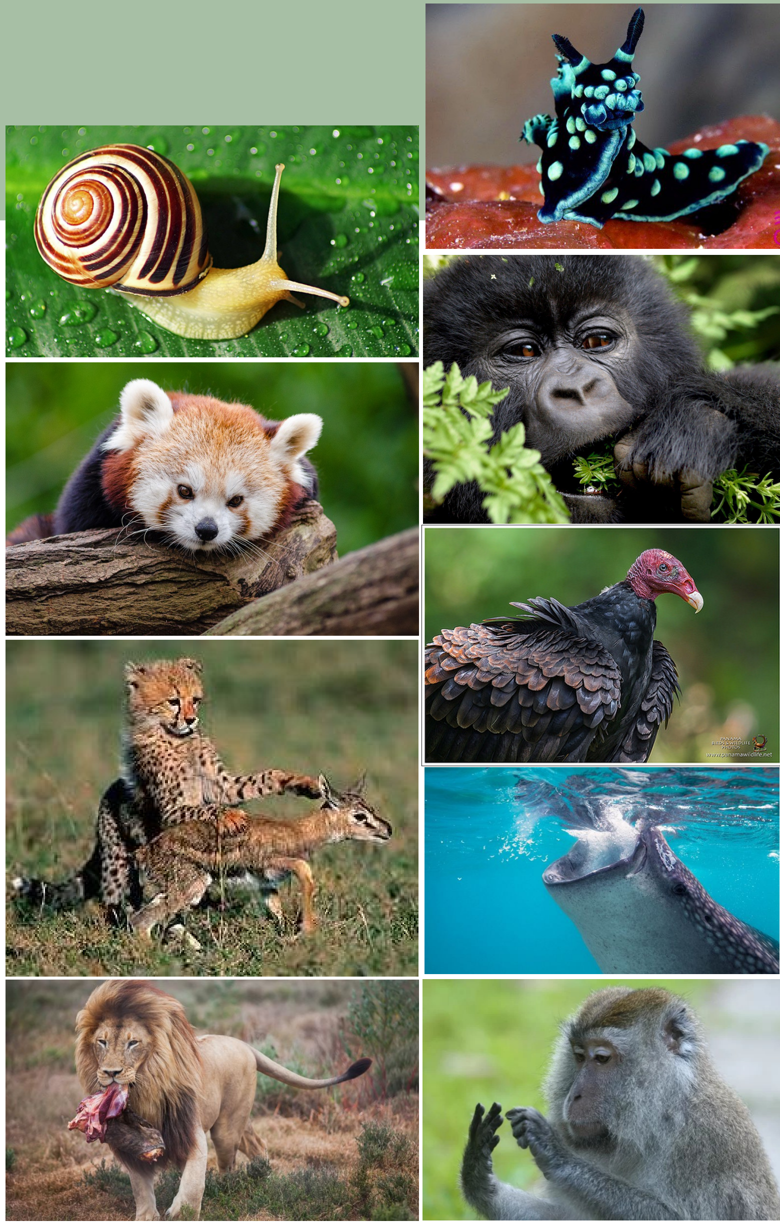
- Mammalian carnivores
- Insect herbivores
- Marine invertebrates that passively filter feed on tiny organisms

**Evolution of animal diets remains poorly understood at the largest phylogenetic scales (e.g. among phyla)**

# Objectives

**(i) Are diets conserved across animal phylogeny?**

Literature typically focuses on the Grinnellian niche (environmental requirements). We provide the broadest test of conservatism in the Eltonian niche.

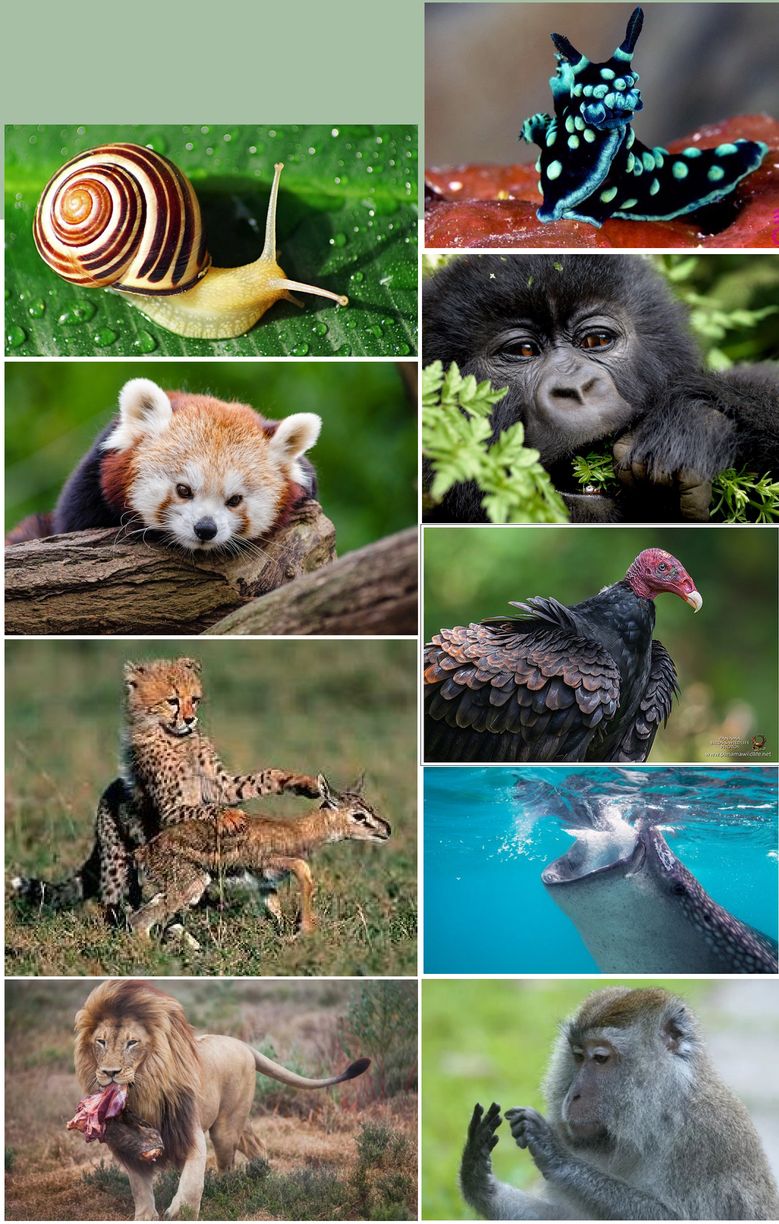


# Objectives

**(ii) Does diet influence rates of species proliferation (diversification) among animal phyla?**

Herbivory influences diversification within some groups (e.g. mammals, hexapods, birds, crustaceans).

It remains unclear whether diet influences diversification patterns among phyla.

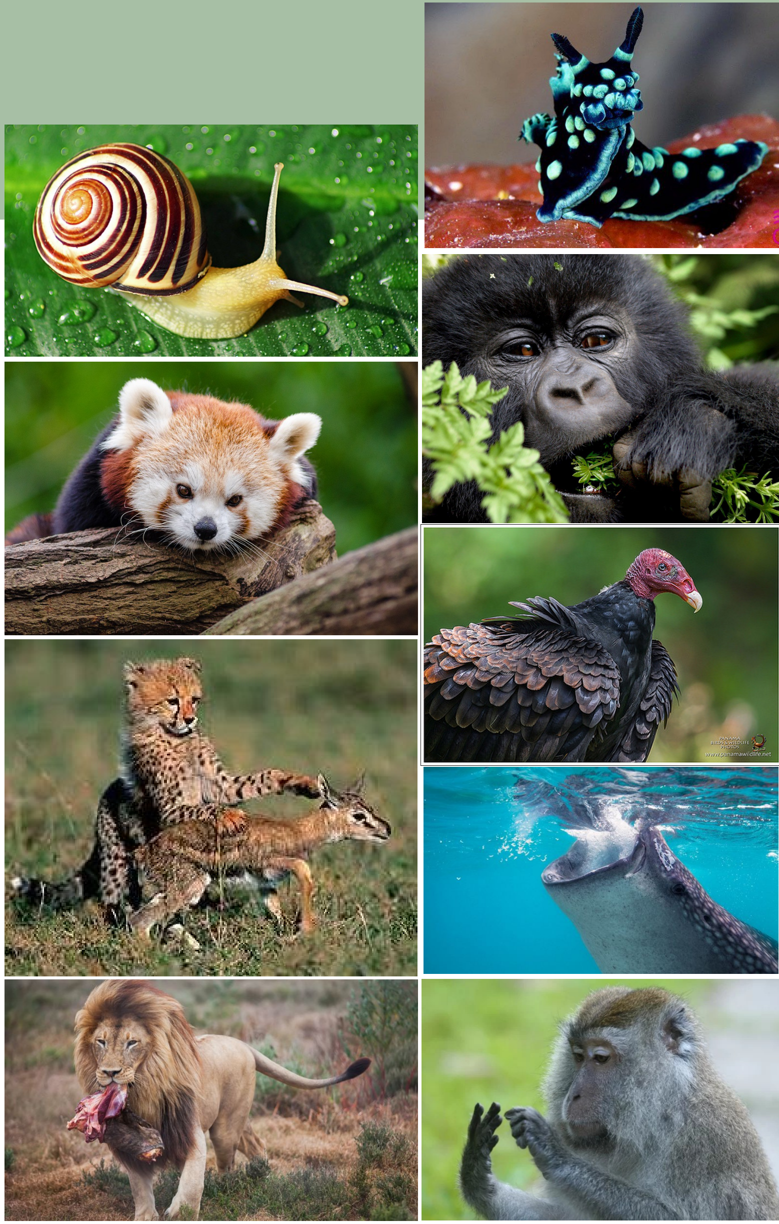


# Objectives

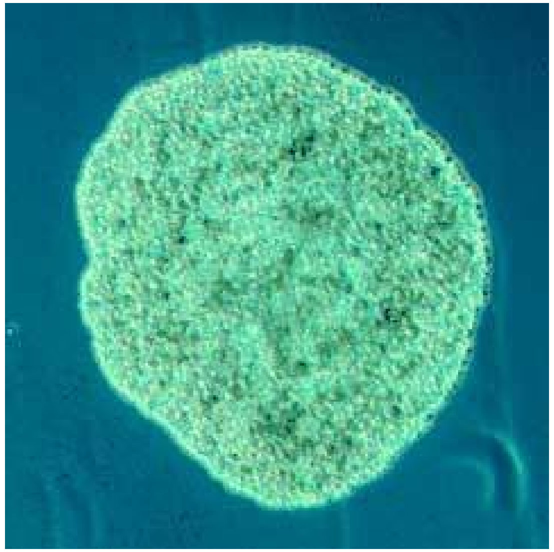
**(iii) What was the ancestral diet of animals and major animal clades?**

Were animals originally carnivores or herbivores?

Many relevant animal phyla do not preserve well (e.g. small, soft-bodied taxa) may be difficult to infer for many fossil taxa.

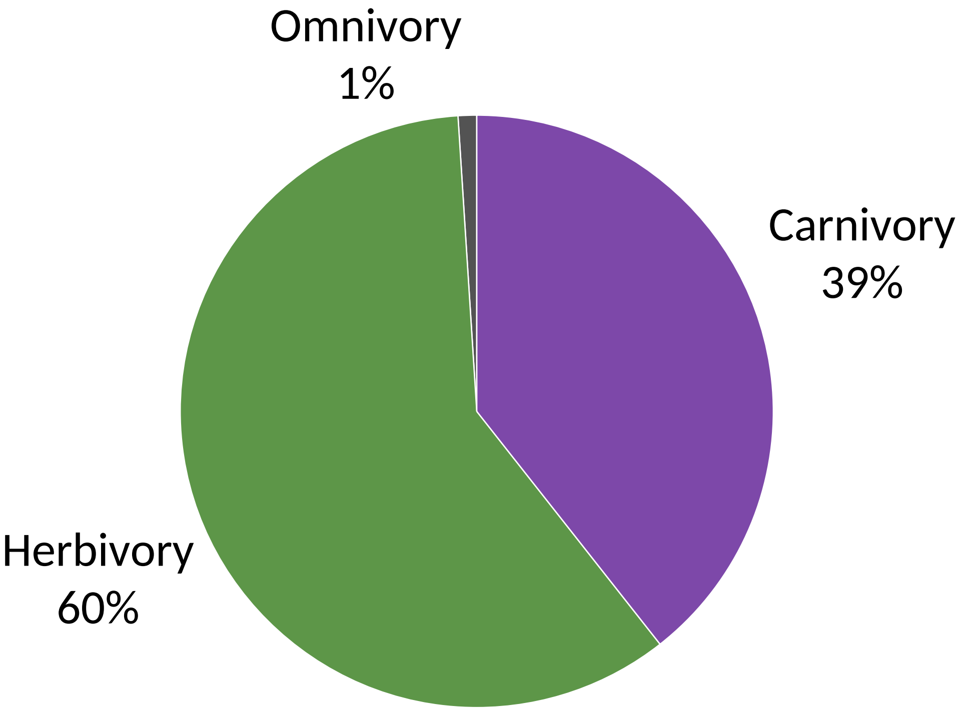


# Diet

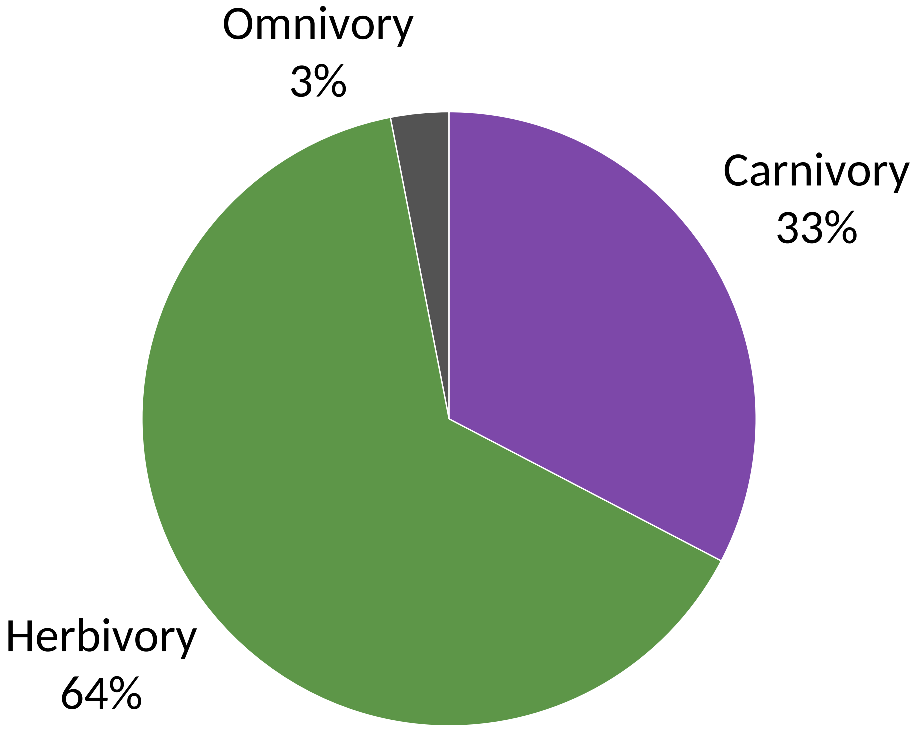


| **Herbivore** | **Carnivore** | **Omnivore** |
|---|---|---|
| Feeding on autotrophs (>90% of diet) | Feeding on heterotrophs (>90% of diet) | Heterotrophs <90% of diet<br>Autotrophs <90% of diet |

# Frequency of trophic strategies in animals



Based on independent literature searches

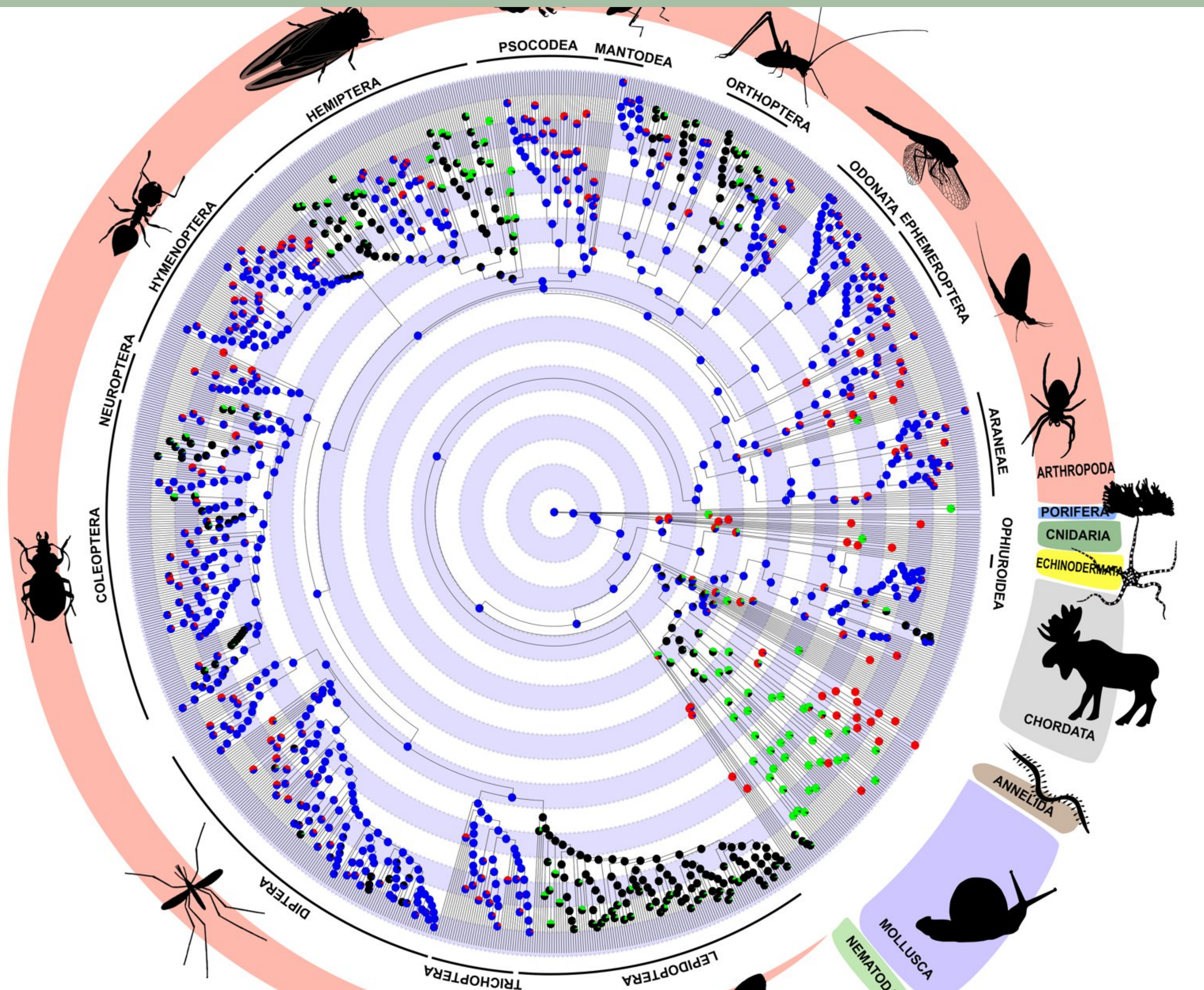


Based on 1,087 taxa sampled in tree

# Phylogenetic signal

Strong phylogenetic signal at broad phylogenetic scales (lambda=0.79,$P<0.0001$)

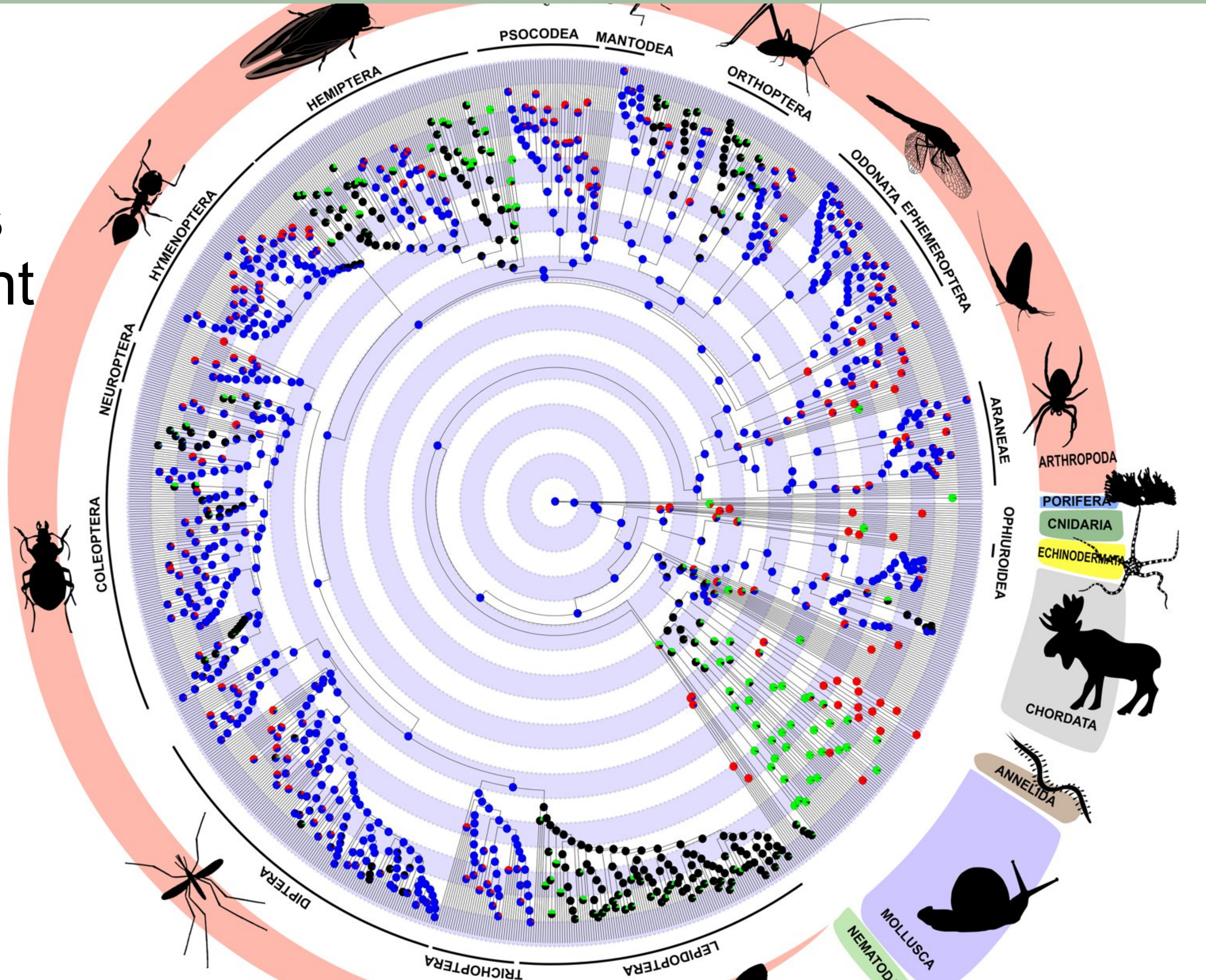
**Diets are evolutionarily conserved, rather than being extremely labile.**

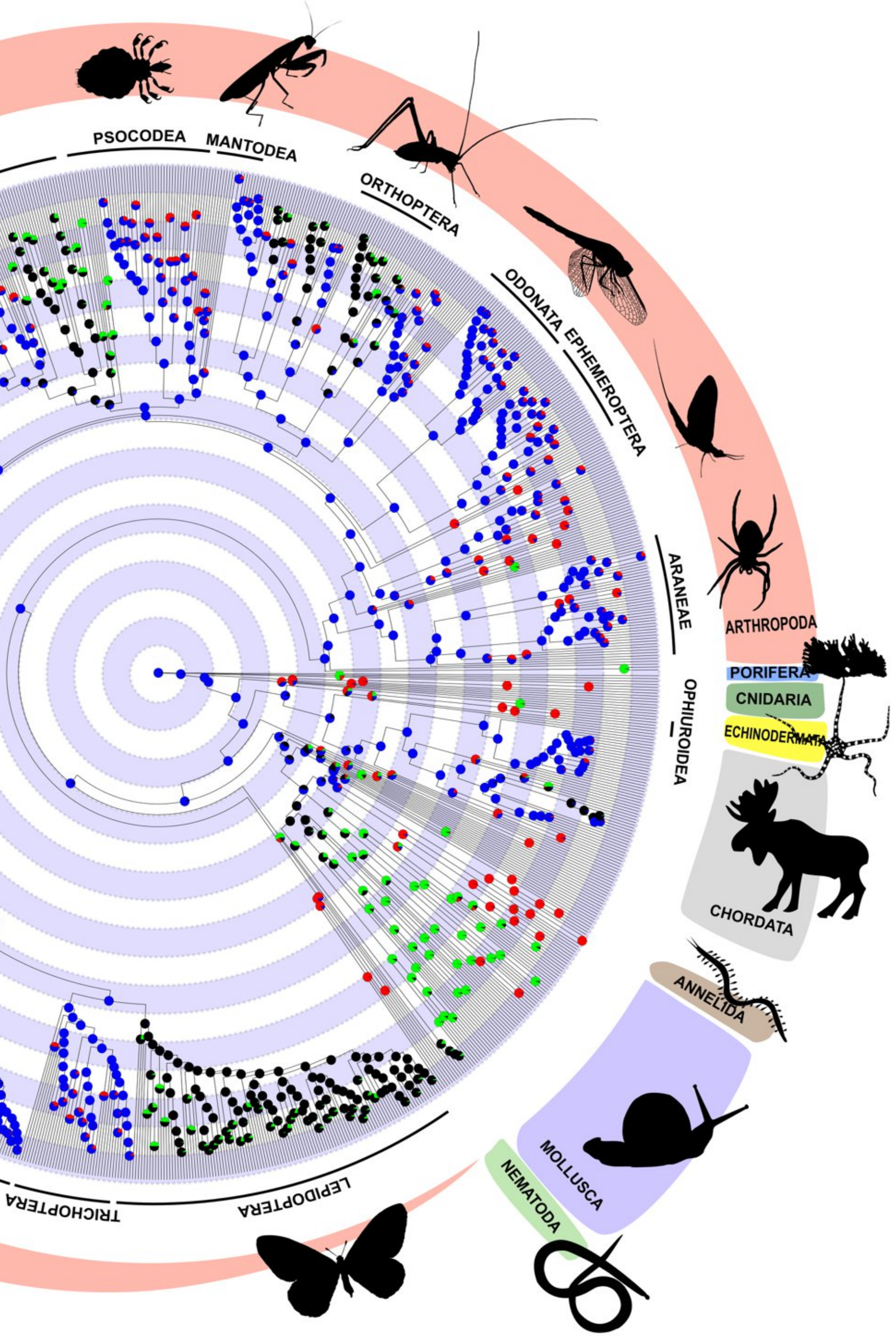


# Diet and diversification

The best-fitting Hidden State Speciation and Extinction models (HiSSE) model supported different rates associated with the inferred hidden states

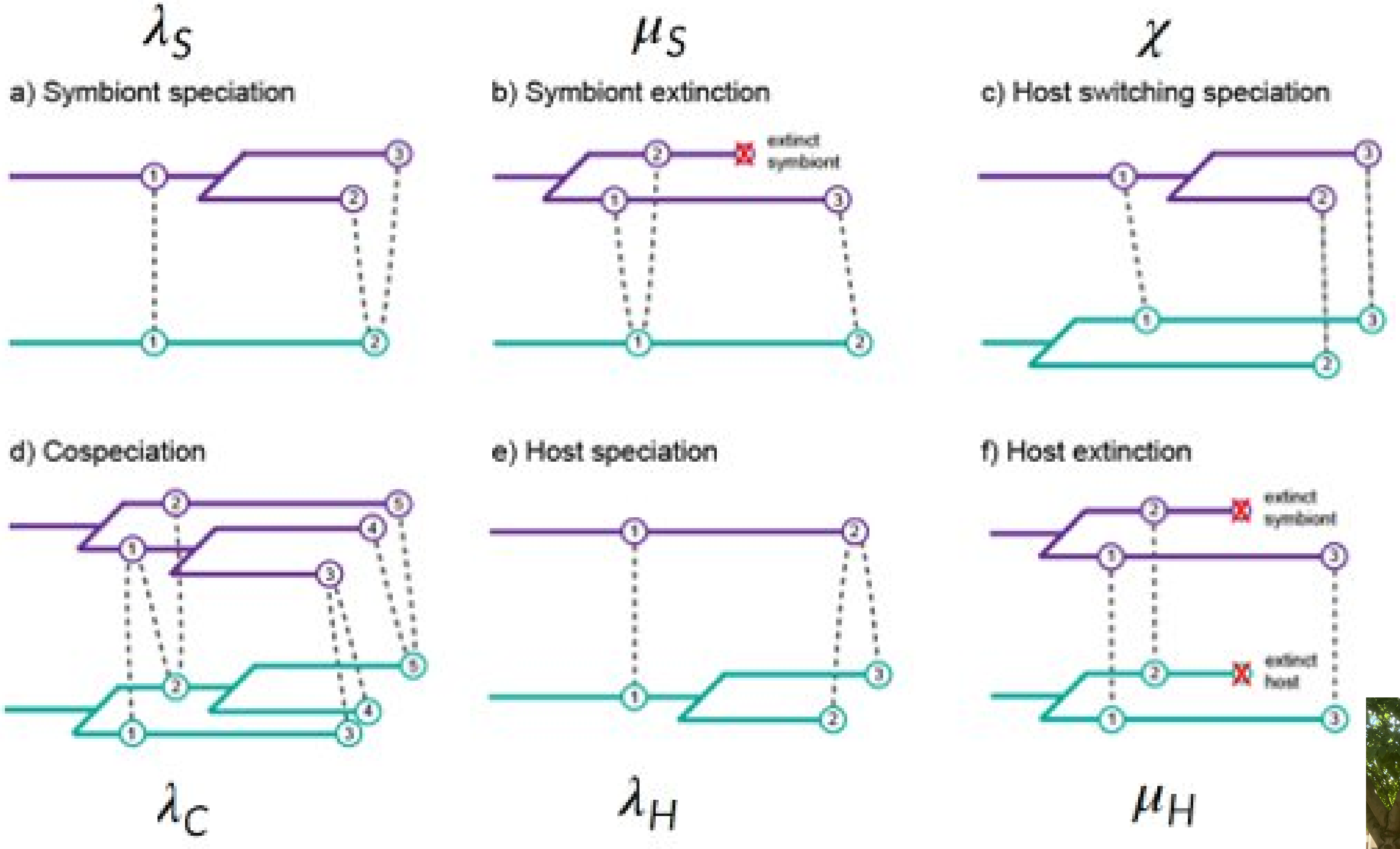
Analyses of net diversification rates of phyla and their proportion of herbivorous species using phylogenetic regression showed **no significant relationships** ($R^2<0.01$; $P>0.05$)



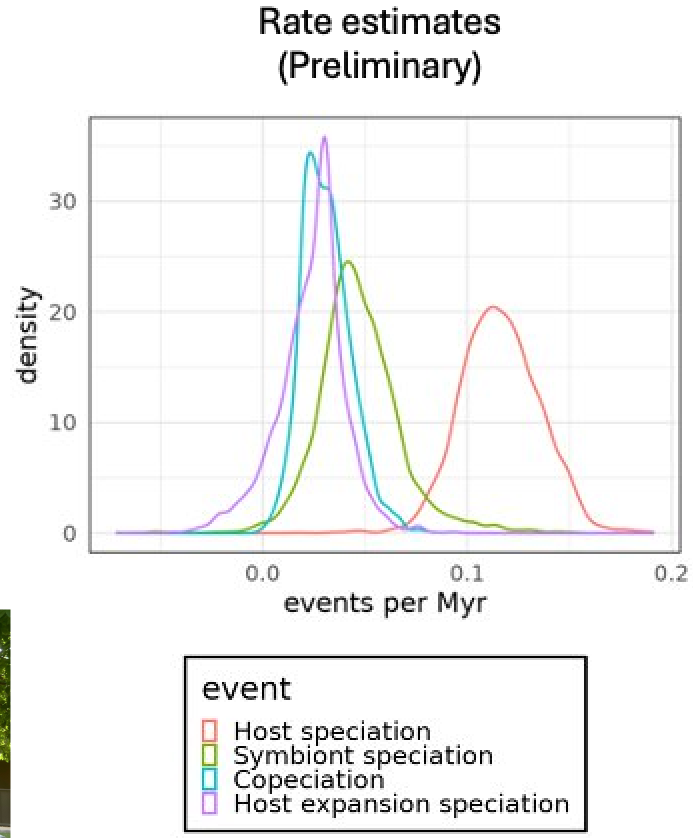


# Other intersections

# ABC and species interactions: What processes explain cophylogenetic patterns?



**Yichao Zeng**
Postdoctoral Researcher

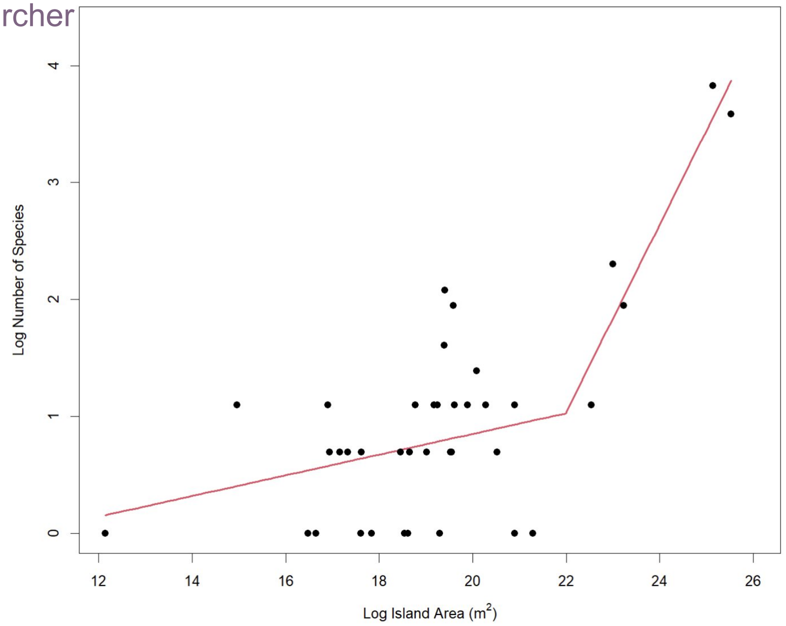


Zeng & Román-Palacios, under review; Sys Bio

# Macroecology: SSARP R Package

- Species-/Speciation-Area Relationship Projector
- Access GBIF or use your own occurrence data to create these relationships
    - Input a phylogenetic tree to create a speciation-area relationship
- New! Input a shapefile to create species- and speciation-area relationships for island-like systems (e.g., lakes, habitat fragments, sky islands)

**Kristen Martinet**
Postdoctoral Researcher

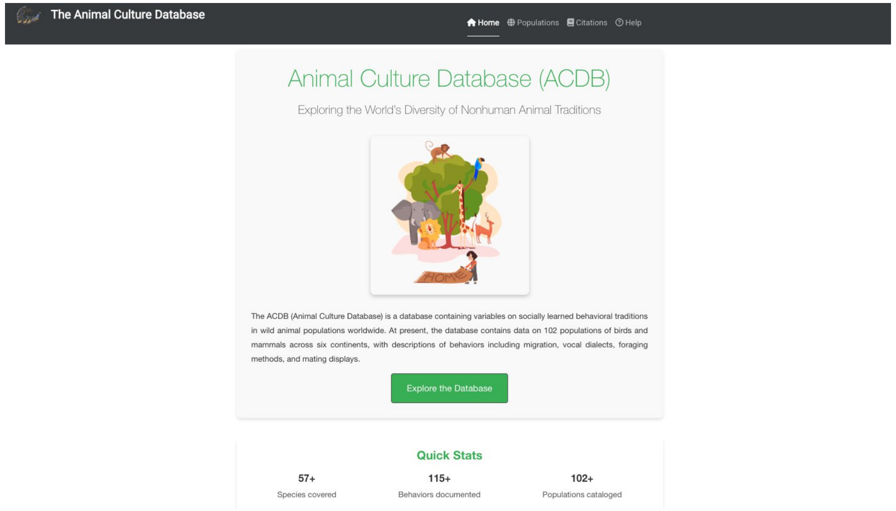


Species-area relationship for *Anolis* using GBIF dat

# Animal Culture Database and ecological covariates

- Comparative database of behavioral traditions in wild animal populations globally
- Includes variables from existing literature on animal behavior on taxonomy, location, forms of social learning (social transmission of behaviors across individuals in a population), behavioral domains (migration, play, mating, communication, etc.)
- Relational SQLite database made available as a website through Shiny app
- Further versions will include data on anthropogenic effects to facilitate research on conservation and animal behavior

**Kiran Basava**
Postdoctoral Researcher



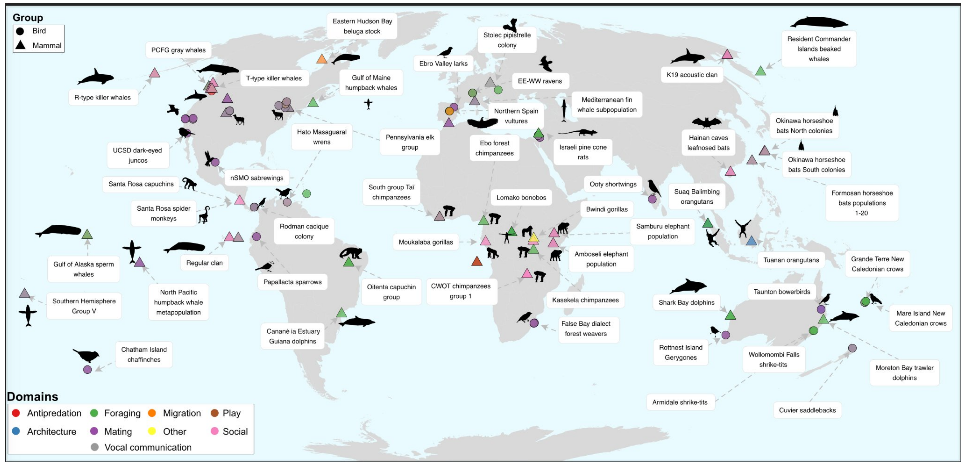
Animal Culture Database (ACDB)

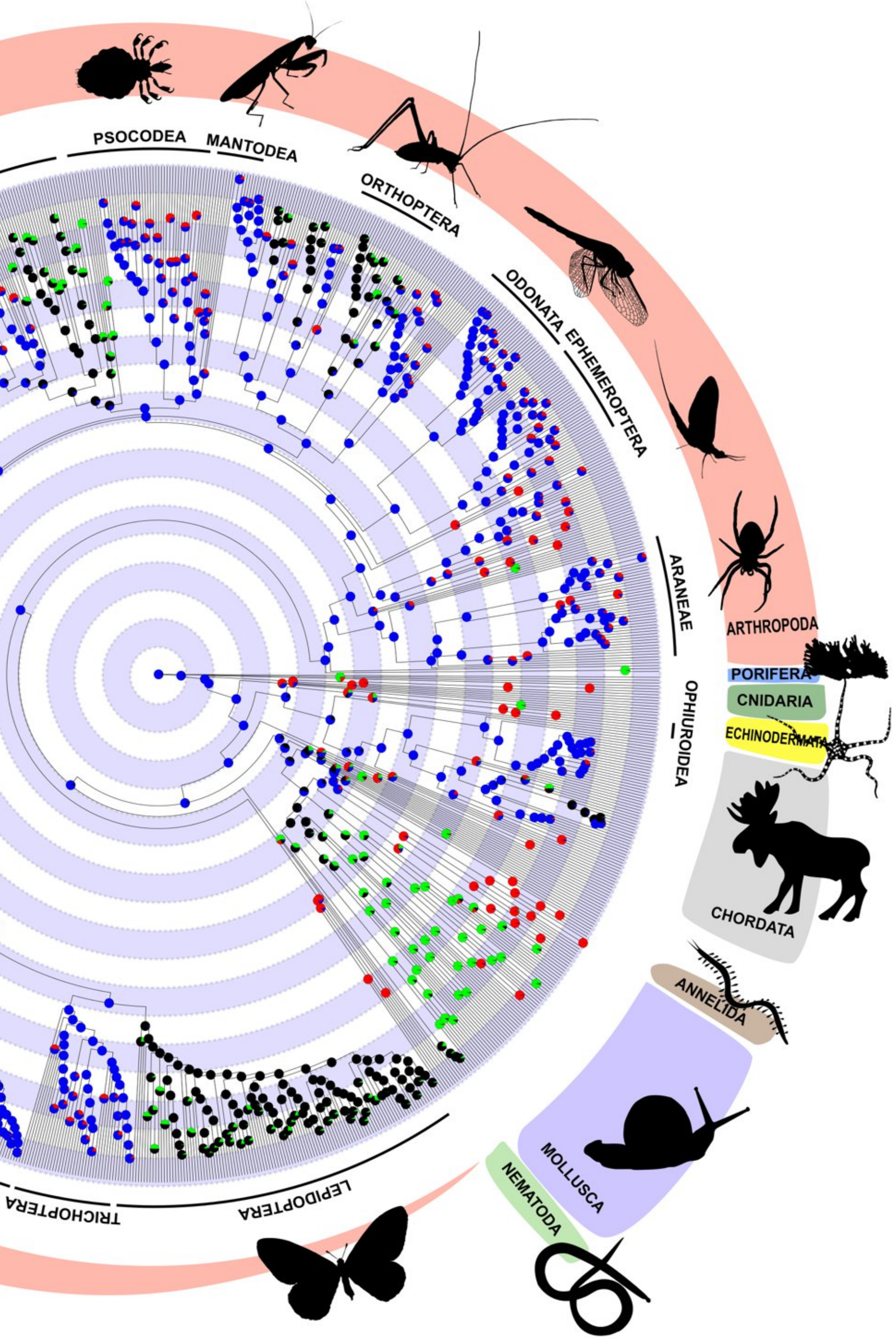
Exploring the World's Diversity of Nonhuman Animal Traditions

The ACDB (Animal Culture Database) is a database containing variables on socially learned behavioral traditions in wild animal populations worldwide. At present, the database contains data on 102 populations of birds and mammals across six continents, with descriptions of behaviors including migration, vocal dialects, foraging methods, and mating displays.

Quick Stats

| 57+ | 115+ | 102+ |
|---|---|---|
| Species covered | Behaviors documented | Populations cataloged |





# Issues with this pipeline

# Issues with this pipeline (in short)

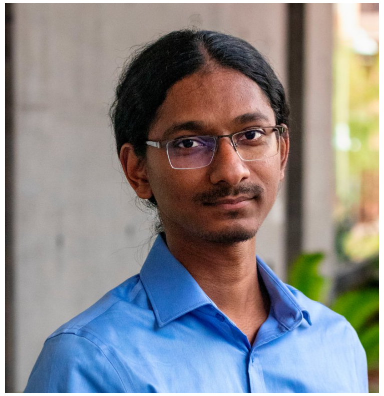
- Data (phylogenetic and traits) are limited for many groups
- Identifiability of phylogenetic signal: many different simulations of evolution can result in similar phylogenetic signals.
- Alternative comparative models of constrained evolution are not often used in calculating phylogenetic signal (i.e. Brownian Motion versus various OU models).
- Phylogenetic signal focuses primarily on the terminals, while largely being uninformative of deeper patterns through the tree.

# Issues with this pipeline

**Current pipeline:** phylogeny is best applied in linear models (PGLMM, PGLS, etc.) to account for shared history; however, we can **infer little about the evolutionary processes or rates** important to understanding ecology using the current phylogenetic pipeline.

**Future pipeline**: models of trait evolution are necessary to understand the processes and rates by which current species, traits, and communities function (i.e. a new pipeline).

# Thank you!



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**Kiran Basava**
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https://bbcs.arizona.edu/)

**Kennedy Gezella**
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Data Diversity Lab

**Alivia Nytko**
Organizer

Cophylogenies
**(ABC)**

Animal culture
**(data)**

Galapagos
**(regressons)**

Diet
**(signal)**

Fish
**(spatial)**

Habitats
**(ancestral states)**

phruta
**(phylo inference)**

treedata.table
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