

Phylogenetic ecology

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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

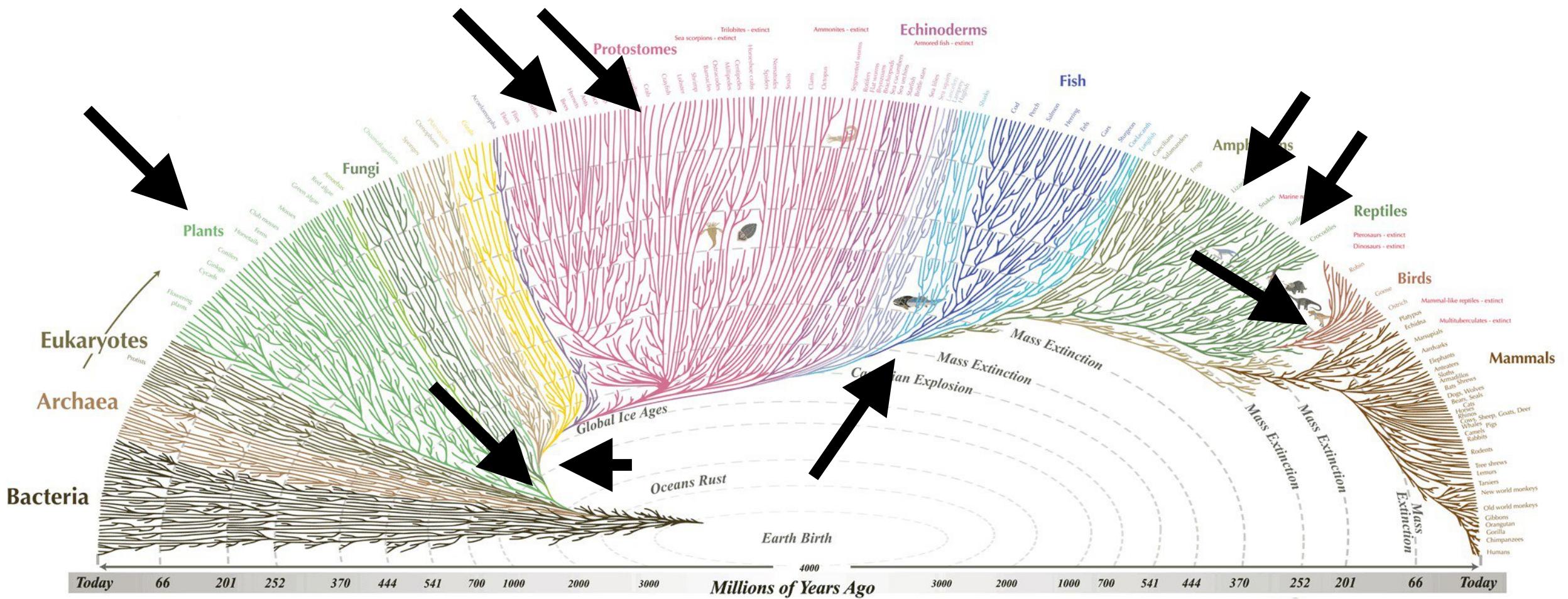
Phylogenetic diversity
How to measure and the effect of spatial scales

04

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

05

Macroevolution
Speciation, extinction, diversification



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

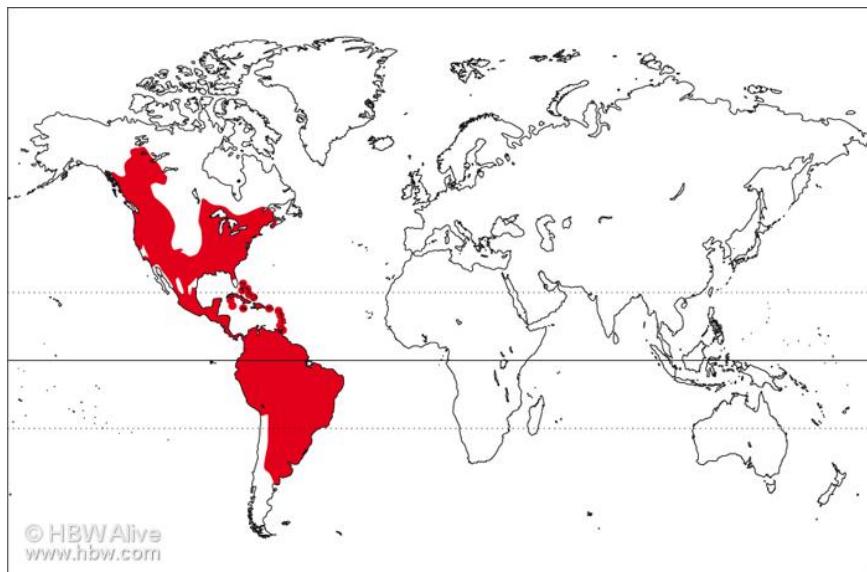
Questions

- 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

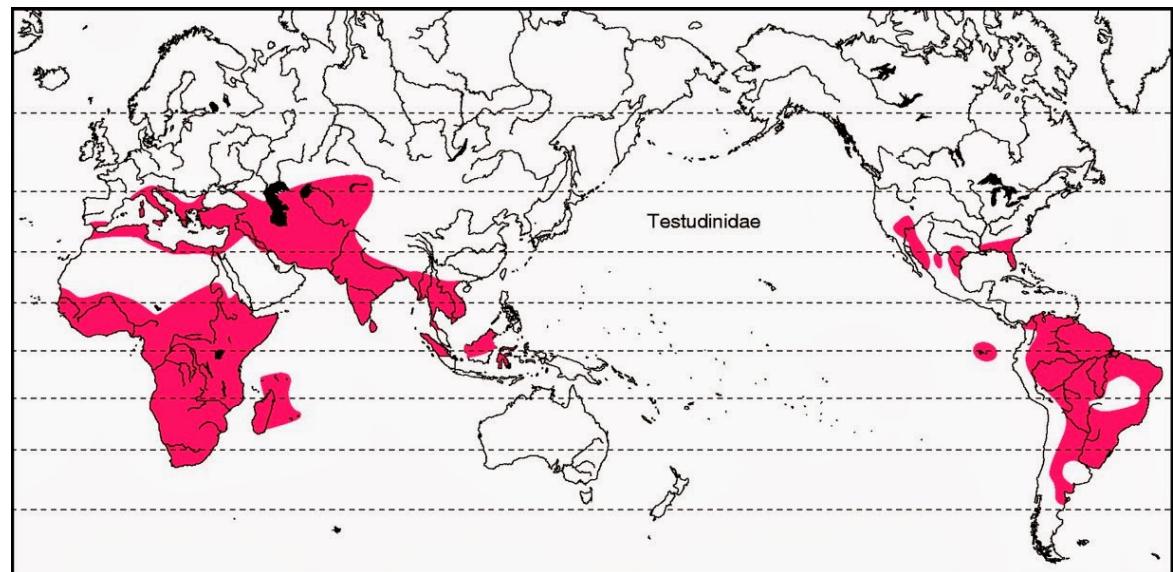
Tanagers (Thraupidae)



~386 species

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

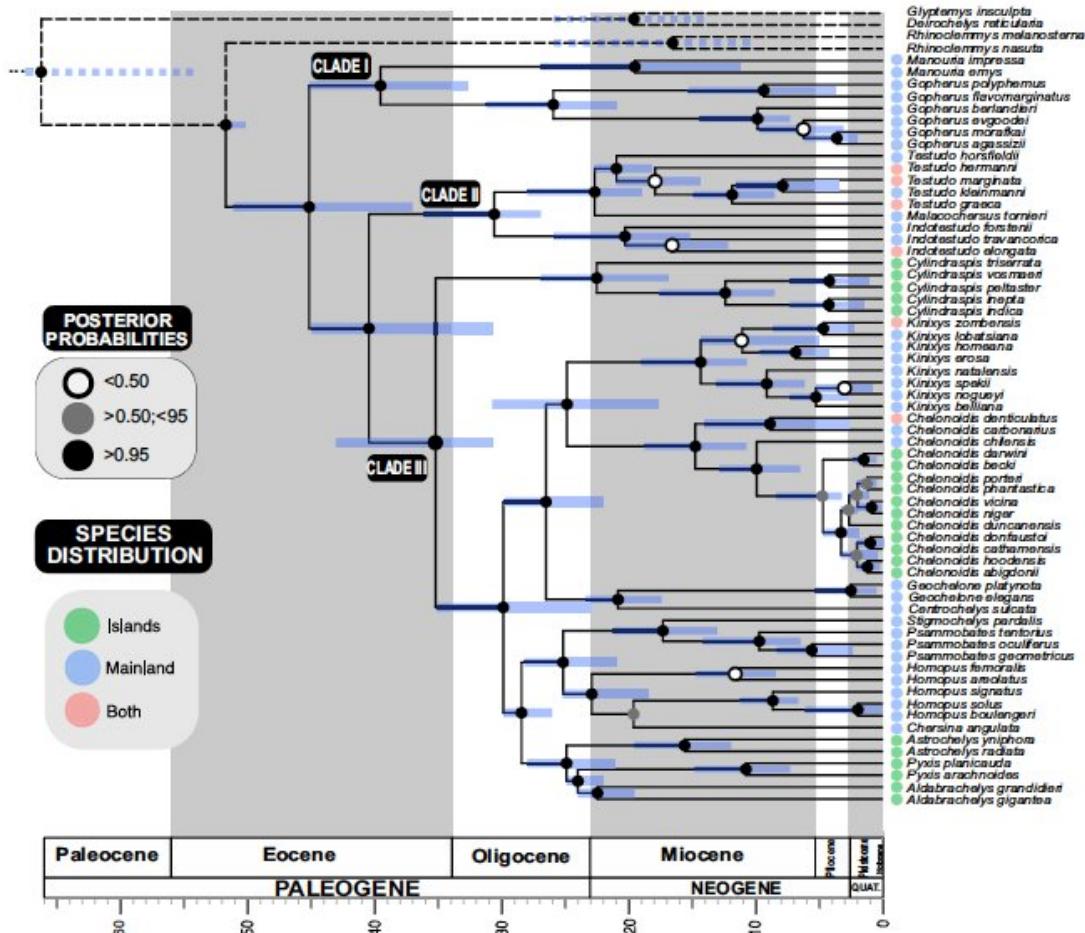
Tortoises (Testudinidae)



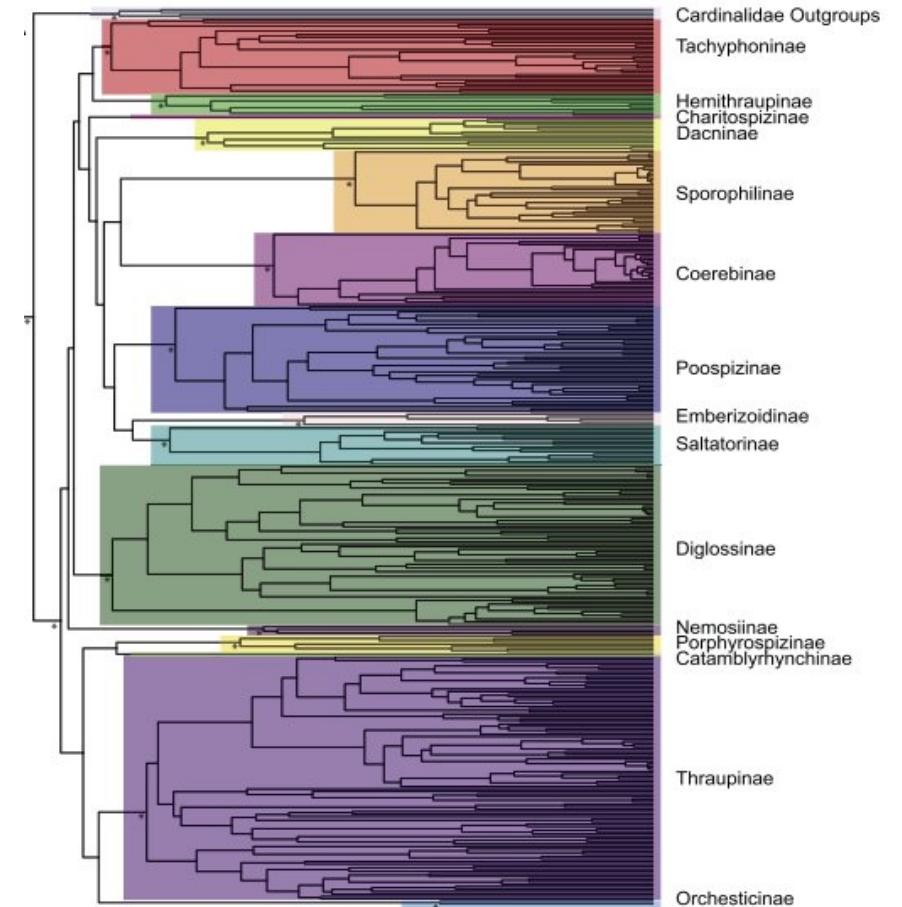
~59 species

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)

Testing for island effects on diversification

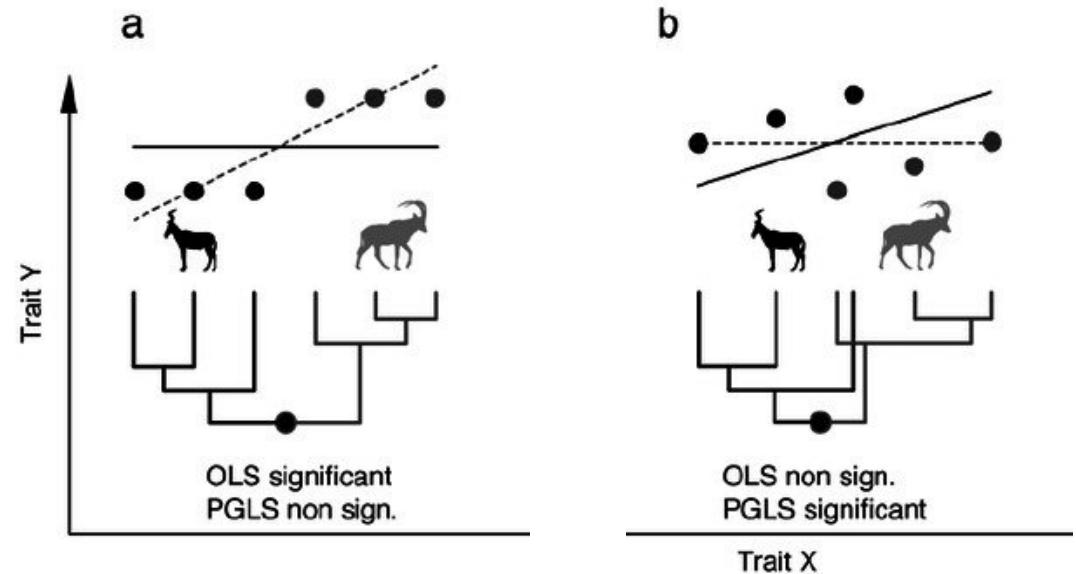
Phylogenetic regressions

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

Are the relationships between variables explained by the phylogeny?



Within clades: similar
Among clades: different

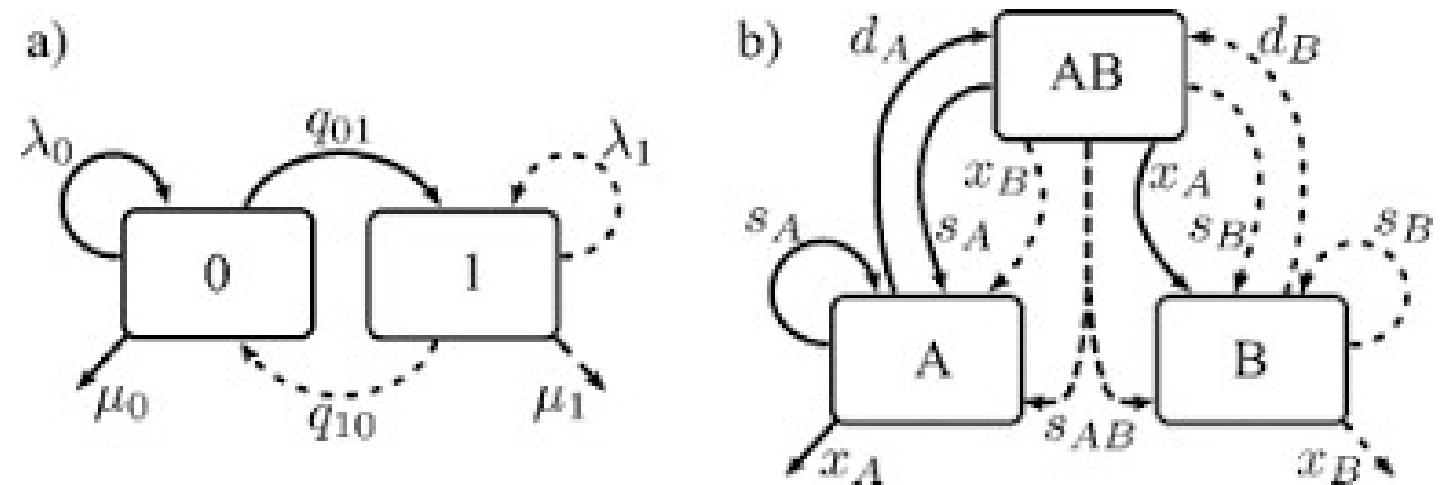
Within clades: different
Among clades: similar

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)*

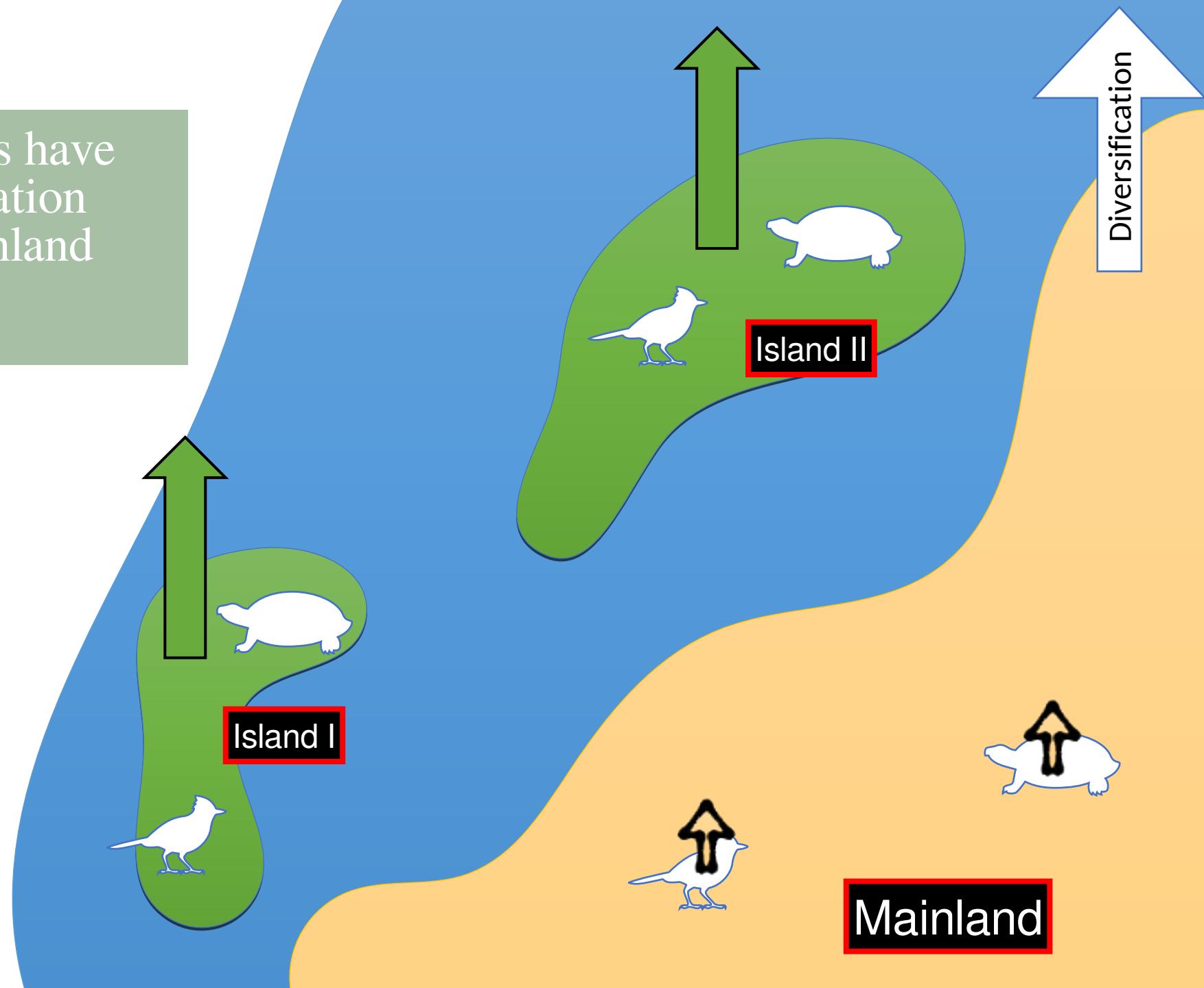


Do lineages on islands have increased diversification rates relative to mainland lineages?

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

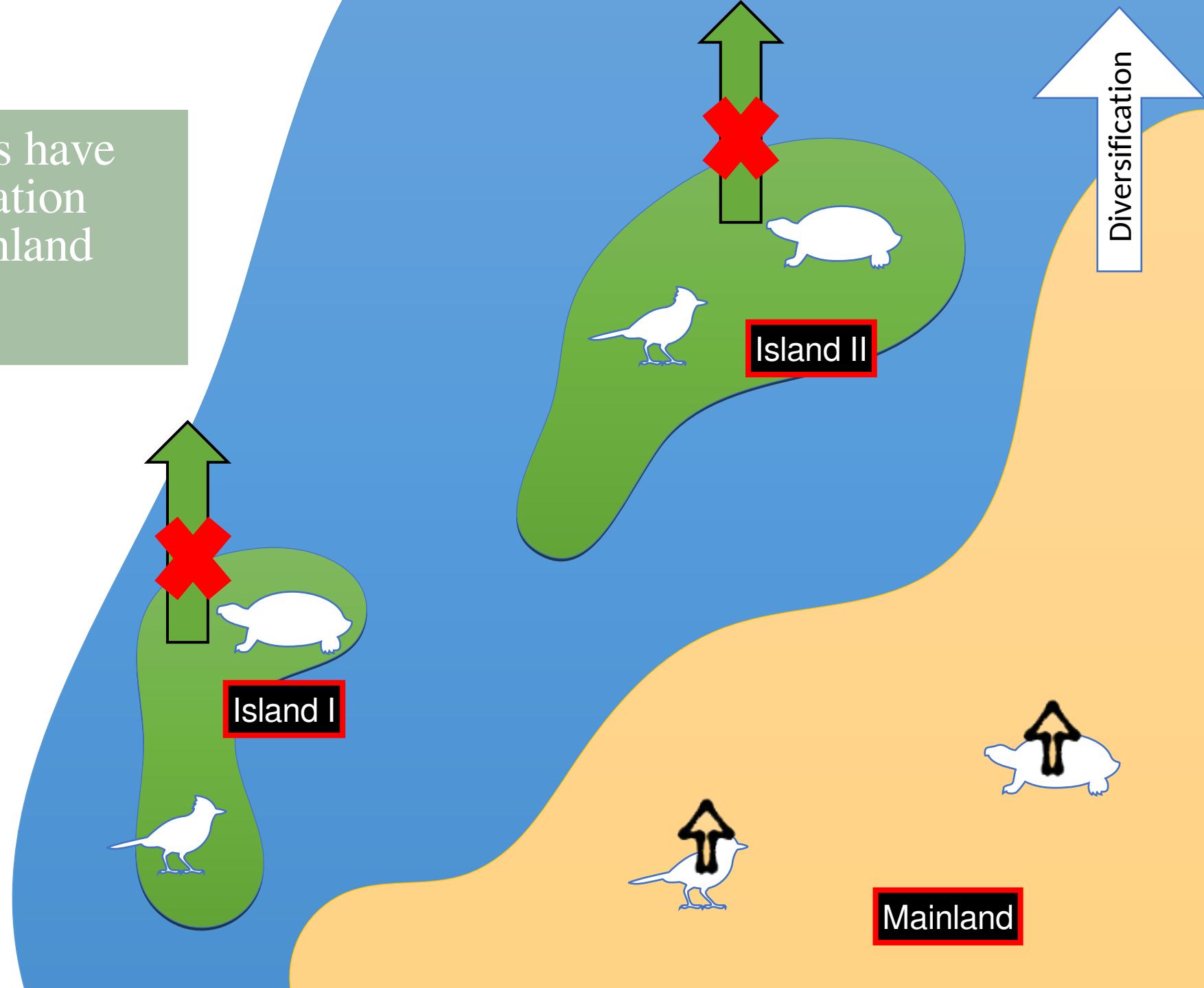
Tortoises: $R^2 < 0.02$, $P > 0.05$

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



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

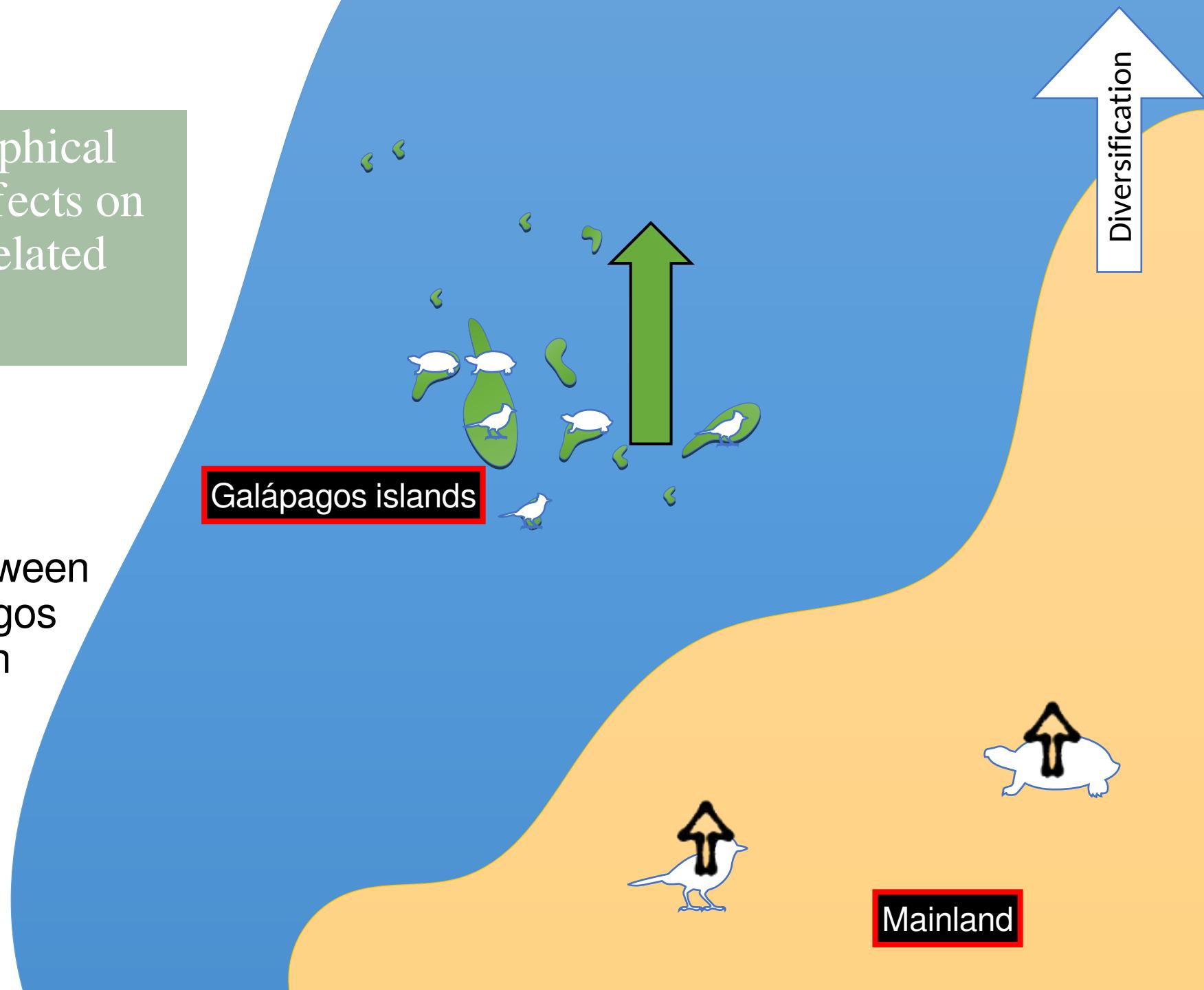
No – Occurring on islands in general did not increase diversification rates in these clades



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

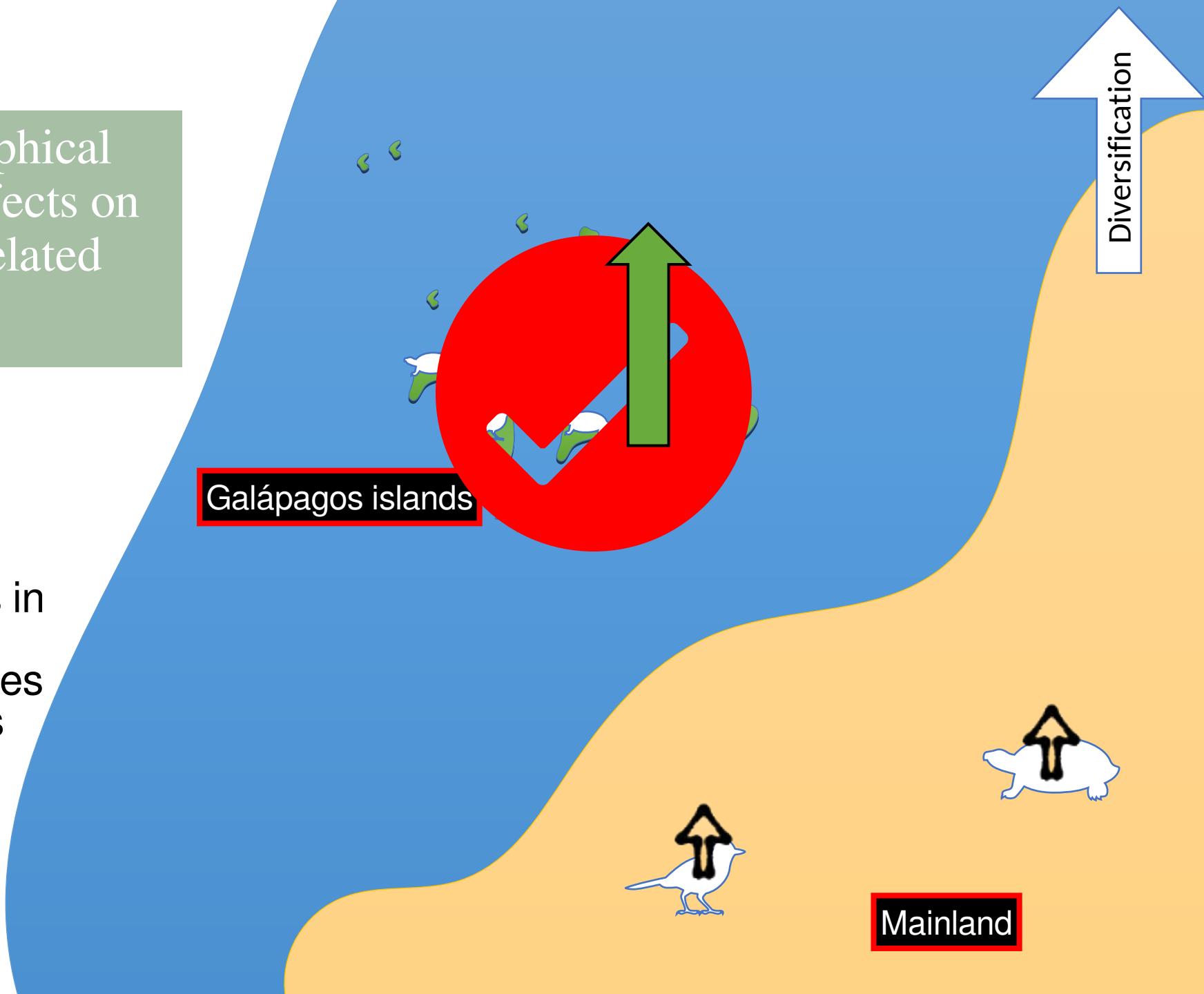
Phylogenetic regressions between the occurrence in the Galápagos and net rates of diversification

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



02

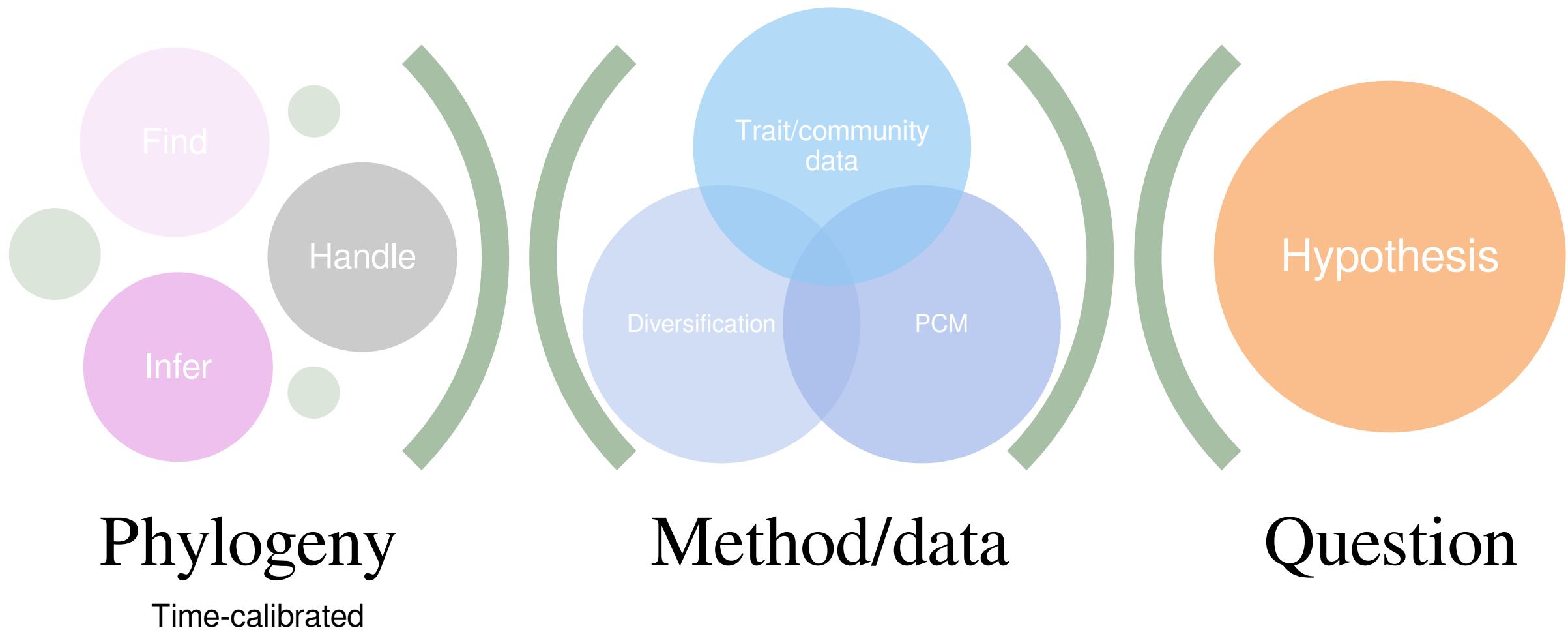
Phylogenies

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 ecology

The pipeline in short...



Building phylogenies

Building phylogenetic trees



phruta (R)

Received: 1 February 2023 | Accepted: 12 May 2023

DOI: 10.1111/2041-210X.14147

APPLICATION

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

Cristian Román-Palacios^{1,2}

Methods in Ecology and Evolution

SuperCRUNCH for phylogenetic datasets

SuperCRUNCH (CLI)

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

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

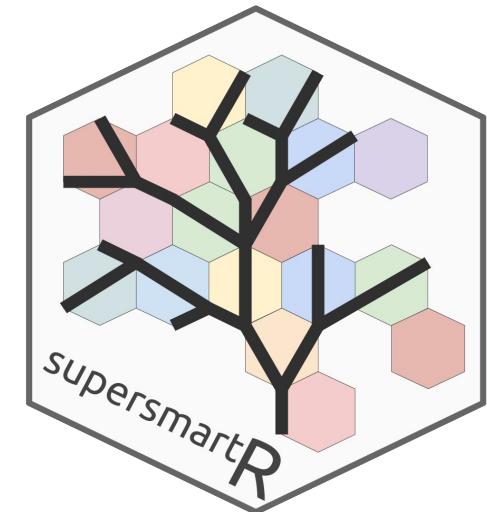
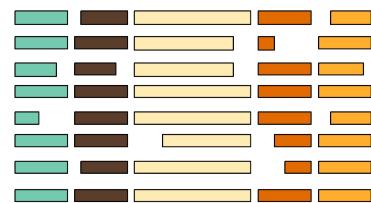
RESEARCH ARTICLE

Methods in Ecology and Evolution

Nature Research Ecology & Evolution

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

Daniel M. Portik^{1,2} | John J. Wiens⁴



supersmartR (R)



Technical Note

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

Dominic J. Bennett^{1,2,*} , Hannes Hettling³, Daniele Silvestro^{1,2}, Alexander Zizka^{1,2}, Christine D. Bacon^{1,2}, Søren Faurby^{1,2}, Rutger A. Vos³ and Alexandre Antonelli^{1,2,4,5}



Finding trees

Finding trees

I



A JOURNAL OF SPACE
AND TIME IN ECOLOGY

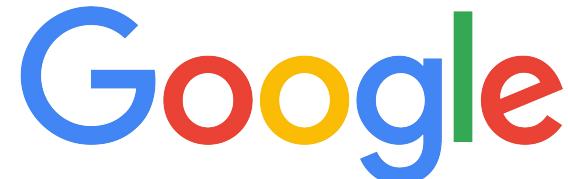
Software note | Open Access | CC

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

IV



species filetype:nex
species filetype:tre*

II



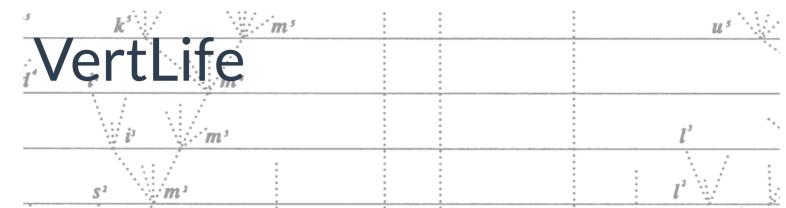
V



III



VI



Handling phylogenetic trees

Using R

Handling trees (in R)

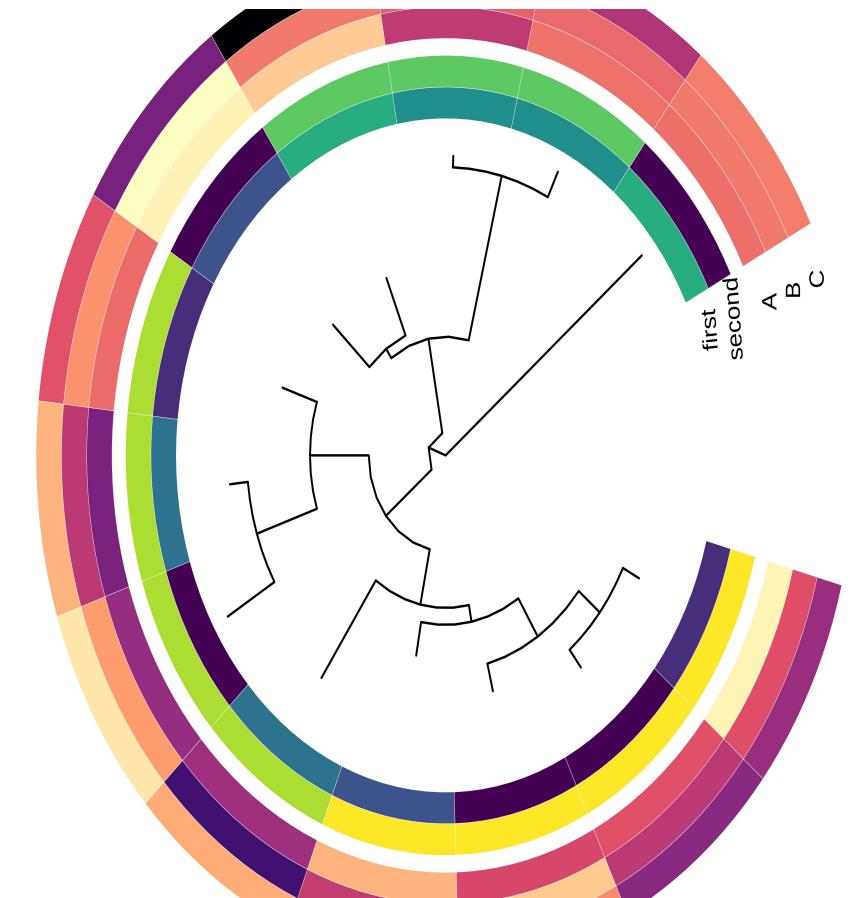
Key packages: **ape** and **picante**

```
> 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)

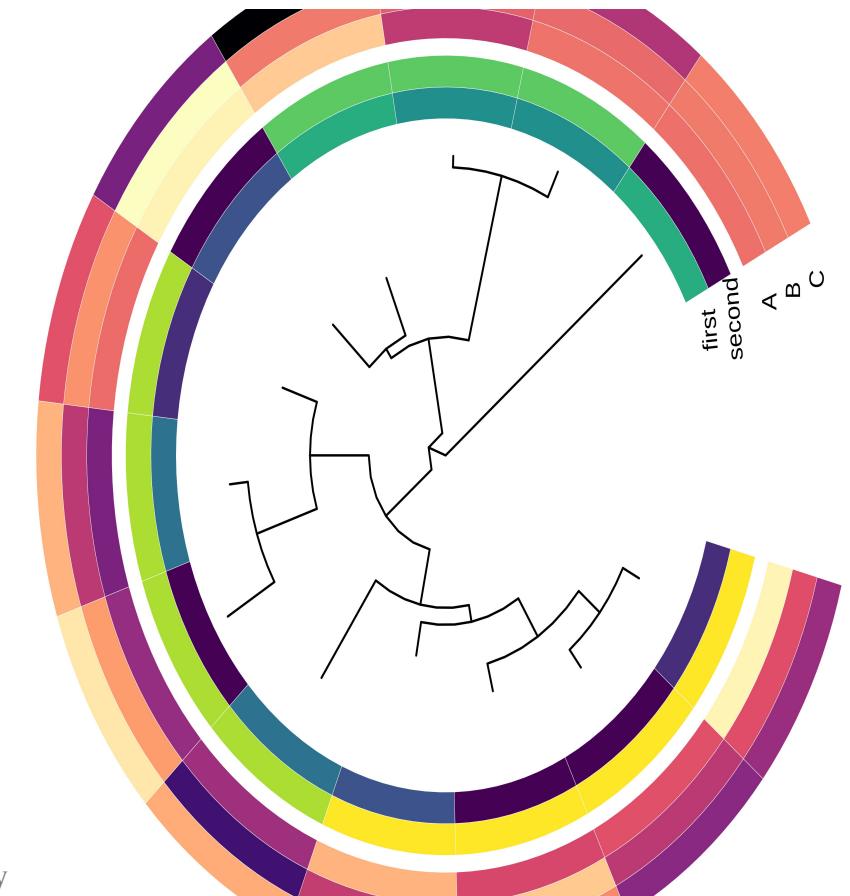
Key packages: **ape** and **picante**

```
> class(tree)
[1] "phylo"

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

$class
[1] "phylo"

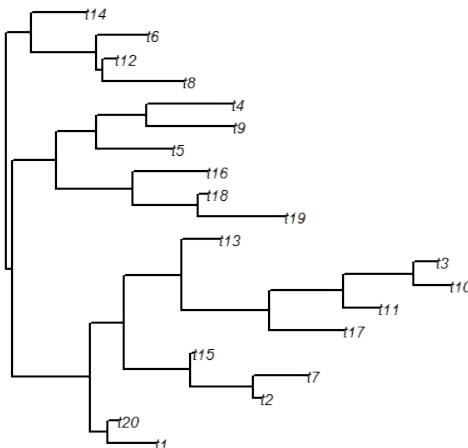
$order
[1] "cladewise"
```



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

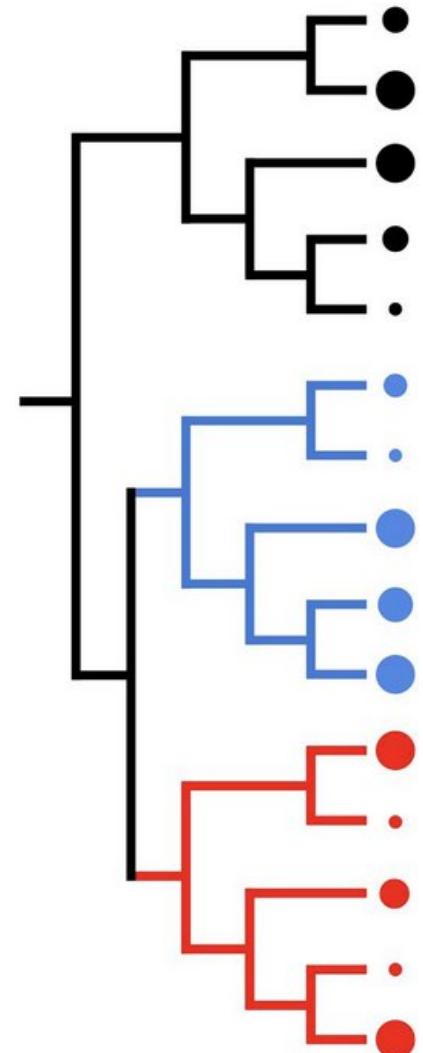
Handling trees (in R)

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

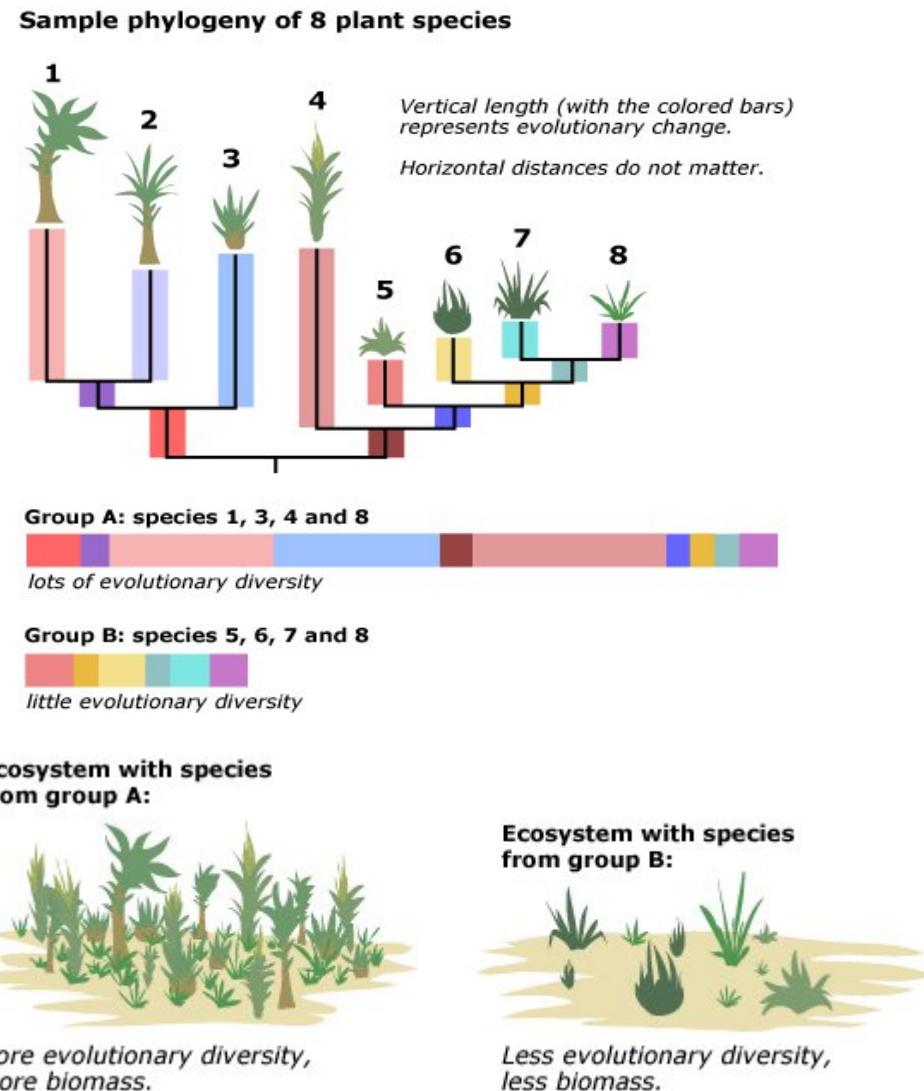
03

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

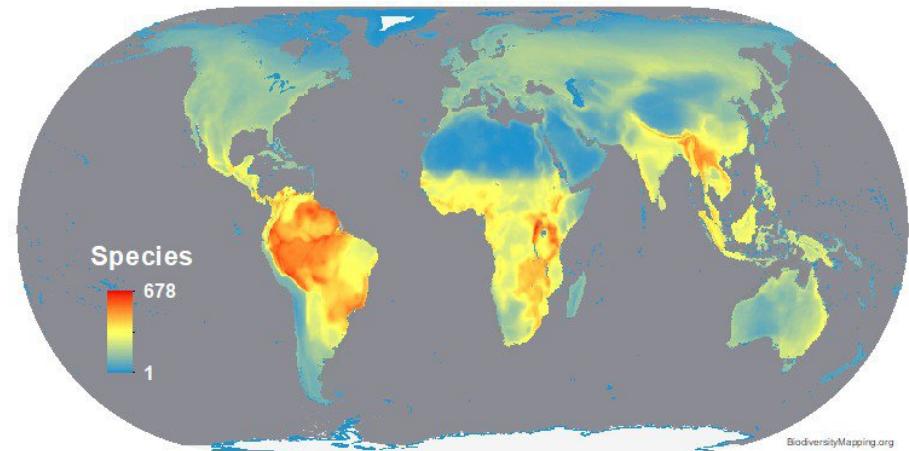


What explains diversity differences across habitats?

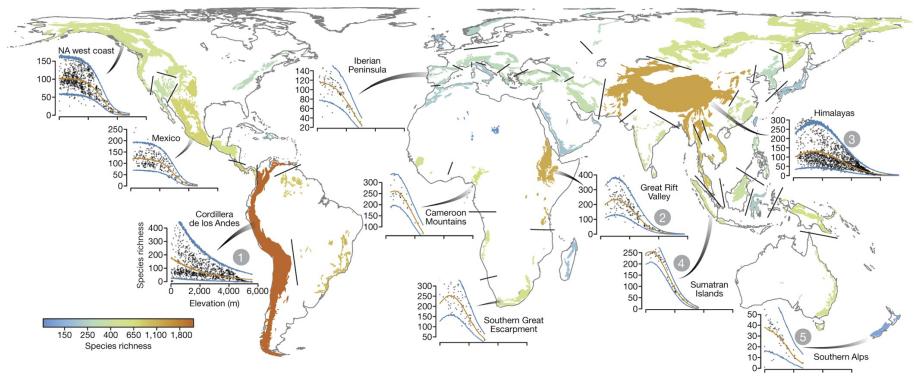
Román-Palacios, C., Moraga-López, D., & Wiens, J. J. (2022). The origins of global biodiversity on land, sea and freshwater. *Ecology letters*, 25(6), 1376-1386.

Global biodiversity patterns

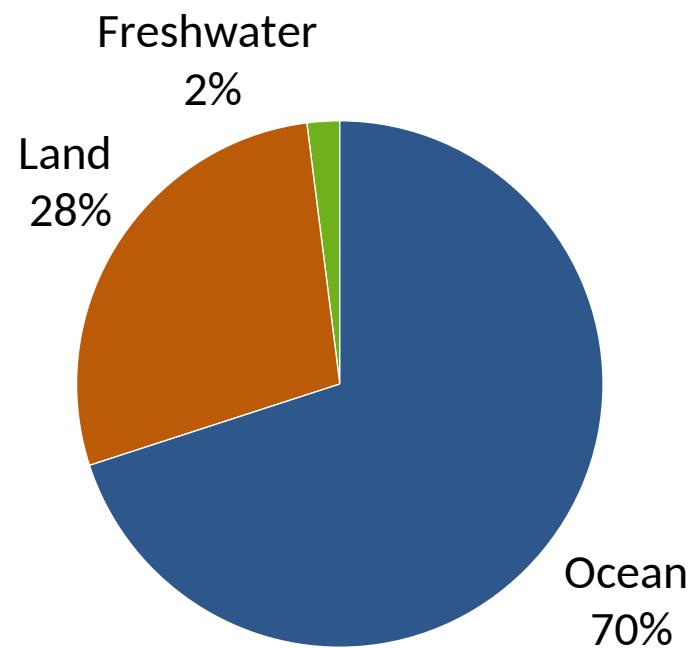
Some are widely studied:
Tropics vs temperate zones
Mountain ranges vs lowlands



But others remain poorly discussed...
Marine, freshwater, and land

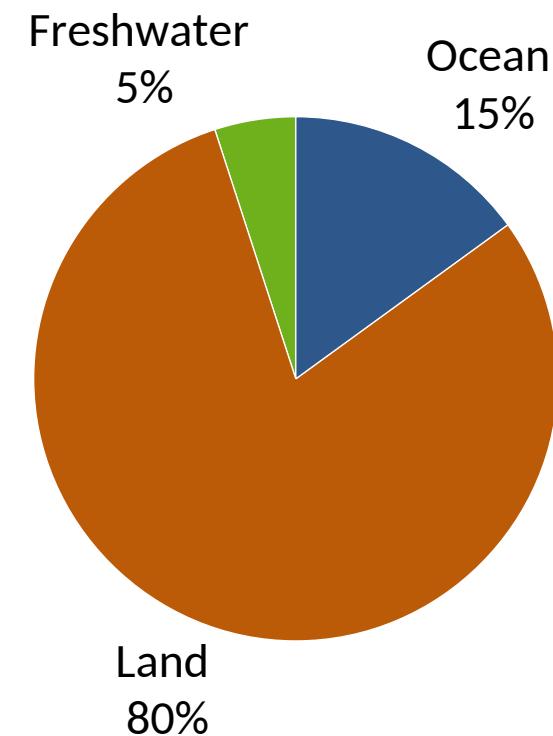


Area vs habitat biodiversity



Surface area

Grosberg et al. (2012)



Species richness

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



Our objectives

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

(2) Test for differences in diversification rates among habitats

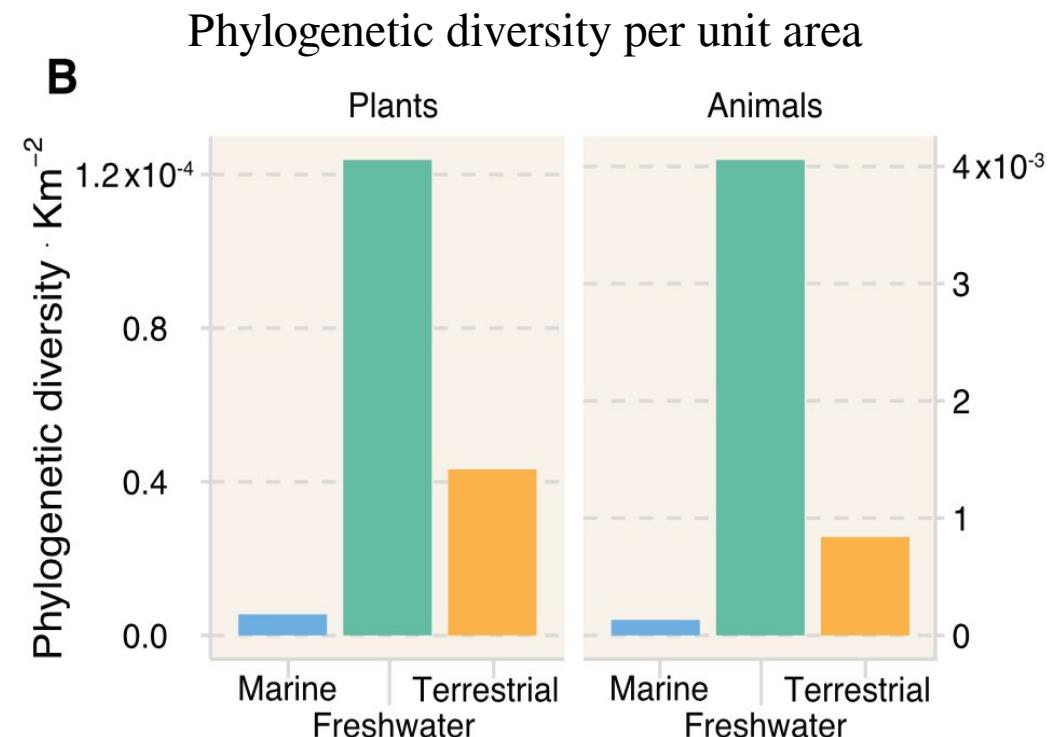
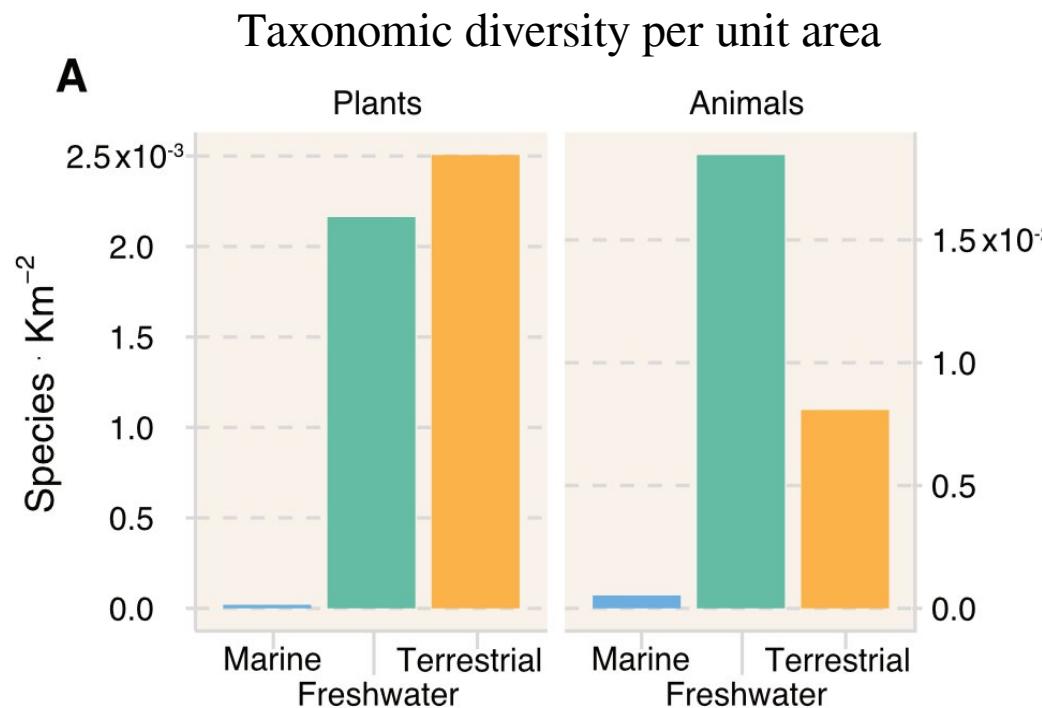
(3) Examine whether times of first colonization to habitats can help explain diversity patterns

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



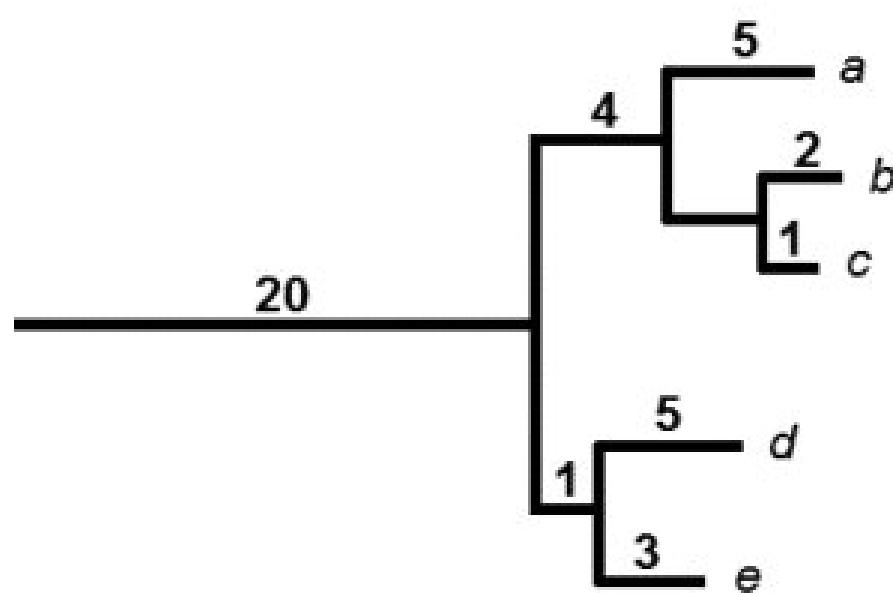
Outstanding diversity by unit area in freshwater

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



Phylogenetic diversity

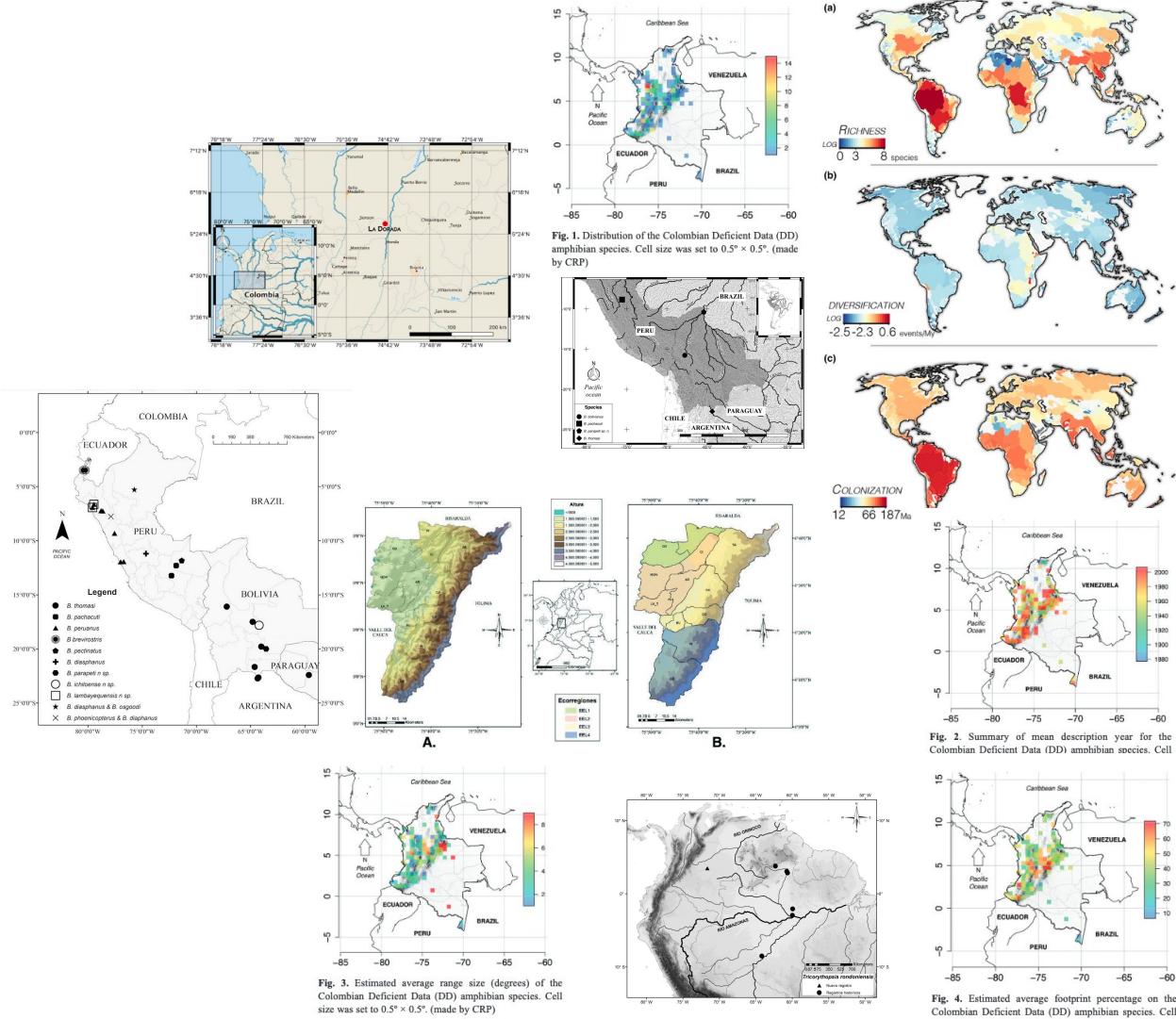
- Faith's (1992) phylogenetic diversity
- Phylogenetic diversity of a set of species as equal to the sum of the lengths of all those branches on the tree that span the members of the set



What about spatial patterns?

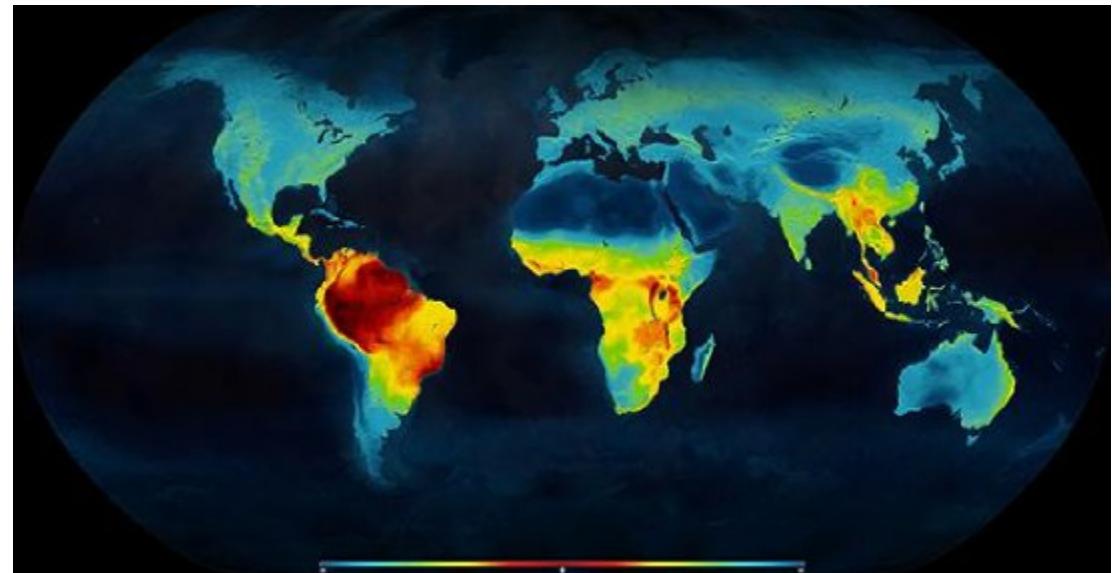
Where to find some of these maps!

- ✓ Elizabeth C. Miller* and **Cristian Román-Palacios***. Evolutionary time best explains the latitudinal diversity gradient of living freshwater fish diversity. *Global Ecology and Biogeography*, 30:749-763.
- ✓ **Cristian Román-Palacios**, and Alejandro Valencia-Zuleta. 2018. *On the Data Deficient amphibians from Colombia*. *Revista de Biología Tropical*, 66:1272-1281.
- ✓ **Cristian Román-Palacios**, Sara Fernández-Garzón, Alejandro Valencia-Zuleta, Andrés F. Jaramillo-Martínez, and Ronald A. Viáfara-Vega. 2017. *Lista anotada de la herpetofauna del departamento del Quindío, Colombia*. *Biota Colombiana*, 18:251-281.
- ✓ **Cristian Román-Palacios**, Sara Fernandez-Garzon, Jenny Johana Gallo-Franco, Alan Giraldo-Lopez, Monica Hernandez-Lopez, and Wilmar Bolivar-Garcia. 2017. *Uso de microhábitat por anuros en un fragmento de bosque seco intervenido del Magdalena medio, Guarinocito, Colombia*. *Boletín Científico Centro De Museos Museo De Historia Natural*, 20:181-196.
- ✓ Molineri, C., Zúñiga, M. D. C., Ramos, B. C., Giraldo, L. P., & Cardona, W. (2016). Three new species of Leptohyphes Eaton (Ephemeroptera: Leptohyphidae) from Colombia. *Iheringia. Série Zoologia*, 106.
- ✓ Zúñiga, M. D. C., Giraldo, L. P., Ramírez, Y. P., Chará, J., & Ramos, B. C. (2015). Neoatriplectides (Trichoptera: Atriplectididae) in Colombia: Notes on its taxonomy, ecology and distribution in the Neotropics. *Revista Colombiana de Entomología*, 41(1), 149-152.
- ✓ del Carmen Zuñiga, M., & Zambrano, N. N. T. (2015). EPHEMEROPTERA: Tricorythopsis rondoniensis (Dias, Salles and Fereira)(Insecta: Ephemeroptera: Leptohyphidae): New distributional record for Colombia and the basin of the Orinoco river (text in Spanish). *Dugesiana*, 22(1).
- ✓ González Córdoba, M., Zuñiga, M. D. C., Torres Zambrano, N. N., & Manzo, M. V. (2015). Primer registro de las especies Neolimnius palpalis Hinton y Piliehmis apama Hinton (Coleoptera: Elmidae: Elminae) para Colombia y la cuenca del río Orinoco.
- ✓ Zúñiga, M. D. C., Giraldo, L. P., Ramírez, Y. P., Chará, J., & Ramos, B. C. (2015). Neoatriplectides (Trichoptera: Atriplectididae) in Colombia: Notes on its taxonomy, ecology and distribution in the Neotropics. *Revista Colombiana de Entomología*, 41(1), 149-152.
- ✓ González Córdoba, M., Zuñiga, M. D. C., Torres Zambrano, N. N., & Manzo, M. V. (2015). Primer registro de las especies Neolimnius palpalis Hinton y Piliehmis apama Hinton (Coleoptera: Elmidae: Elminae) para Colombia y la cuenca del río Orinoco.



Introduction and background

- Species richness decreases from the equator to the poles – the latitudinal biodiversity gradient is one of Earth's most pervasive patterns.
- Three processes directly affecting regional richness: *in situ* speciation, local extinction, and dispersal.
- Freshwater fishes, representing nearly one-quarter of all vertebrates, are ideal for testing the relative contributions of these processes.
- The paper compares two hypotheses:
 - Faster diversification rates in the tropics
 - More time for diversification due to earlier colonization in tropical regions



Methods – Data sources and phylogeny

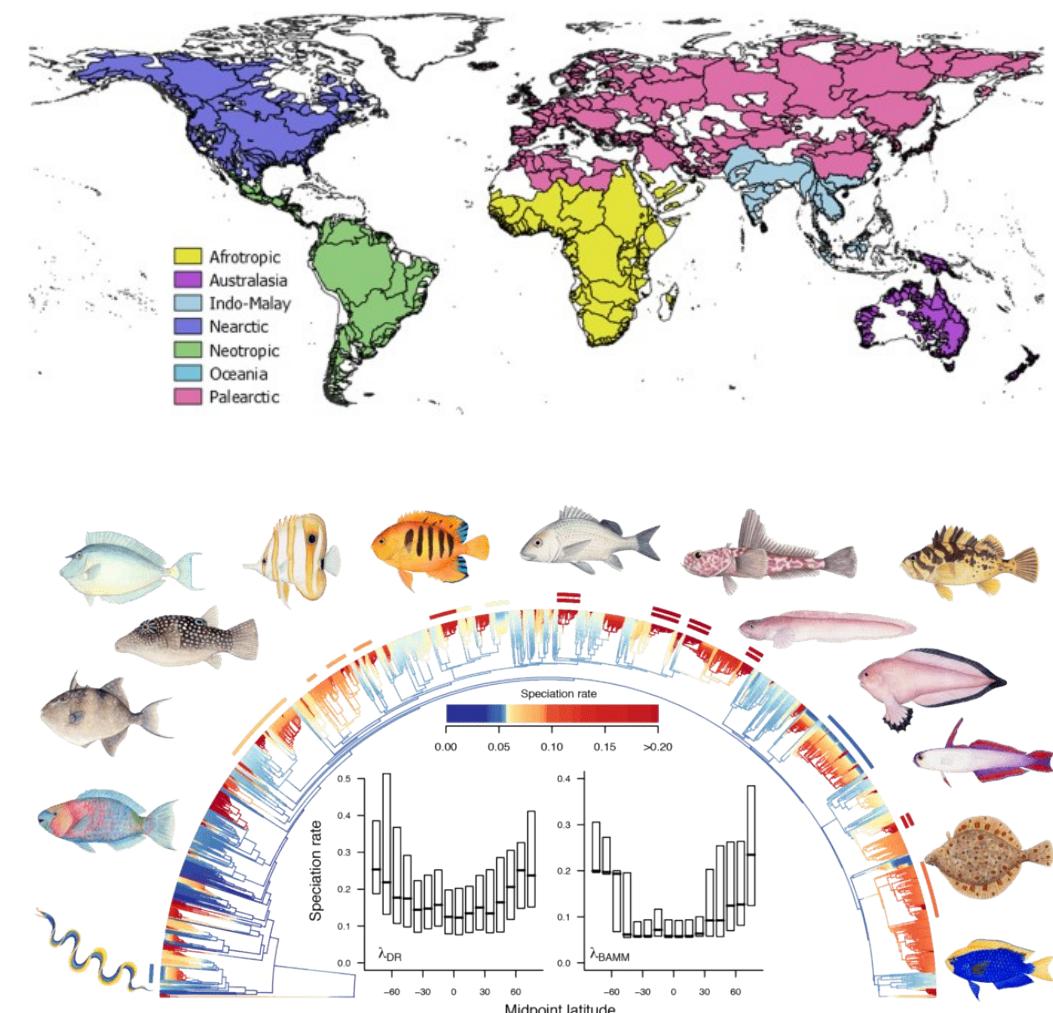
We needed...estimates of basin-specific species richness, diversification rates, and colonization (time for speciation).

Occurrence data:

- Expert-vetted records for 14,947 freshwater fish species across 3,119 drainage basins (Tedesco et al., 2017).

Phylogenetic data:

- A mega-phylogeny of actinopterygians from Rabosky et al. (2018) including 11,638 species (~37% of known ray-finned fishes).



Diversification and colonization times

Diversification rates:

- Calculated using tip-based methods (BAMM and the DR statistic).
- Mean rates per basin based on species co-occurring in each drainage.
- Time for speciation:
 - Inferred from ancestral range reconstructions using a DEC model (via BioGeoBEARS).
 - Regional colonization times were averaged across 100 stochastic maps.
- Additional predictor: Basin surface area

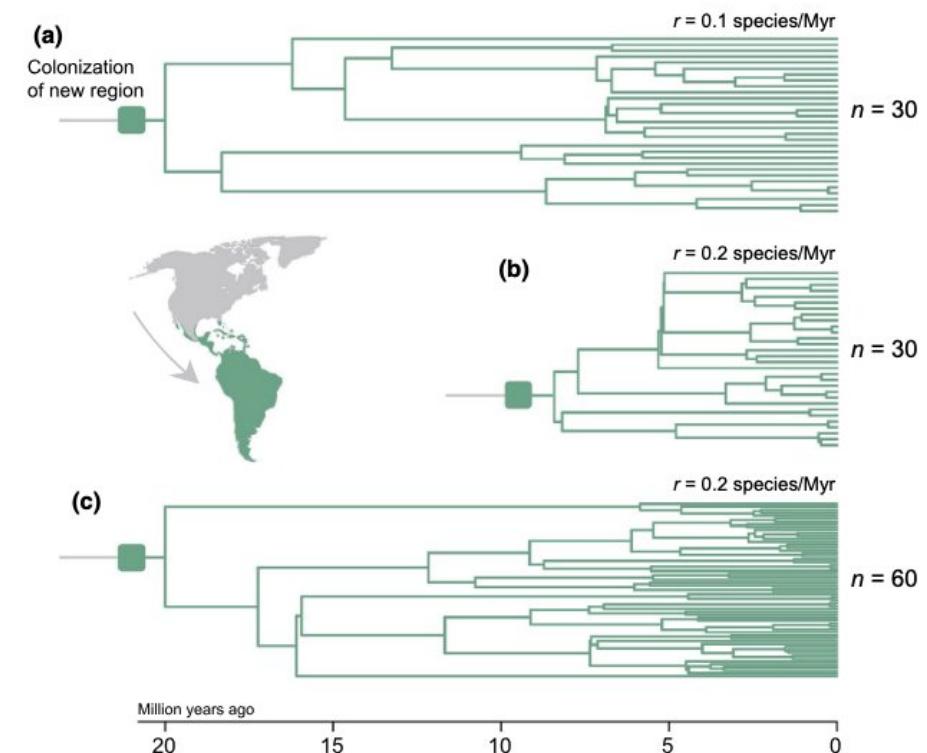


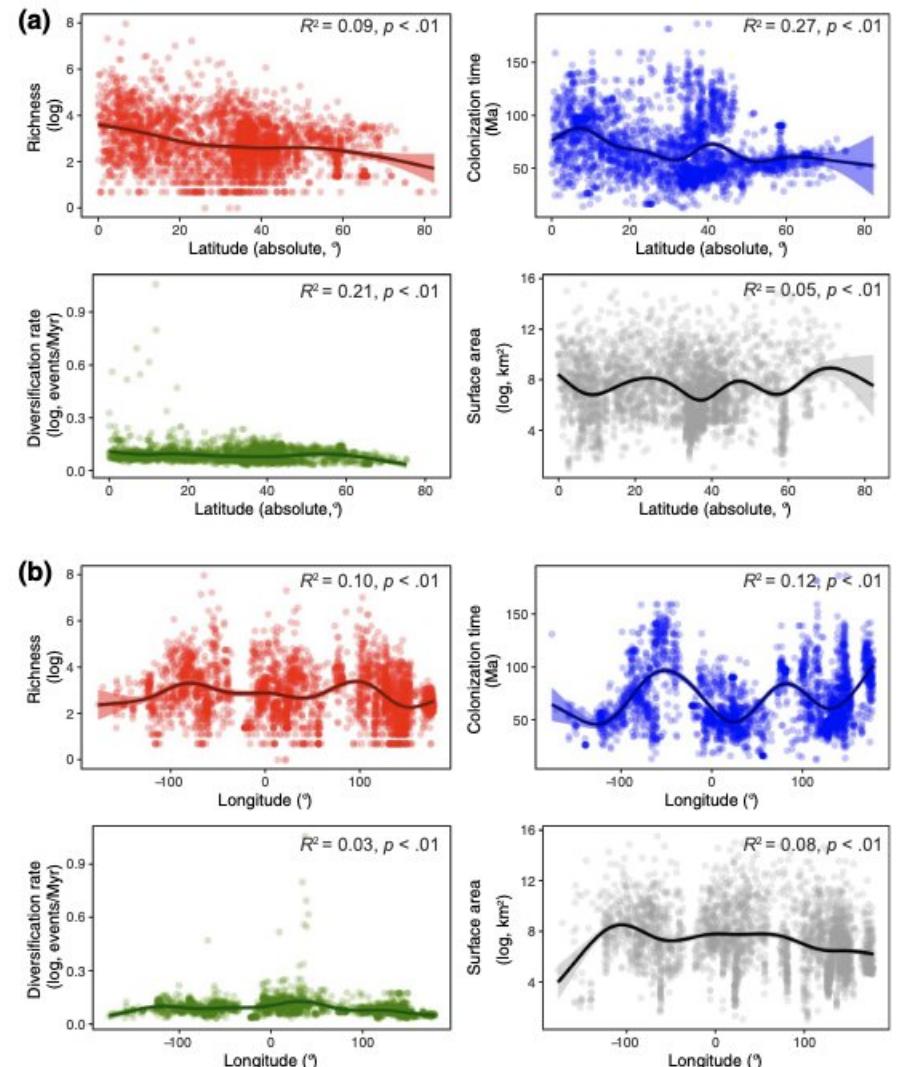
FIGURE 1 Schematic diagram illustrating alternative pathways to build species richness through *in situ* speciation. In all three examples, a lineage colonizes a region and diversifies with no further immigration or emigration. In (a), the lineage colonizes the region relatively early and diversifies at a modest rate. In (b), the lineage colonizes later, but diversifies at a faster rate and achieves the same species richness as (a). In (c), the lineage colonizes relatively early and diversifies quickly, achieving high richness. Although diversification rates are constant in these simple examples, these scenarios are also applicable to cases where rates change through time (Pontarp & Wiens, 2017)

Statistical analyses

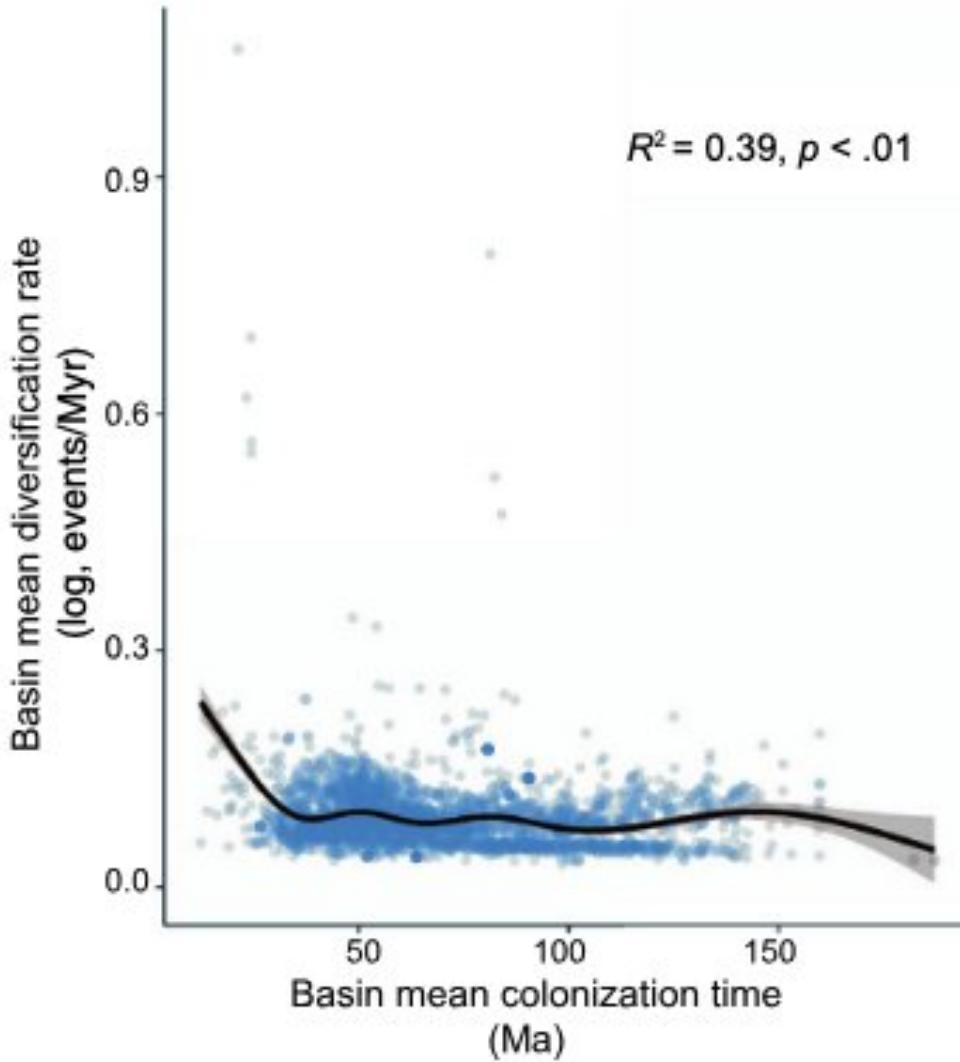
- Generalized additive models (GAMs) were used to relate:
 - Species richness, diversification rates, colonization (time for speciation) vs latitude and longitude.
 - Richness vs individual and combined effects of predictors.
 - Relationships among diversification rates, time for speciation, and basin area.
 - While accounting for spatial autocorrelation....

Latitudinal patterns in richness and predictors

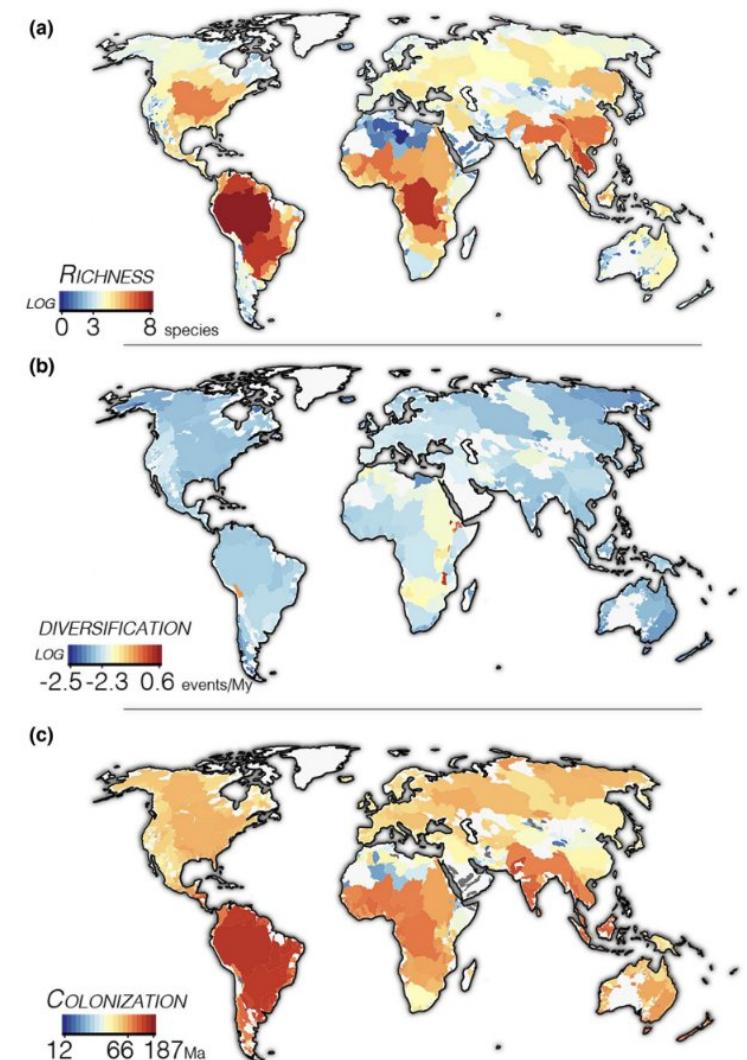
- Species richness shows a negative latitudinal gradient.
- Diversification rates and colonization times vary with latitude.
 - Lower latitudes tend to have older colonization times.
- Basin surface area is positively related to richness but is poorly related to latitude.



Importance of time and diversification

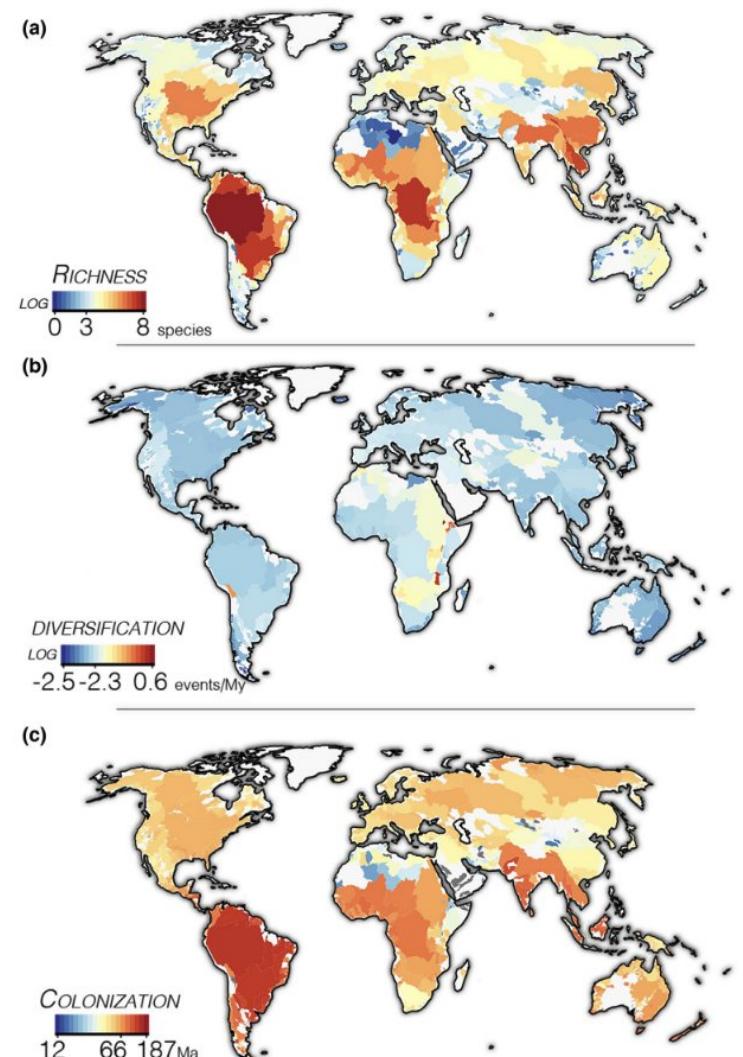


Diversification rates and colonization times are inversely related (recent colonizations correlate with faster rates).



Importance of time and diversification

- Variance in species richness globally is explained by:
 - Diversification rates: $R^2 \approx 0.34\text{--}0.36$
 - Time for speciation: $R^2 \approx 0.32\text{--}0.33$
- When controlling for basin area, models show increased explanatory power ($R^2 > 0.53$).
- Time for speciation contributes 2.3–6.1 times more to richness patterns than diversification rates.
- Don't forget: Diversification rates and colonization times are inversely related (i.e. richness is controlled by different mechanisms in different basins).



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 constraints
 - 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

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

Diet evolution

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, Quindío 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.

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 (<i>Oscillatoria</i> 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
Dipteroptera: 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 ($r=0.12$, $p=0.615$)

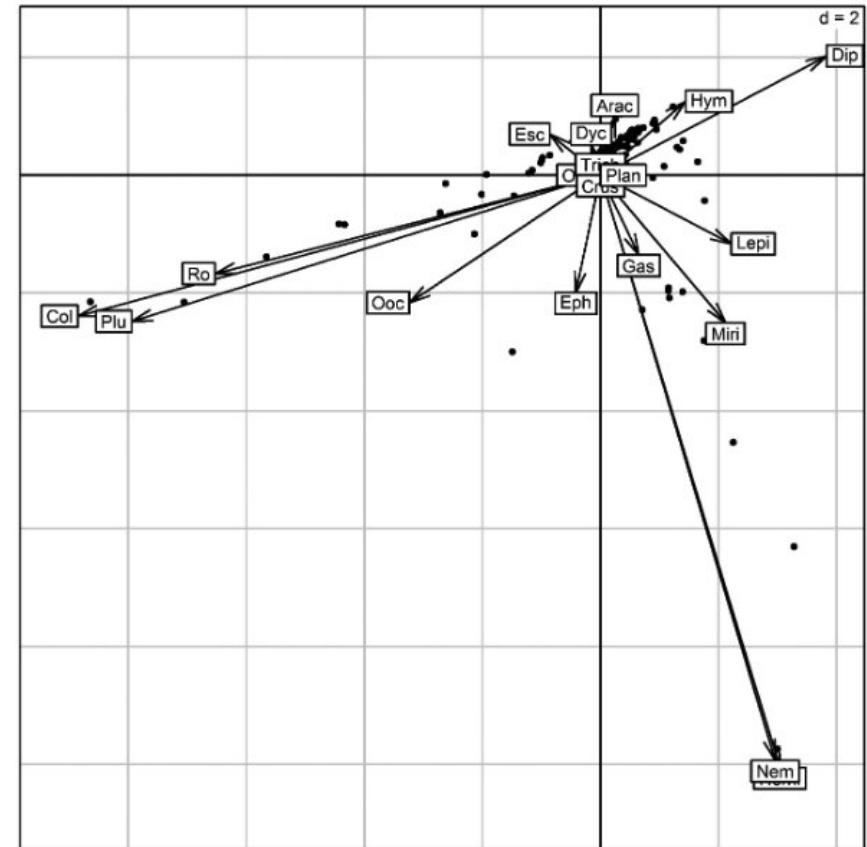


Figure 2. Biplot of prey and stomachs obtained from a Centered Principal Component Analysis (first factorial plane) for *Hemibrycon brevispini*, in La Venada Creek, Quindío River. Dots represent stomachs. Where, Hym: Hymenoptera, Dip: Diptera, Hemi: Hemiptera, Col: Coleoptera, Eph: Ephemeroptera, Odo: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

What was the big
picture...?

CITATION

Trophic diversity in animals

Remarkable diversity of diets and associated lifestyles:

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

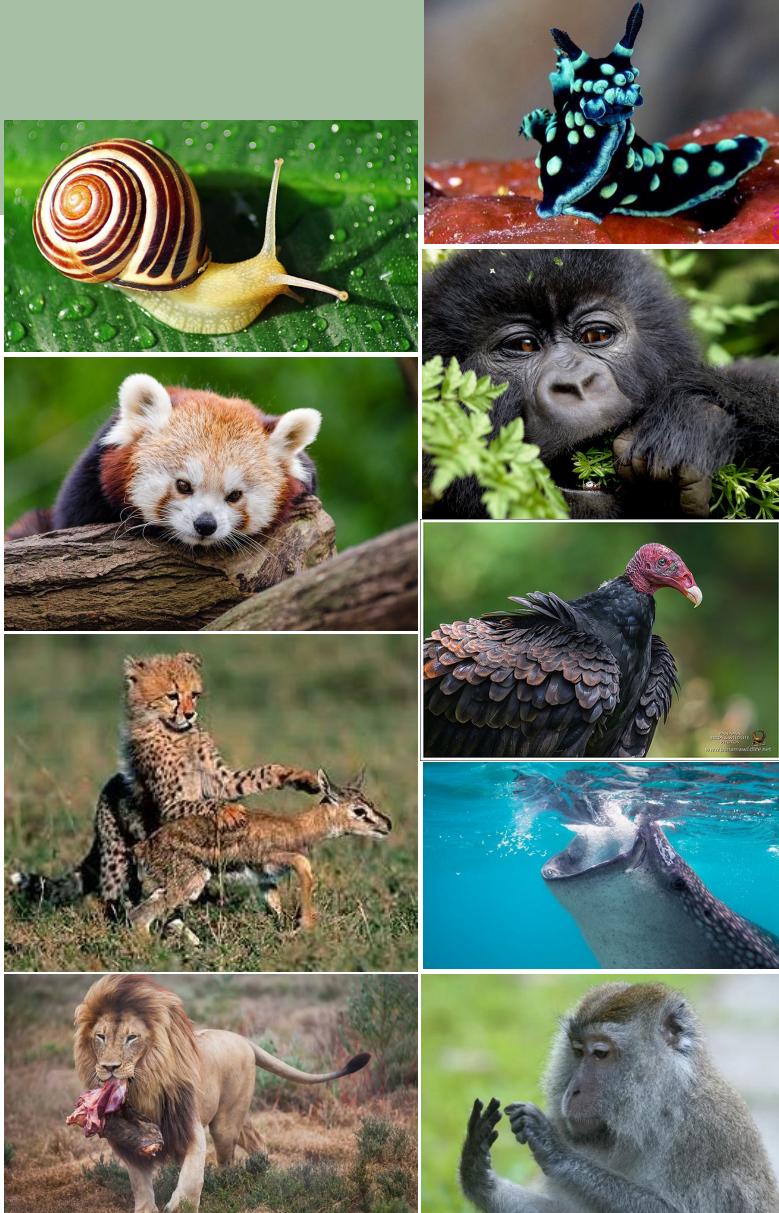
Evolution of animal diets remains poorly understood at the largest phylogenetic scales (e.g. among phyla)



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.

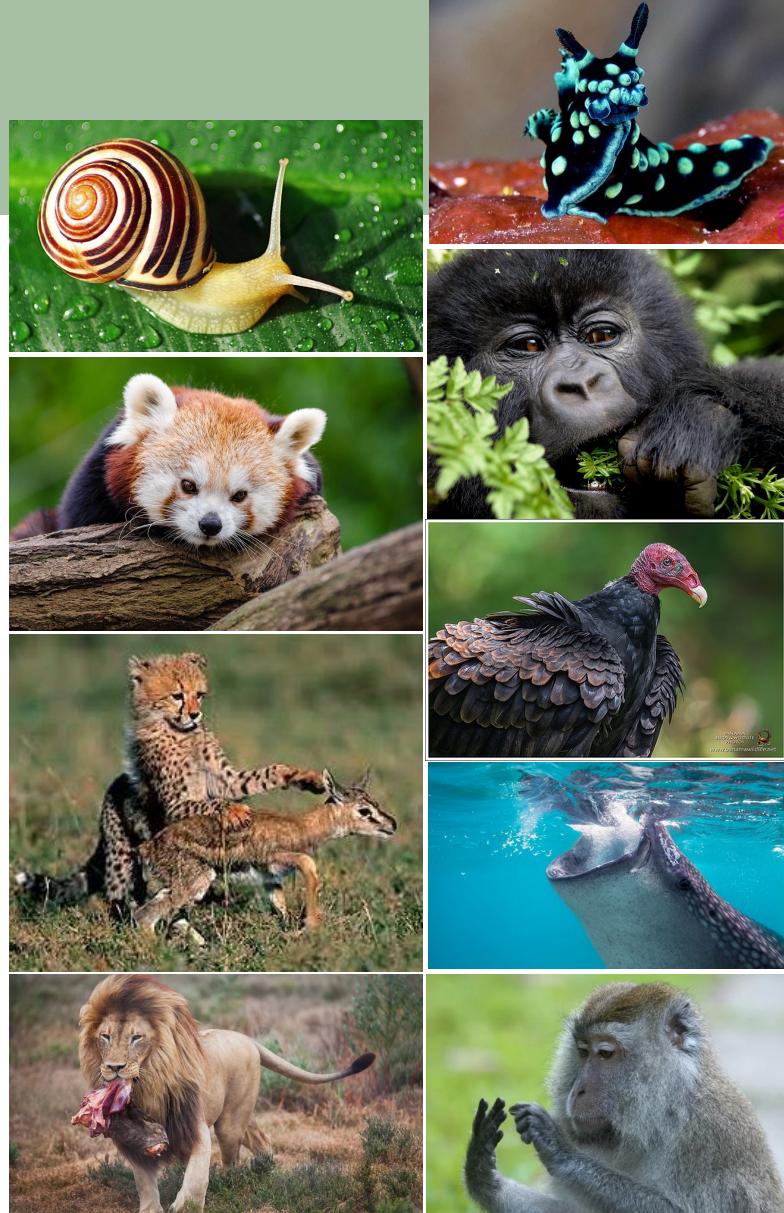


Objectives

(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



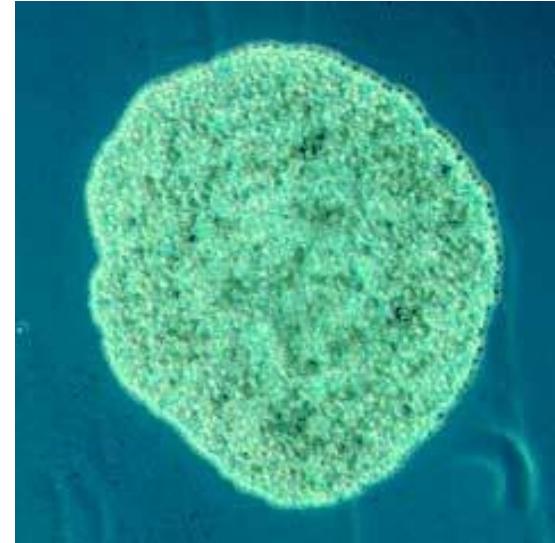
Herbivore

Feeding on autotrophs
(>90% of diet)



Carnivore

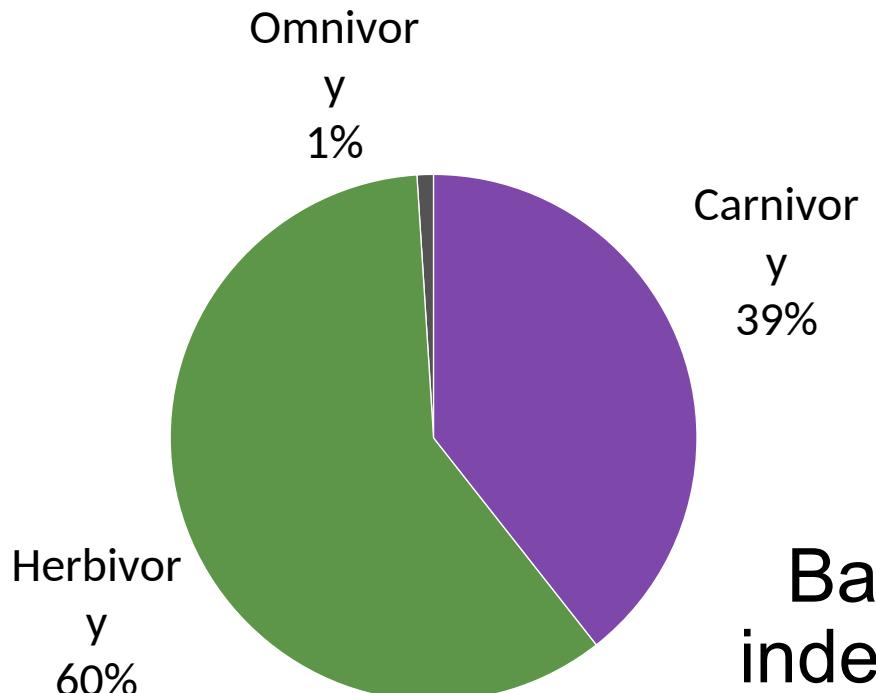
Feeding on heterotrophs
(>90% of diet)



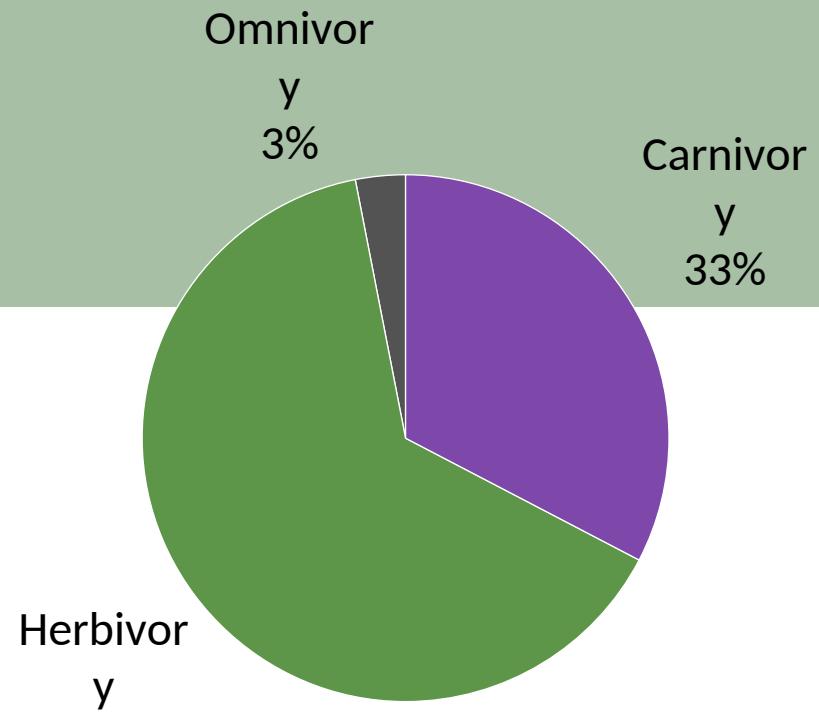
Omnivore

Heterotrophs <90% of diet
Autotrophs <90% of diet

How frequent is each diet among all animals?



Based on
independent
literature searches



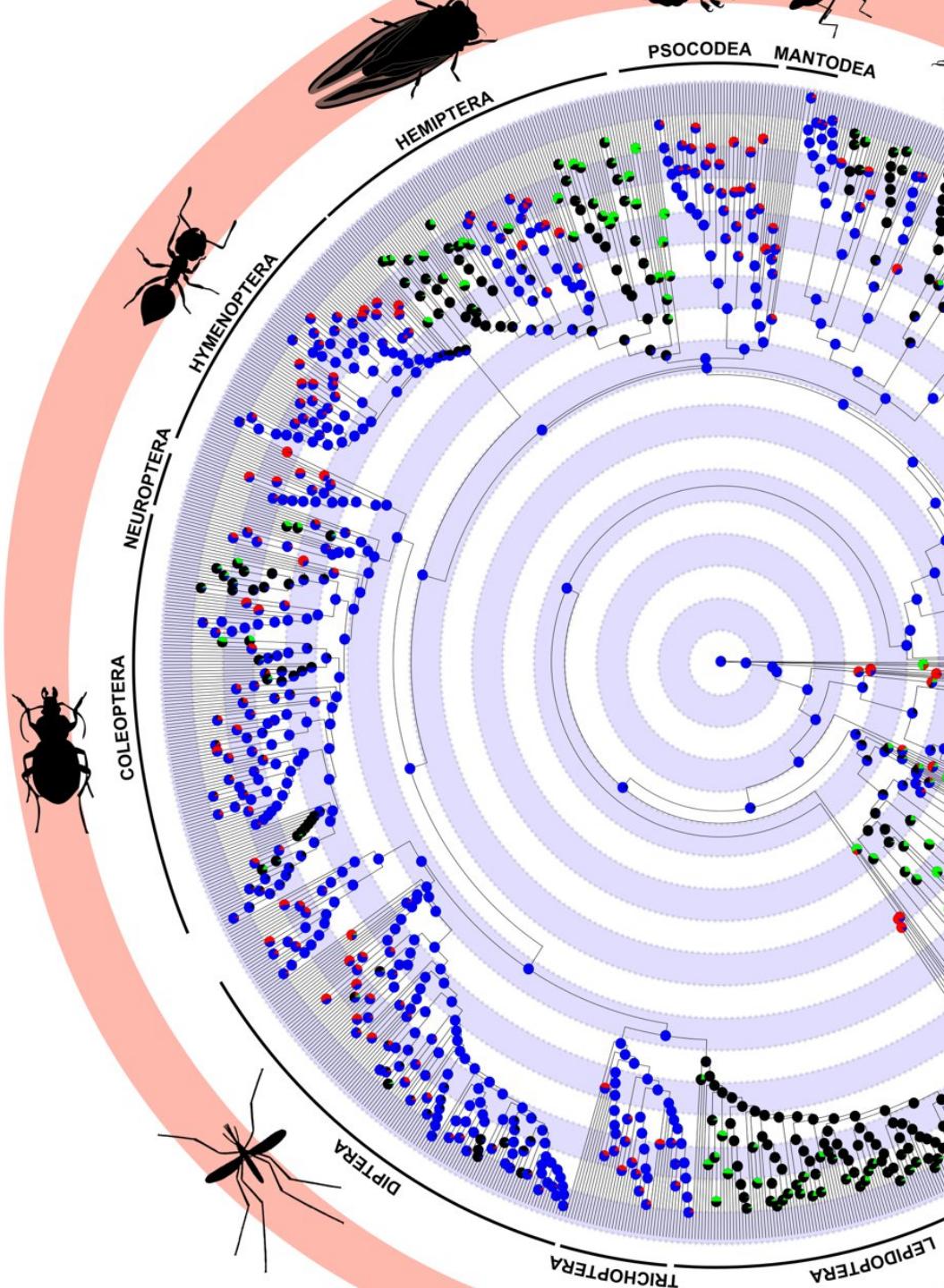
Based on 1,087 taxa
sampled in tree

Phylogenetic signal

Phylogenetic signal

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

Diets are evolutionarily conserved, rather than being extremely labile.

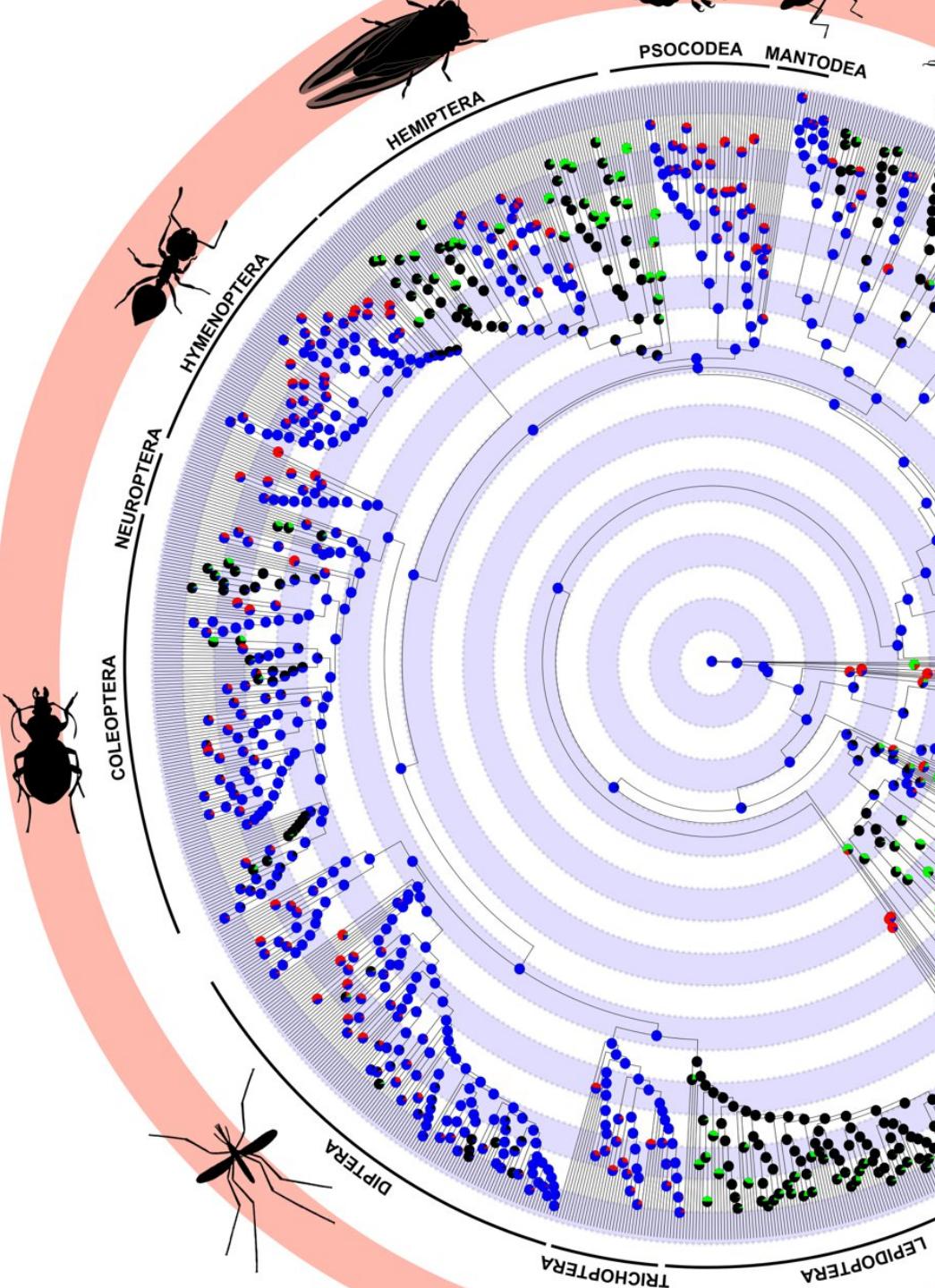


HiSSE

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** ($R^2 < 0.01$; $P > 0.05$)

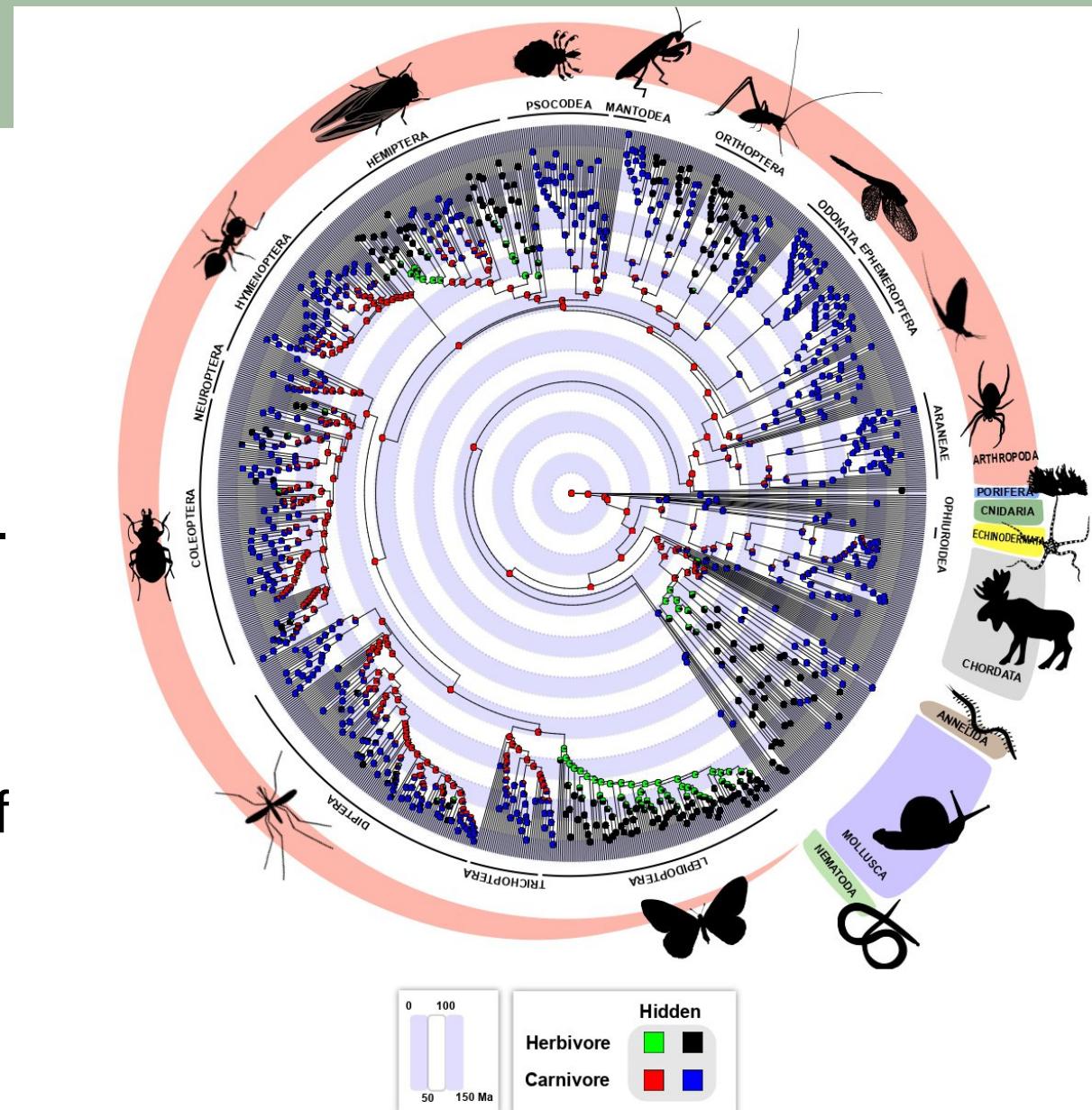


Take-home

Diet is highly conserved at broad phylogenetic scales across animals.

Diet does not significantly influence large-scale patterns of animal diversity.

The ancestor of all animals was most likely carnivorous (i.e. fed on heterotrophs), as were the ancestors of many of the largest animal groups (like arthropods, chordates, and molluscs).



Phylogenetic diversity

Explaining global diversity on land, sea, and freshwater

Maps, phylogenies GAMs

Miller, E. C., & Román-Palacios, C. (2021). Evolutionary history explains the latitudinal diversity gradient of living diversity. *Global Ecology and Biogeography*, 30.

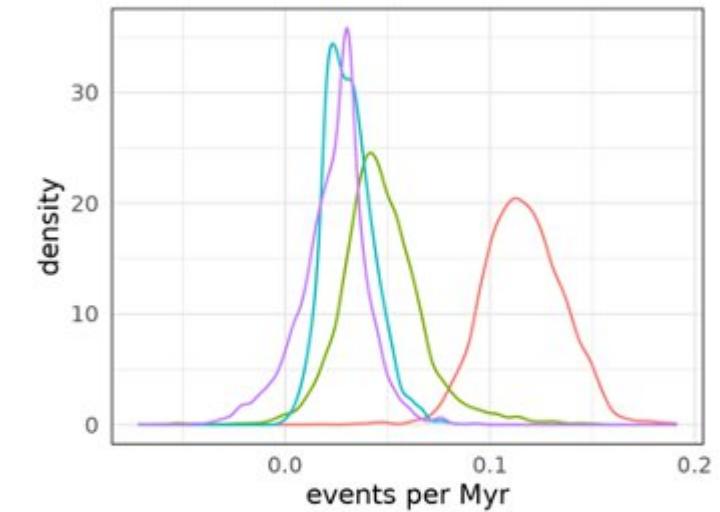
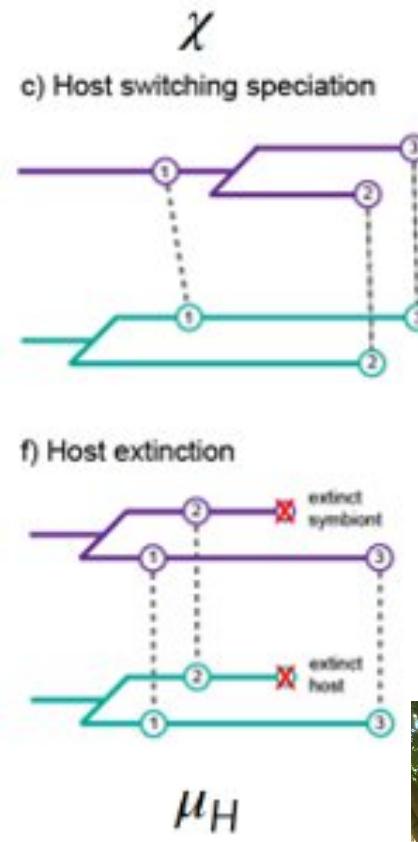
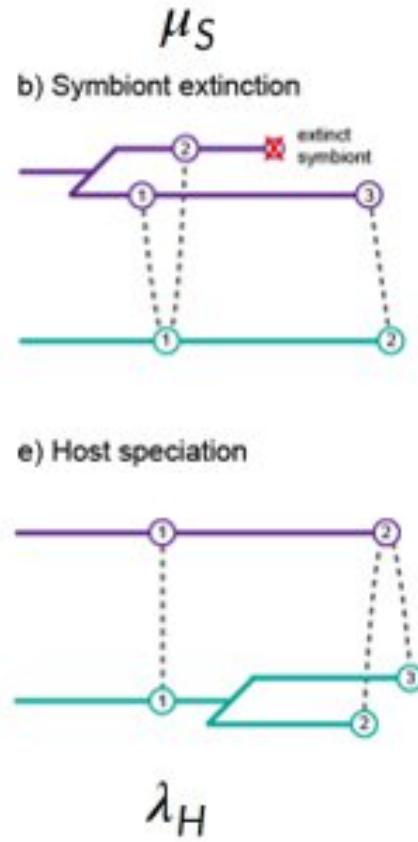
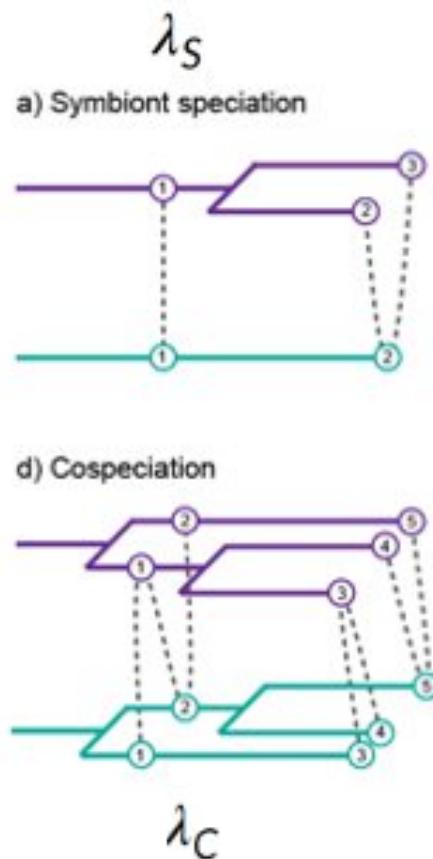
Phylogenetic regression

Román-Palacios, C., & Wiens, J. J. (2018). The Tortoise effect: Testing for island effects on diversification using two island radiations. *Journal of biogeography*, 45(8), 1703–1714.

Other intersections: .

ABC and species interactions: What processes underly cophylogenetic patterns? How frequent are they?

Rate estimates
(Preliminary)



event

- Host speciation
- Symbiont speciation
- Cospeciation
- Host expansion speciation

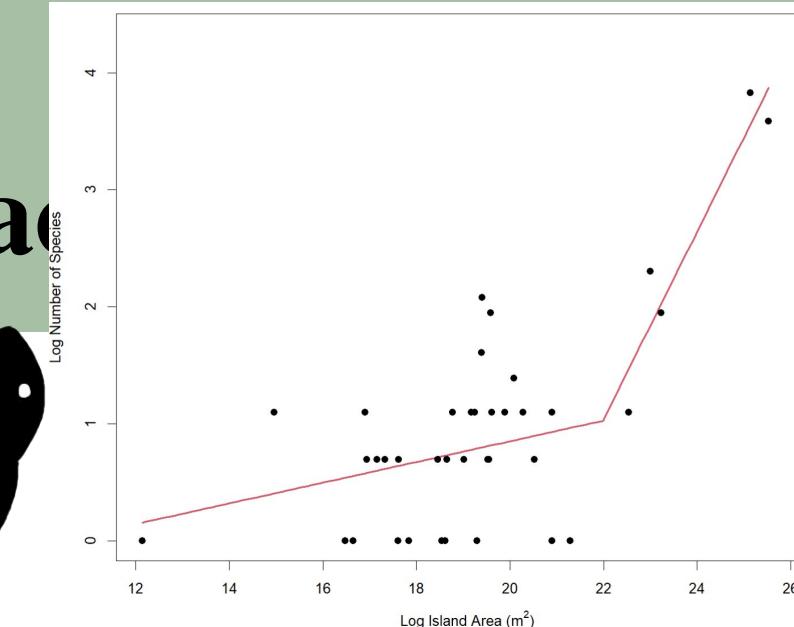
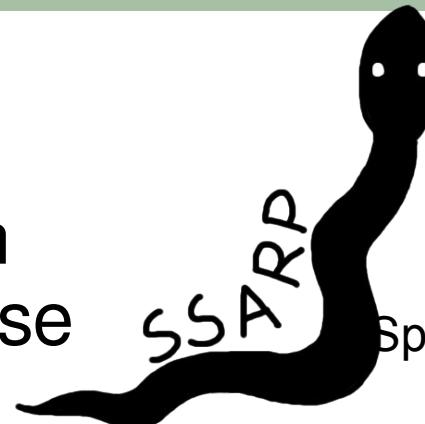


Yichao Zeng
Postdoctoral Researcher

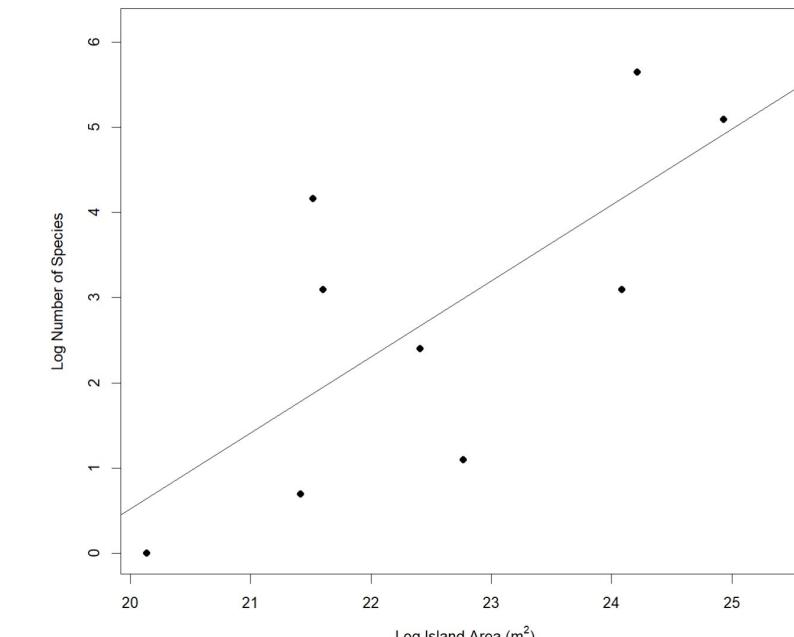
Zeng & Román-Palacios, *In prep.*

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)



Species-area relationship for *Anolis* using GBIF data



Species-area relationship for African cichlids using GBIF data

Animal chromosome count database

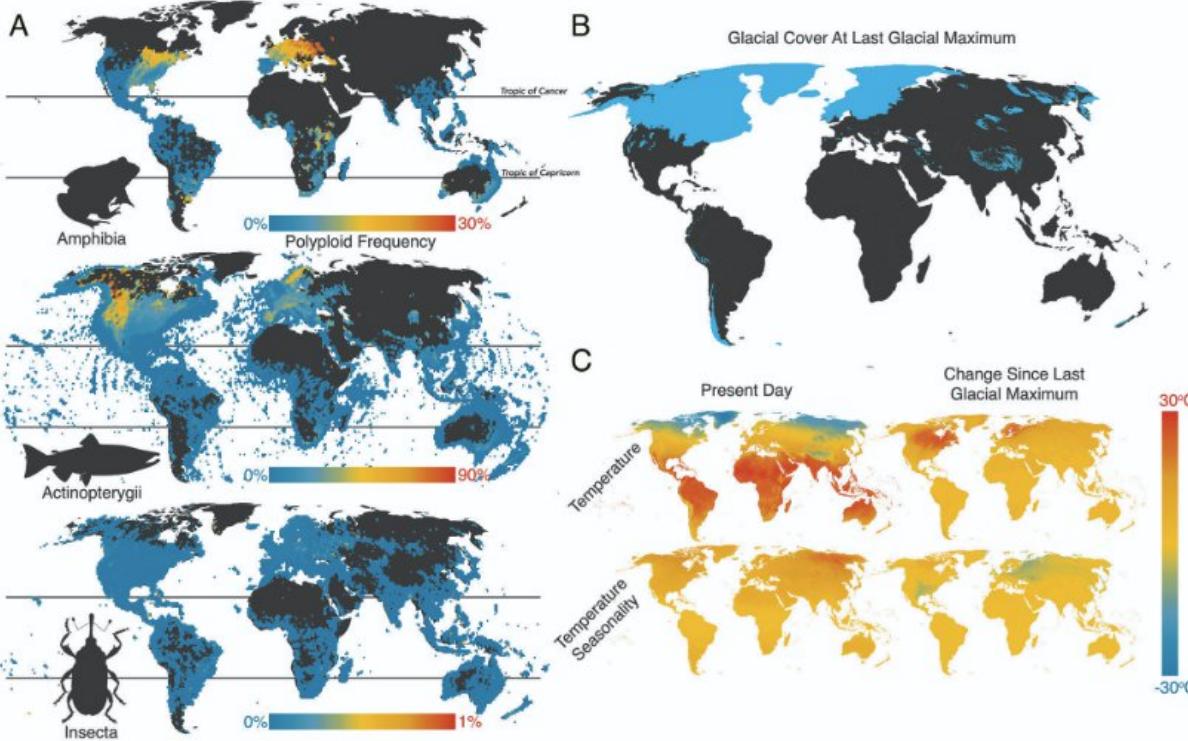


Fig. 2. (A) Global heatmap of polypliod species in each focal clade (excluding cells with species richness <10). (B) Estimated glacial cover at last glacial maximum (LGM). (C) Mean annual temperature and temperature seasonality (SD), estimated for modern day as well as change from LGM.

Curated

Phylum	Total richness	Species in the ACC	Richness in ACC (%)	Curated
Acoela	140	0	0	FALSE
Arthropoda	1302809	9755	0.7	TRUE
Brachiopoda	392	0	0	FALSE
Bryozoa	6008	2	0	TRUE
Chaetognatha	170	4	2.4	TRUE
Chordata	85423	4134	4.8	TRUE
Cnidaria	10203	18	0.2	TRUE
Ctenophora	187	0	0	FALSE
Echinodermata	7550	26	0.3	TRUE
Entoprocta	171	2	1.2	TRUE
Gastropoda	794	0	0	FALSE
Gnathostomulida	97	0	0	FALSE
Hemichordata	103	0	0	FALSE
Kinorhyncha	196	0	0	FALSE
Mollusca	84977	122	0.1	TRUE
Nematoda	25033	35	0.1	TRUE
Nematomorpha	339	7	2.1	TRUE
Nemertea	1358	10	0.7	TRUE
Onychophora	183	0	0	FALSE
Phoronida	16	2	12.5	TRUE
Placozoa	1	0	0	FALSE
Platyhelminthes	29487	306	1	TRUE
Porifera	8659	8	0.1	TRUE
Rotifera	2049	4	0.2	TRUE
Sipuncula	205	3	1.5	TRUE
Tardigrada	1167	1	0.1	FALSE
Xenoturbellida	2	0	0	FALSE

The ACC

A database of animal chromosome counts

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[Contact Us](#)

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Currently v1.0.0

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More ...

Animal Culture Database (ACDB) and ecological covariates

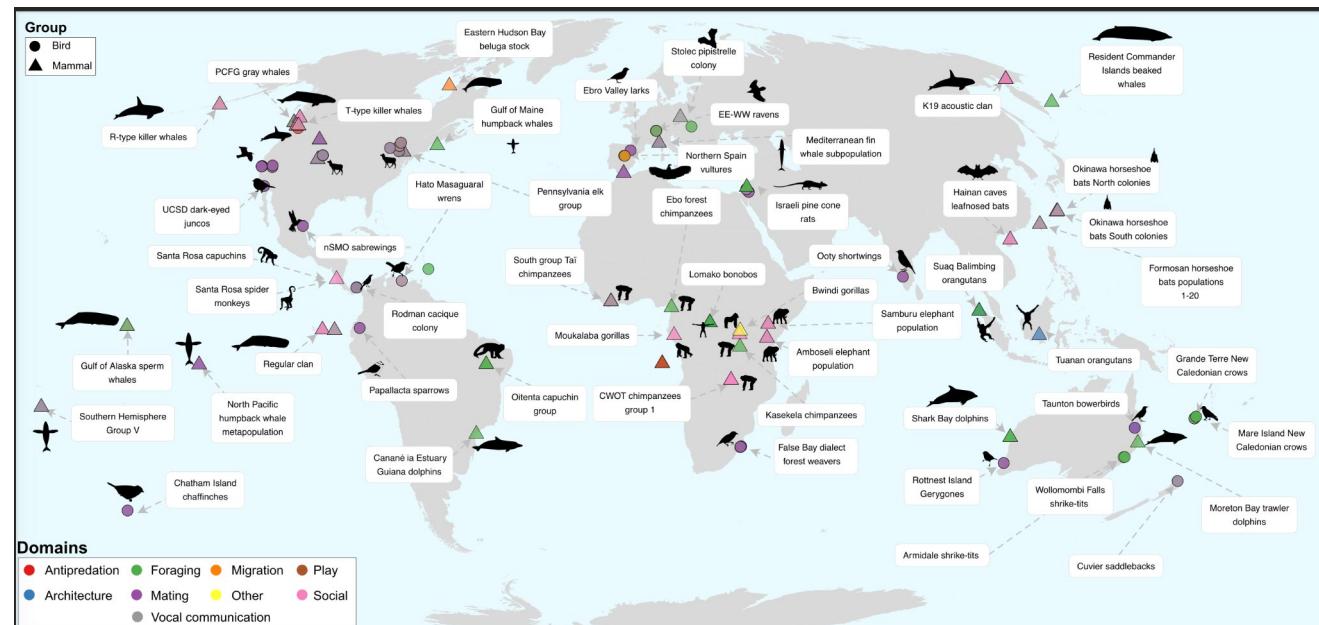
- Comparative database of behavioral traditions in wild animal populations globally
- Includes variables from existing literature on animal behavior on taxonomy, location, forms of social learning (social transmission of behaviors across individuals in a population), behavioral domains (migration, play, 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



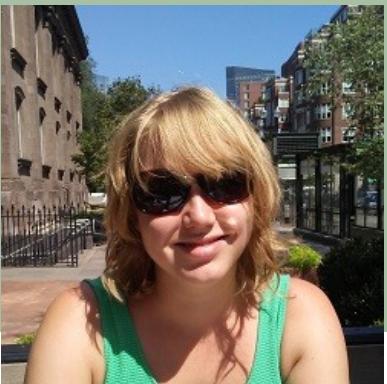
Kiran Basava
Postdoctoral Researcher

The Animal Culture Database (ACDB) 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.

[Explore the Database](#)



Resources



April Wright,
Southeastern Louisiana University

Josef Uyeda,
Virginia Tech

R package: treedata.table

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.

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 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 Wright³ and Josef Uyeda⁴

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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/>).

Released through
ROpenSci – “good”
coding practices!
Published!

Salphycon, phruta

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

APPLICATION

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

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²Center for Diverse Leadership in Science, University of California–Los Angeles, Los Angeles, California, USA

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Handling Editor: Tiago Quental

Methods in Ecology and Evolution

Abstract

1. Current practices for assembling phylogenetic trees often recur to sequence data stored in GenBank. However, the molecular and taxonomic make-up of sequences deposited in GenBank is generally not very clear.
2. PHRUTA, a newly developed R package, is designed to primarily improve access to genetic data stored in GenBank. Functions in PHRUTA further enable users to assemble single- and multi-gene molecular datasets, and run basic phylogenetic tasks, all within R.
3. The structure of the functions implemented in PHRUTA aim to allow users to assemble simple workflows for particular tasks, which are in turn expected to increase reproducibility of relatively simple phylogenies.
4. To support the use of PHRUTA by researchers in different fields with variable levels of coding expertise, this paper presents the first version of SALPHYCON, a shiny web app that aims to increase access to the fundamental functions in the PHRUTA R package.

KEY WORDS

Phylogenetics, R package, reproducibility, workflow

Etymology

phruta

Fruta (Spanish for fruit) + phylogenetics

salphycon

Salpicon (~fruit salad in Colombian Spanish) + phylogenetics

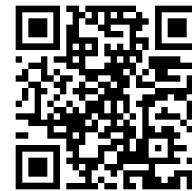
Palenquera



- **Common perspective:** Palenqueras are the Black woman ones who sells fruits in particular Colombian touristic areas (e.g. Cartagena)
- **In reality:** Palenque, northern Colombia, was the first free African town in the Americas. Tons of dignity in this community...
- Logo, Greek mythology – Atlas? To carry something fundamental...



Salphycon



- A salpicon from my hometown...
- Why salphycon? a bunch of fruits (taxa)...



The workflow in short...

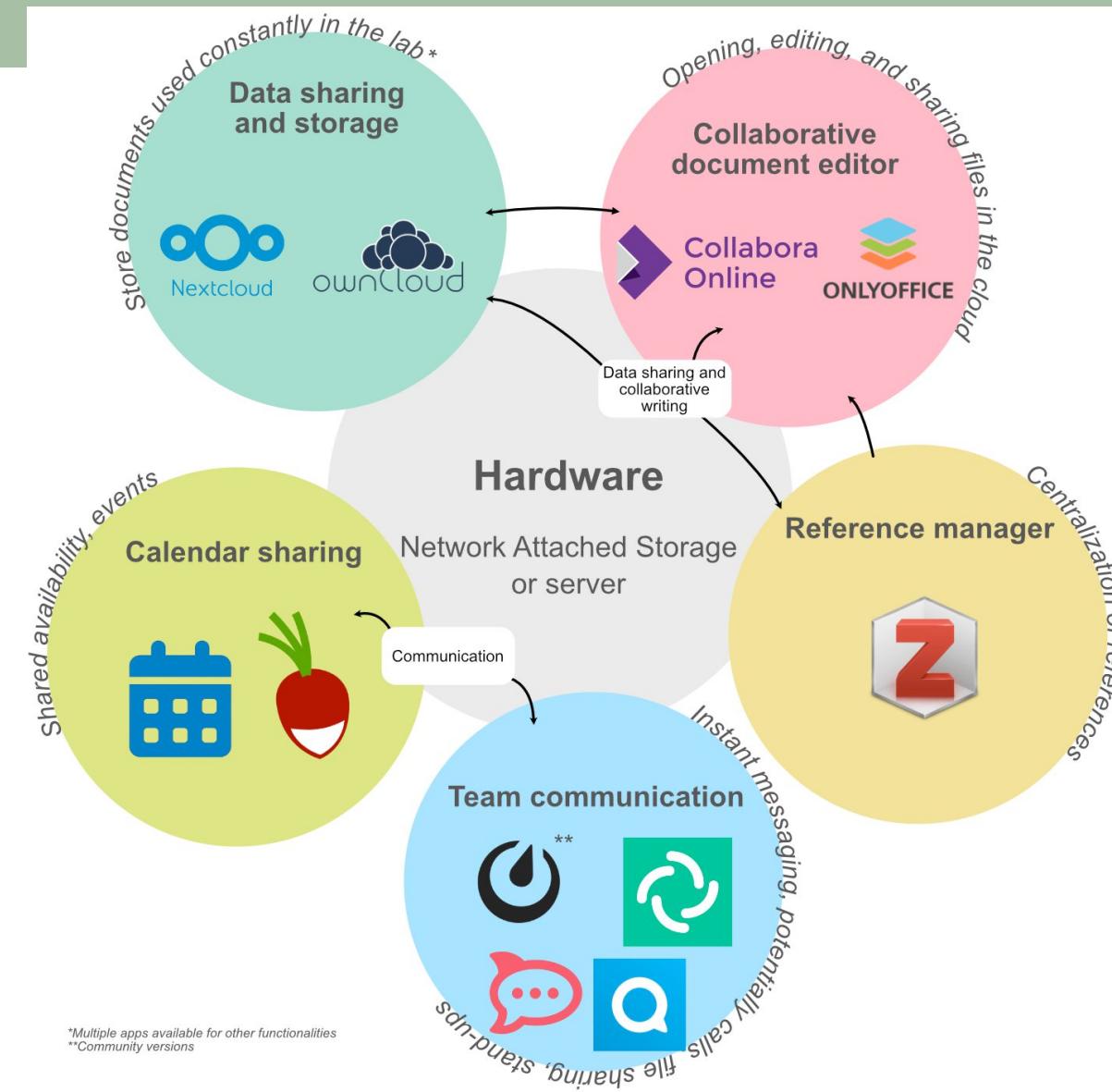


Code?



 GitLab

- Nextcloud – file storage & sharing
- OnlyOffice – collaborative writing
- Mattermost – team communication
- Zotero – reference management
- Radicale – calendar coordination
- Optional: GitLab/Gitea, JupyterHub, Etherpad



Docmost

Wiki and documentation?

LaTex and general writing



Proofs received at
2:35 pm today :)



EDUCATION

LabOps: A flexible self-hosted workflow of open source tools for efficient collaboration within research laboratories

Héctor D. García-Verdugo , Cristian Román-Palacios *

College of Information Science, University of Arizona, Tucson, Arizona, United States of America

* cromanpa@arizona.edu



LabOps GitHub repo



No preprint – it was rejected from arXiv and bioRxiv :)

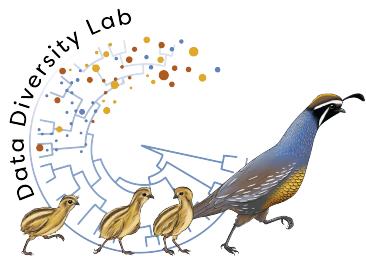
Issues with this pipe

- Many times, ecologists infer evolutionary processes or rates from phylogenetic signal which can be problematic, as many different simulations of evolution can result in similar phylogenetic signals.
- For example, a high phylogenetic signal is often associated with evolutionary conservatism or a strong selective regime, while a low phylogenetic signal is associated with evolutionary liability. However, both processes of strong stabilizing selection and divergent selection result in low phylogenetic signal, uncorrelated with evolutionary rate (Revell et al. 2008, *Syst. Biol.*).
- Other comparative models of constrained evolution are also not often used in calculating phylogenetic signal (i.e. Brownian Motion versus various OU models).
- When we examine phylogenetic signal, we are also only interested in what is happening at the tips without discovering the majority of the evolution through the tree.
- Therefore, using the 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.
-
- This is why 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).

Other topics...

- Randomizations, null distributions, hypothesis testing
- Character divergence and geographic overlap
- Community-wide trait dispersion
- Phylogenetic information to make better conservation decisions
 - Preserving evolutionary history
 - Quantifying evolutionary history
 - Prioritization

Current lab members



Cristian Román-Palacios, Ph.D.
Principal Investigator, Assistant Professor



MD Nafis UI Alam (Michael)
PhD student



Kiran Basava
Postdoctoral Researcher



Ian Estacio
Postdoctoral Researcher
(BBCS;
<https://bbcs.arizona.edu/>)



Kennedy Gezella
Student Staff Support



Kristen Martinet
Postdoctoral Researcher

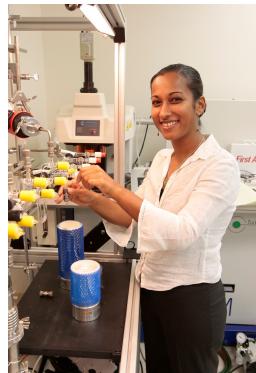


College of
Information Science

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UC- Los Angeles**



**Dr. Rosie Gillespie,
Professor,
UC-Berkeley**



**Dr. Michael Barker,
Associate Professor,
UArizona**



Center for Diverse
Leadership in Science

