

Generalizing Bayesian phylogenetics to infer shared evolutionary events

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phyletica.org/slides/lib.pdf



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The Phyleticians

Postdocs

- ▶ Perry Wood, Jr
- ▶ Brian Folt
- ▶ Jesse Grismer

Graduate students

- ▶ Tashitso Anamza
- ▶ Matt Buehler
- ▶ Kerry Cobb
- ▶ Kyle David
- ▶ Randy Klabacka
- ▶ Morgan Muell
- ▶ Tanner Myers
- ▶ Claire Tracy
- ▶ Branna Sipley
- ▶ Aundrea Westfall



Undergraduate students

- ▶ Laura Lewis
- ▶ Mary Wells
- ▶ Hailey Whitaker
- ▶ Noah Yawn
- ▶ Charlotte Benedict
- ▶ Eric Carbo
- ▶ Ryan Cook
- ▶ Andrew DeSana
- ▶ Miles Horne
- ▶ Jacob Landrum
- ▶ Nadia L'Bahy
- ▶ Jorge Lopez-Perez
- ▶ Holden Smith
- ▶ Virginia White
- ▶ Kayla Wilson

The last 5 years



Generalizing Bayesian phylogenetics to infer shared evolutionary events

The next 5 years

- ▶ My vision for a position at the LIB



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- ▶ Phylogenetics is rapidly becoming the statistical foundation of biology



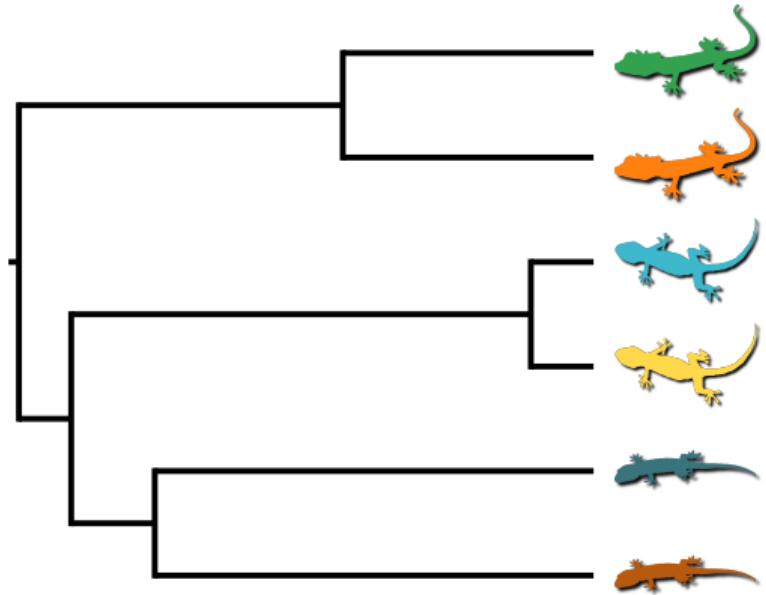
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- ▶ Phylogenetics is rapidly becoming the statistical foundation of biology
- ▶ “Big data” present exciting possibilities and challenges

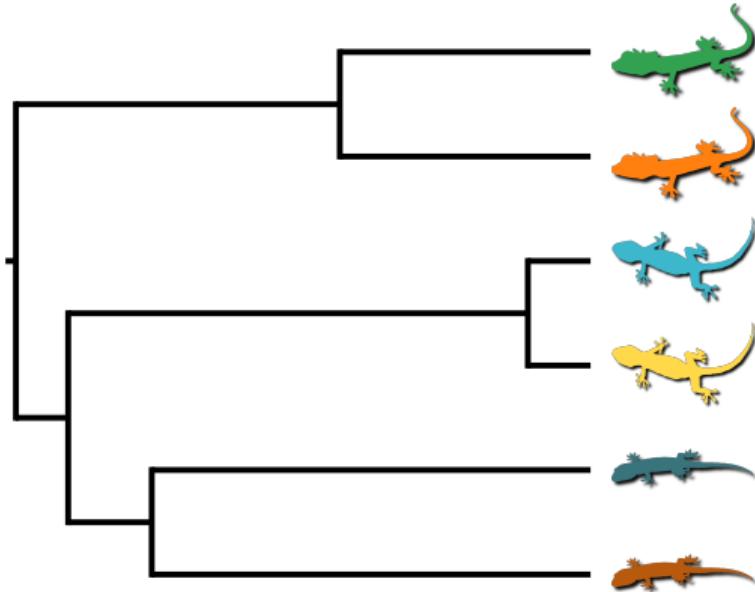


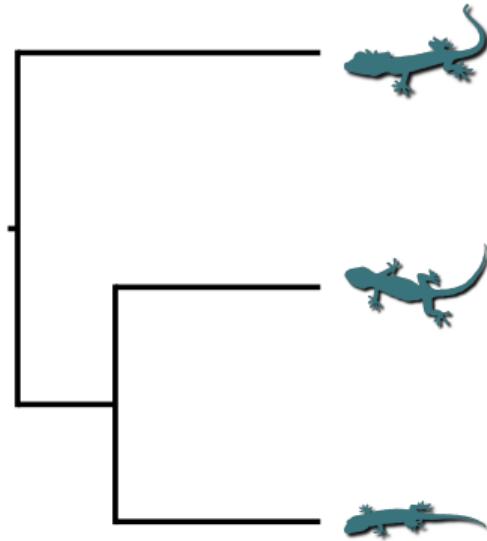
- ▶ Phylogenetics is rapidly becoming the statistical foundation of biology
- ▶ “Big data” present exciting possibilities and challenges
- ▶ Many opportunities to develop new ways to study biology in light of phylogeny

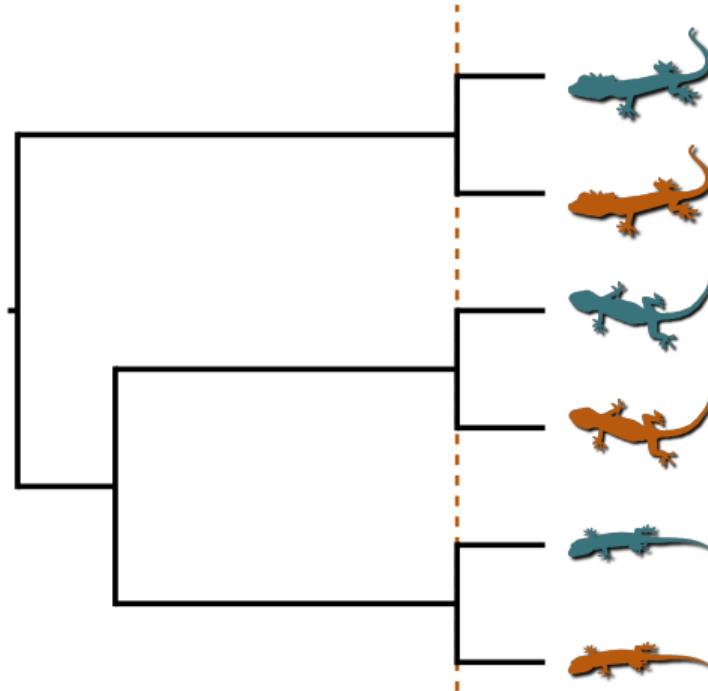




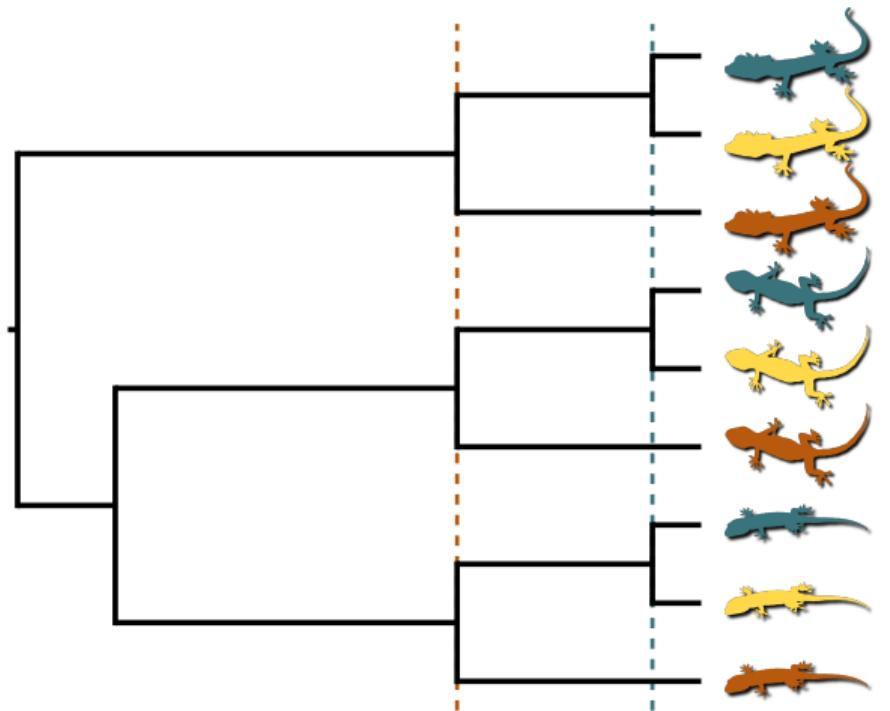
- ▶ **Assumption:** All processes of diversification affect each lineage independently and only cause bifurcating divergences.





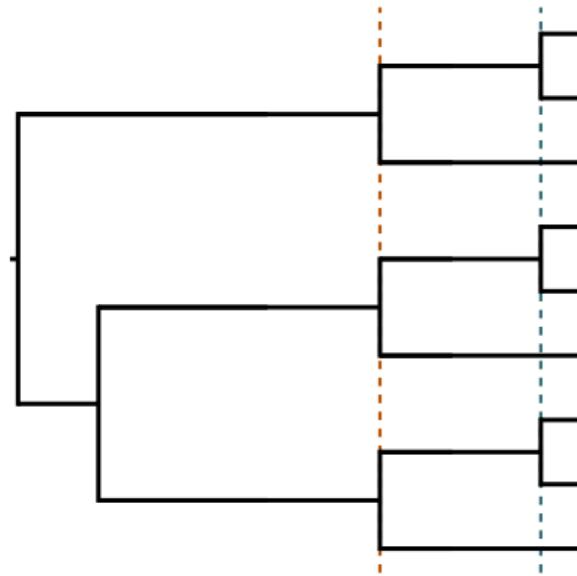


J. R. Oaks (2019). *Systematic Biology* 68: 371–395
J. R. Oaks, C. D. Siler, and R. M. Brown (2019). *Evolution* 73: 1151–1167



Biogeography

- ▶ Environmental changes that affect whole communities of species

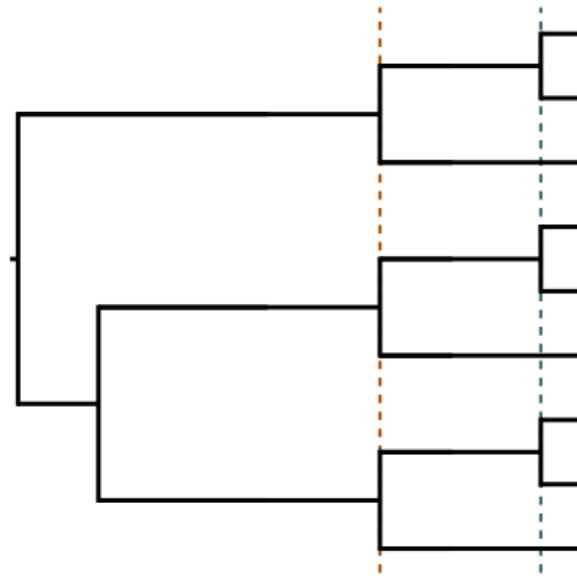


Biogeography

- ▶ Environmental changes that affect whole communities of species

Genome evolution

- ▶ Duplication of a chromosome segment harboring gene families



Biogeography

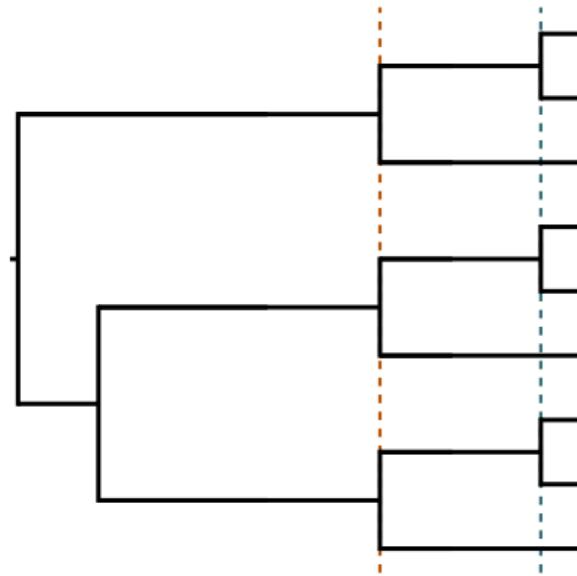
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Epidemiology

- ▶ Transmission at social gatherings



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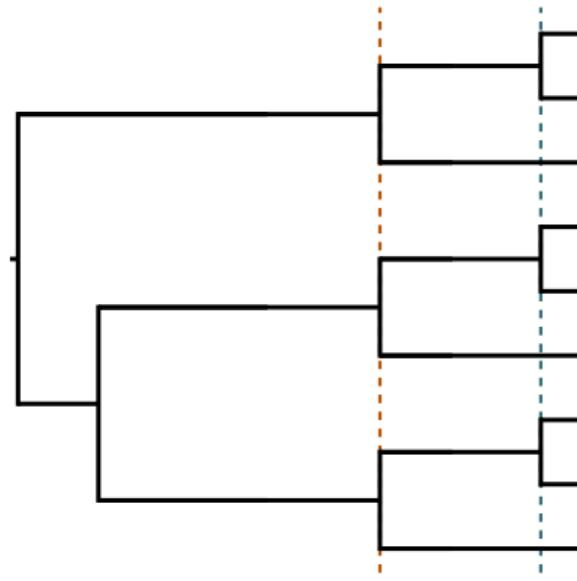
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Endosymbiont evolution (e.g., parasites, microbiome)

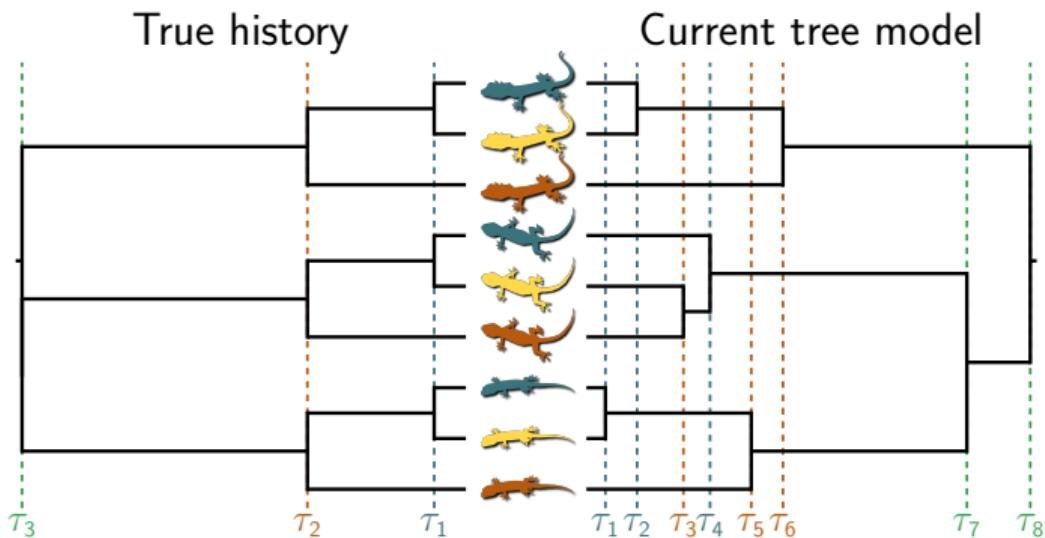
- ▶ Speciation of the host
- ▶ Co-colonization of new host species



Why account for shared divergences?

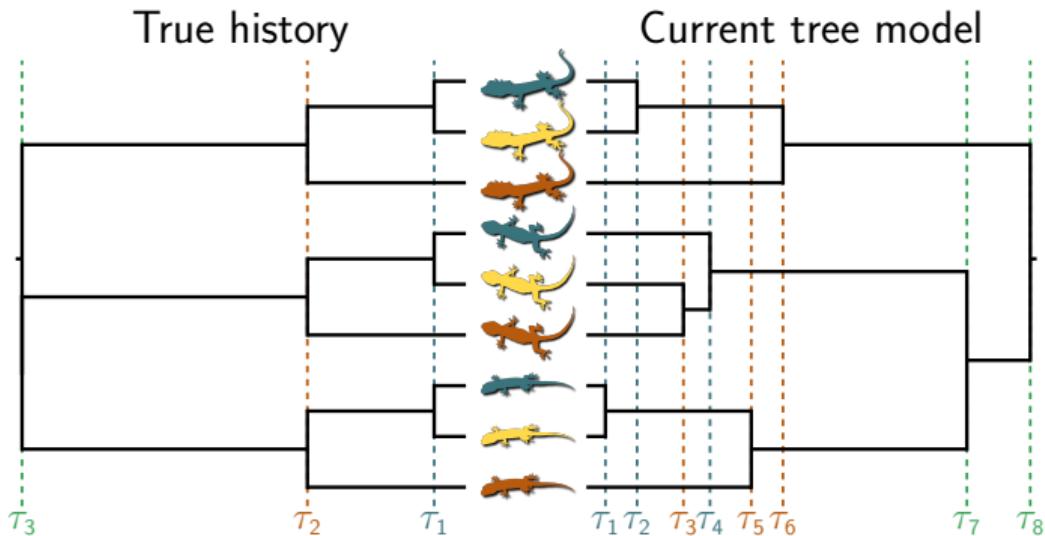
Why account for shared divergences?

1. Improve inference



Why account for shared divergences?

1. Improve inference
2. **Provide a framework for studying processes of co-diversification**



Biogeography

- ▶ Environmental changes that affect whole communities of species

Genome evolution

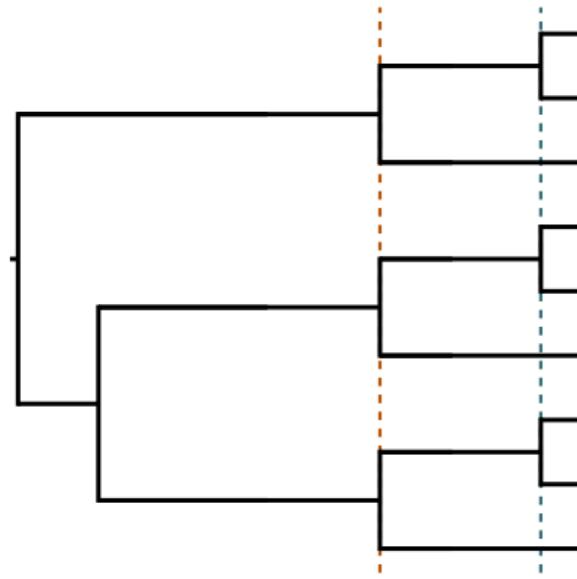
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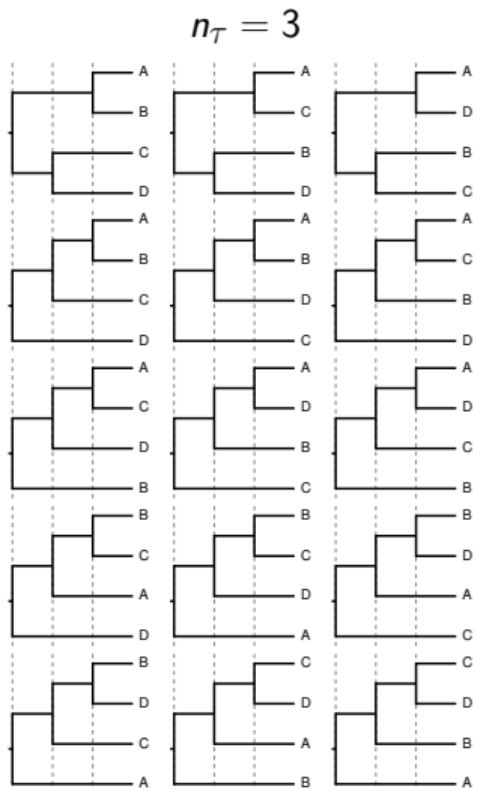
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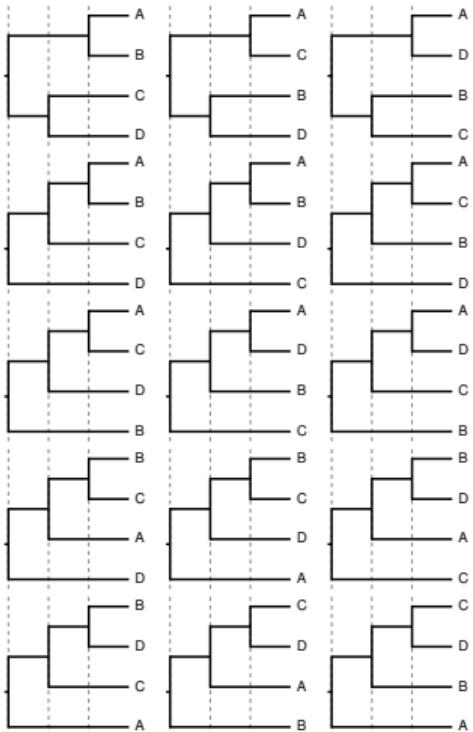
Generalizing tree space

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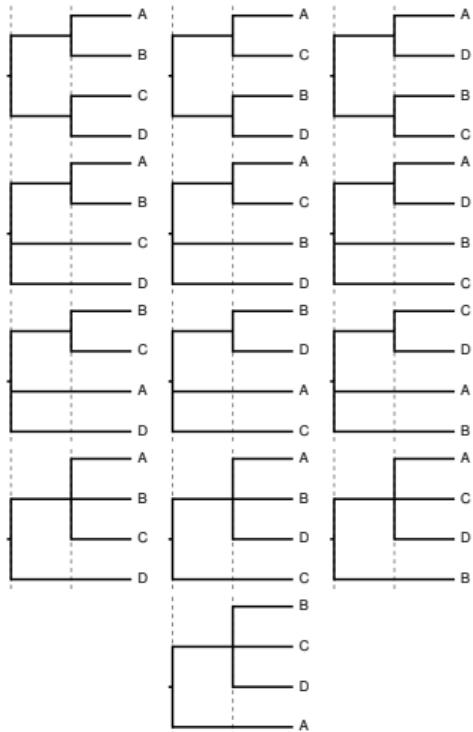


Generalizing tree space

$$n_T = 3$$



$$n_T = 2$$

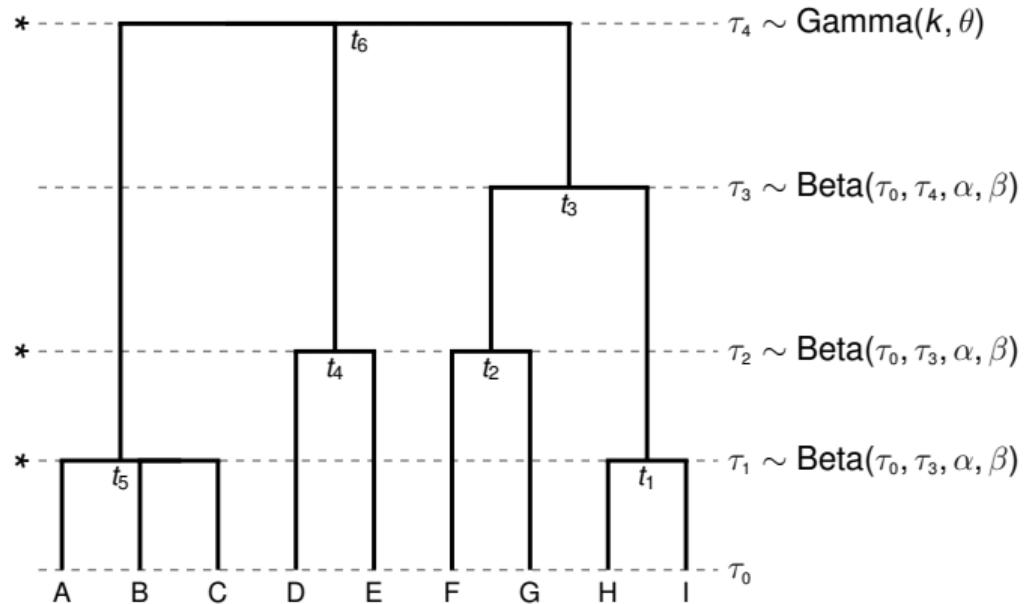


$$n_T = 1$$

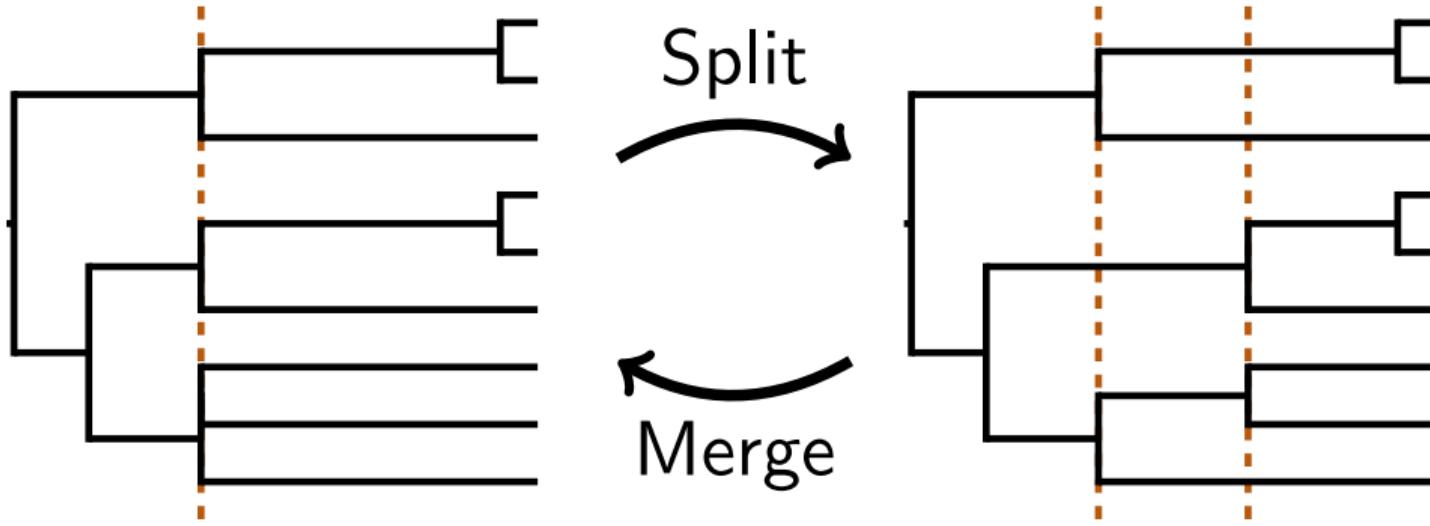


Generalized tree distribution

- ▶ All topologies equally probable
- ▶ Parametric distribution on age of root
- ▶ Beta distributions on other div times

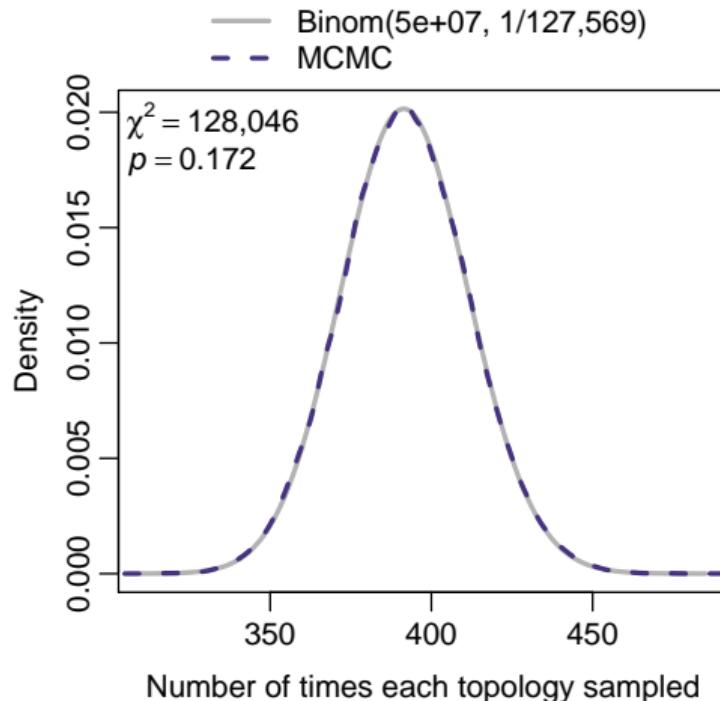


Inferring trees with shared divergences



Reversible-jump MCMC

Validating rjMCMC with 7-leaf tree



The rjMCMC algorithms sample the expected generalized tree distribution

PhycoEval

Phylogenetic coevality

J. R. Oaks and P. L. Wood, Jr. (2021). *bioRxiv*

Ecoevolity

Estimating evolutionary coevality

J. R. Oaks (2019). *Systematic Biology* 68: 371–395

► Tree model

- rjMCMC sampling of generalized tree distribution

¹ D. Bryant et al. (2012). *Molecular Biology and Evolution* 29: 1917–1932

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- ▶ **Tree model**
 - ▶ rjMCMC sampling of generalized tree distribution
- ▶ **Likelihood model**
 - ▶ CTMC model of characters evolving along genealogies
 - ▶ Infer species trees by analytically integrate over genealogies¹

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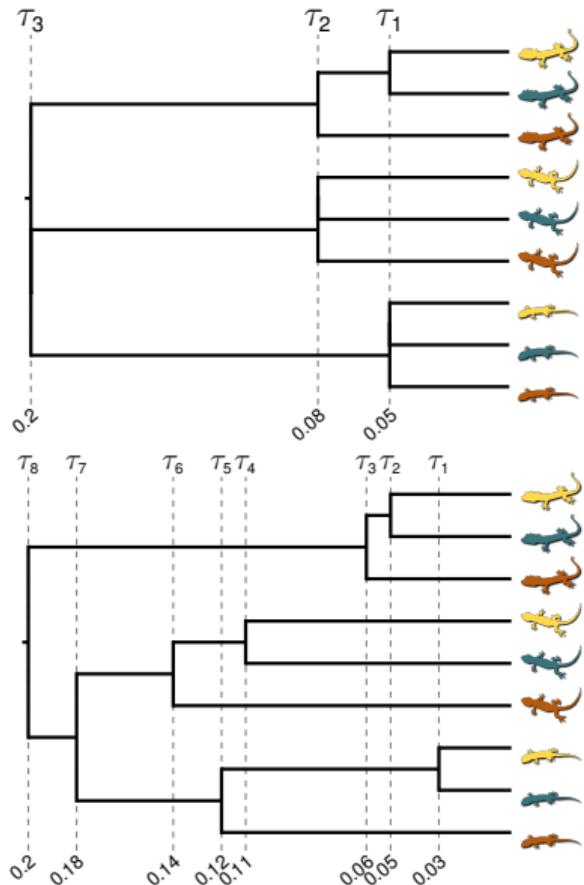
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- ▶ **Likelihood model**
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 - ▶ Infer species trees by analytically integrate over genealogies¹
- ▶ *Goal: Co-estimation of phylogeny and shared divergences from genomic data*

¹ D. Bryant et al. (2012). *Molecular Biology and Evolution* 29: 1917–1932

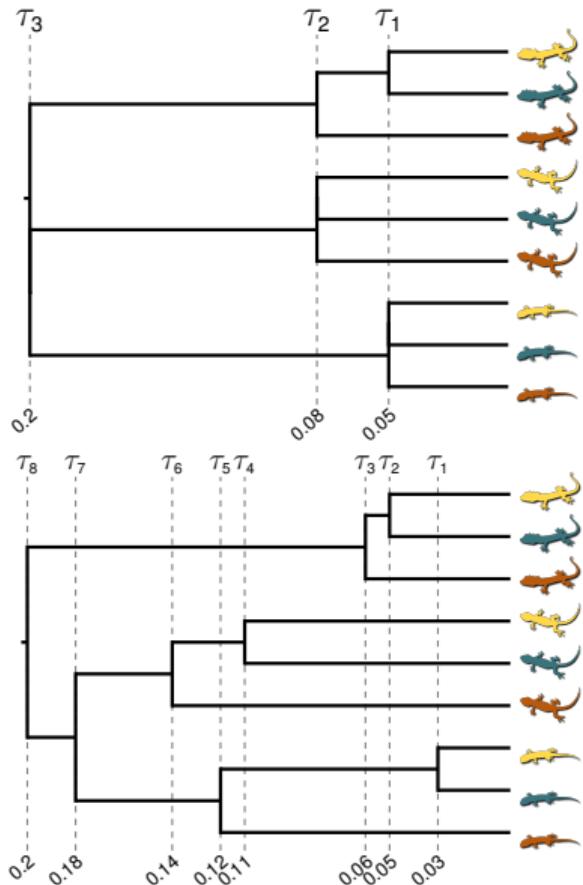
Methods: Simulations

- ▶ Simulated 100 data sets with 50,000 characters
- ▶ Strict clock



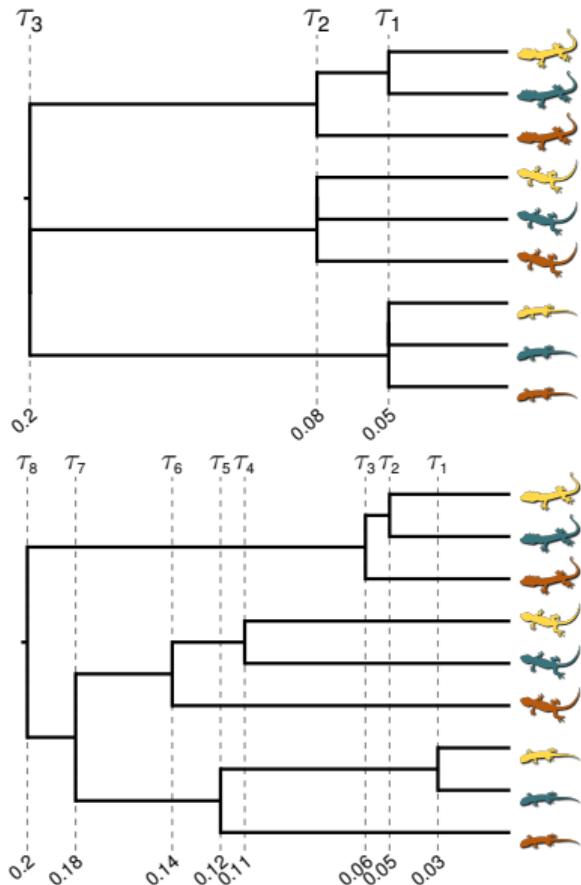
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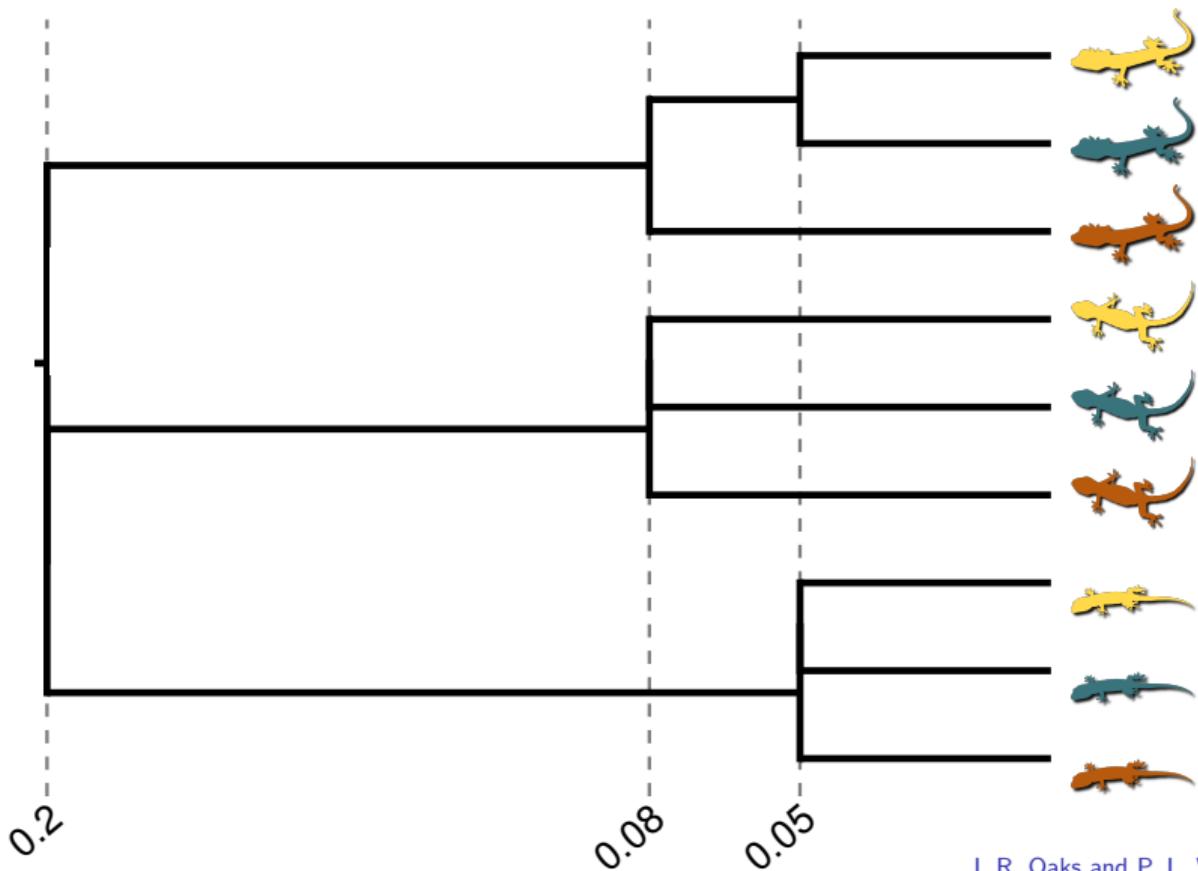
- ▶ Simulated 100 data sets with 50,000 characters
- ▶ Strict clock
- ▶ Analyzed each data set with:
 - ▶ M_G = Generalized tree model
 - ▶ M_{IB} = Independent-bifurcating tree model

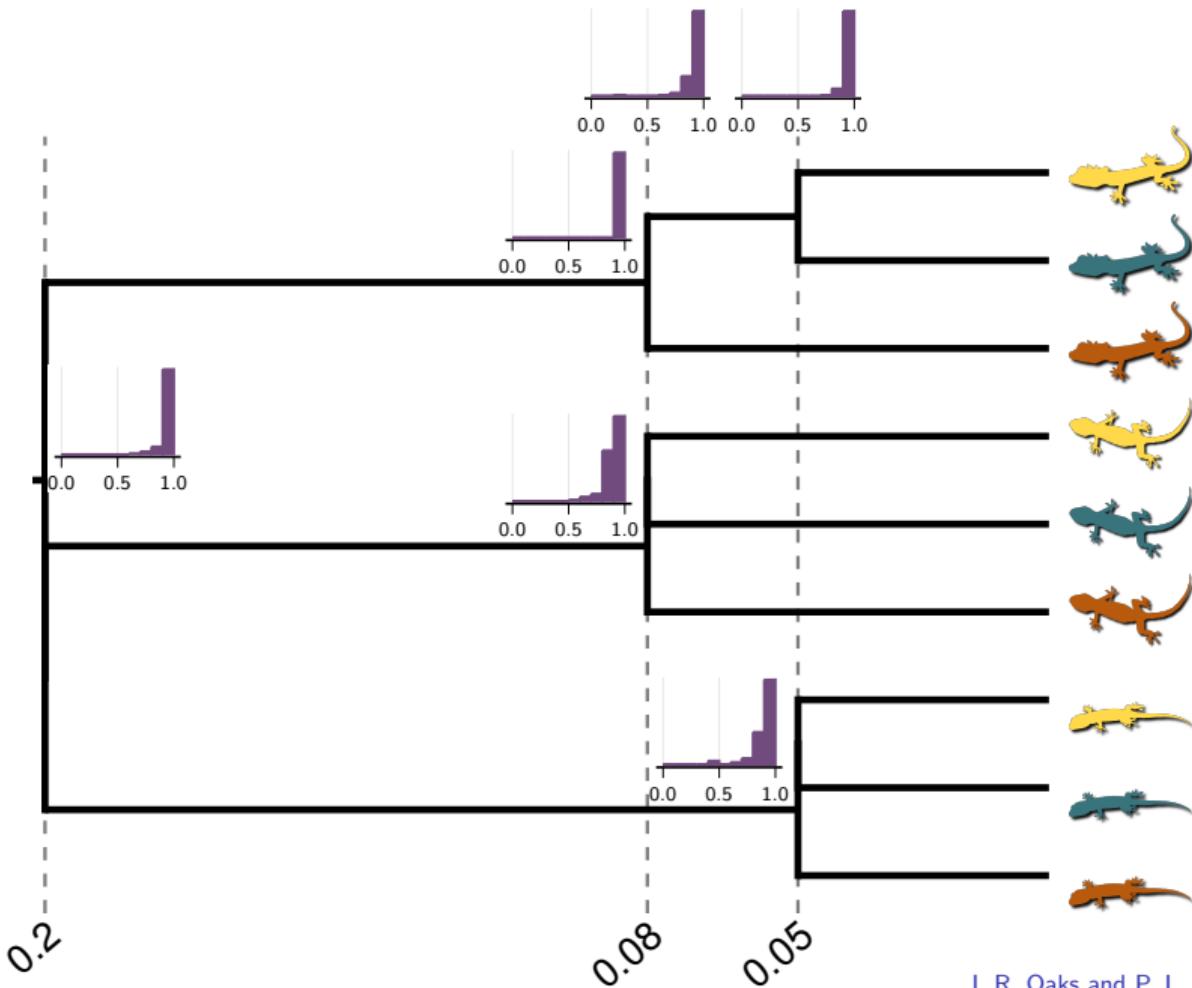


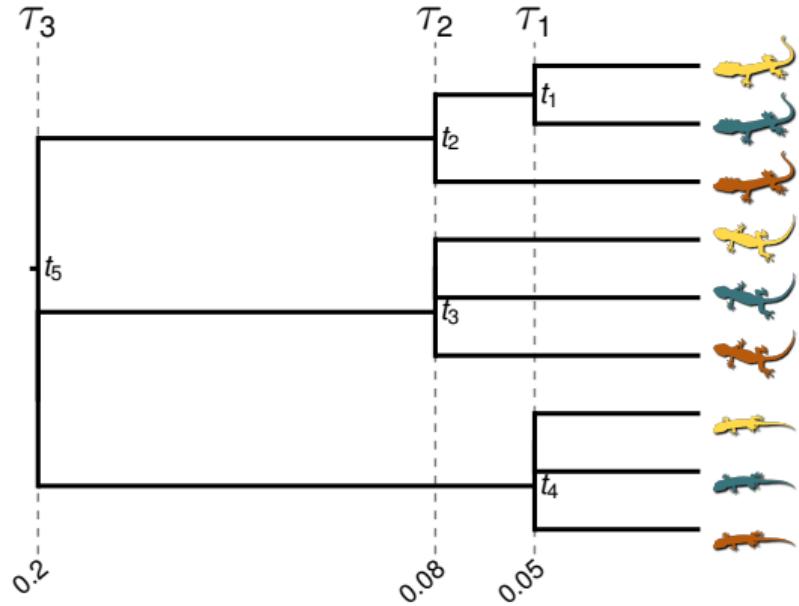
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- ▶ Simulated 100 data sets where topology and div times randomly drawn from M_G and M_{IB}



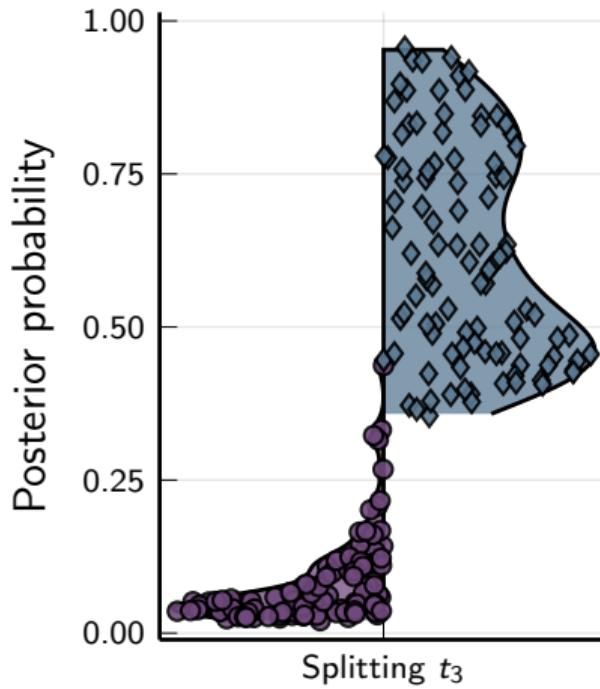
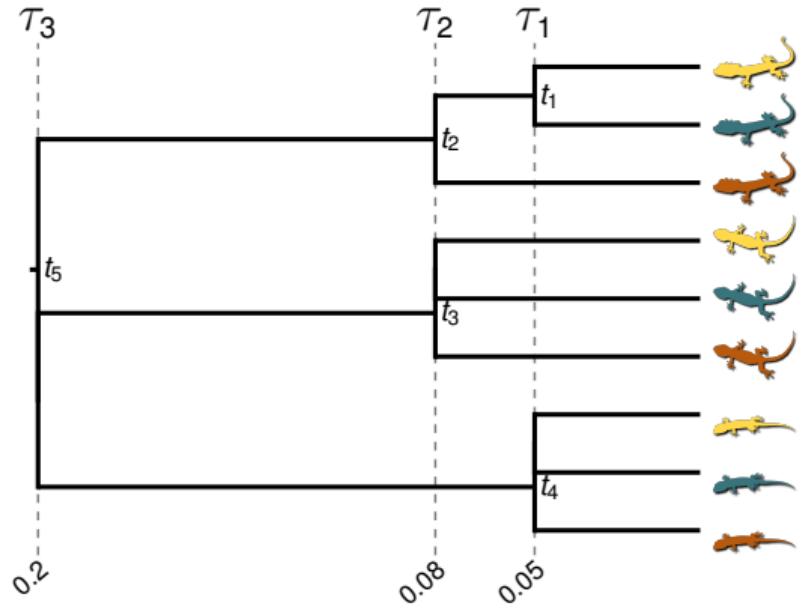






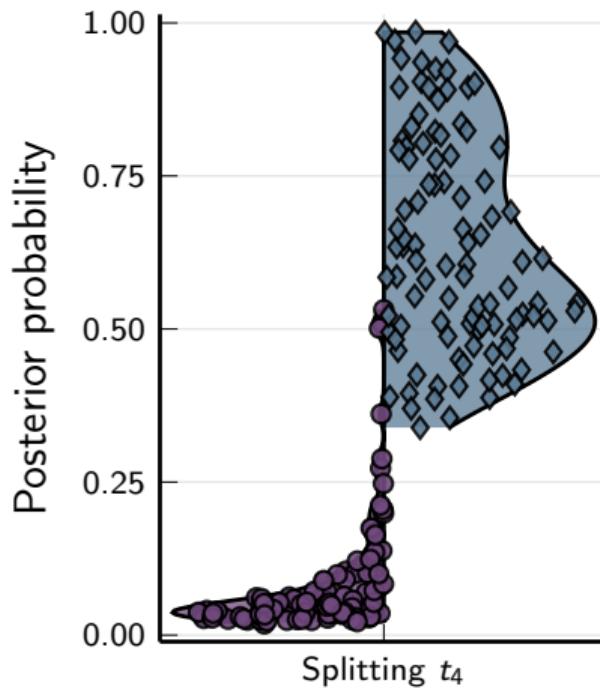
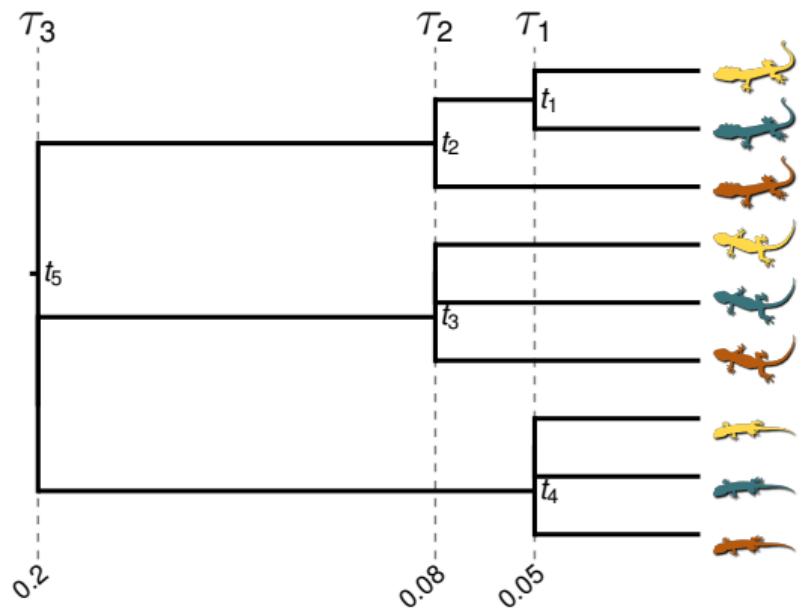
● M_G = Generalized model

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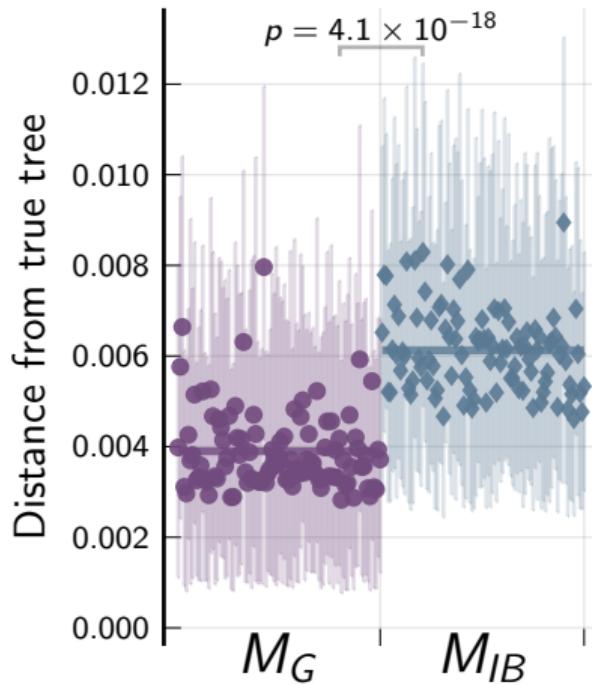
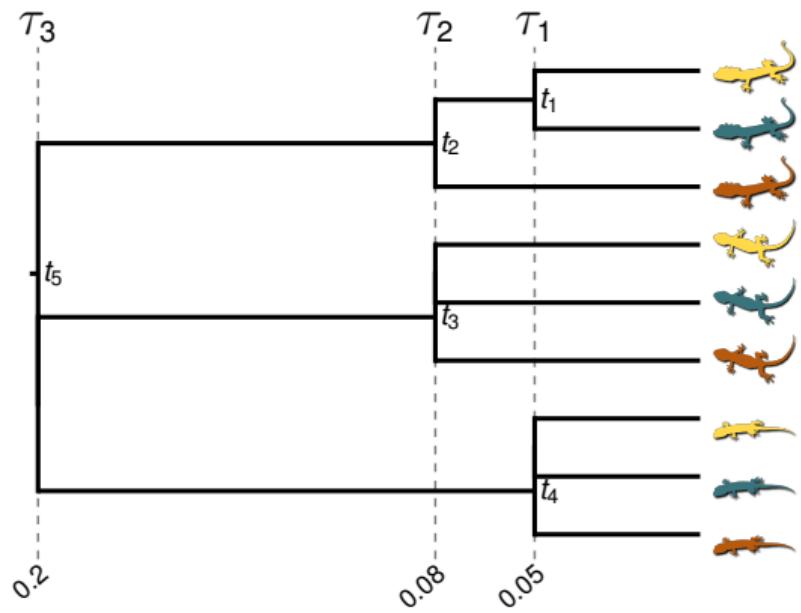
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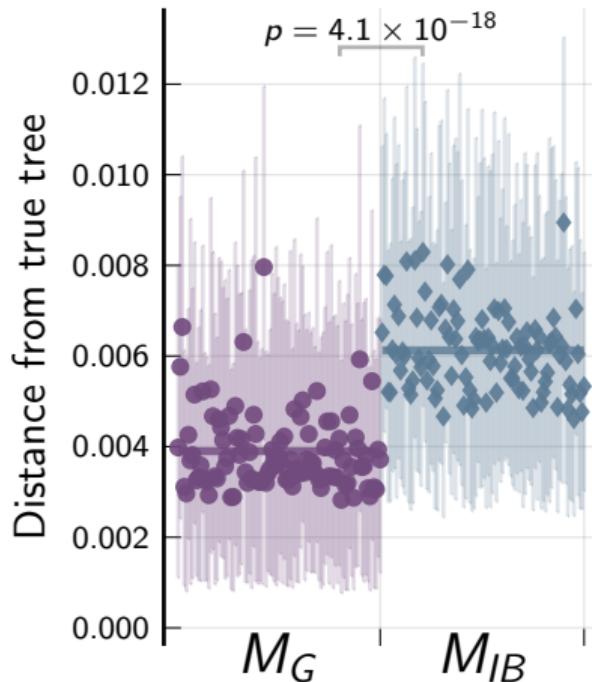
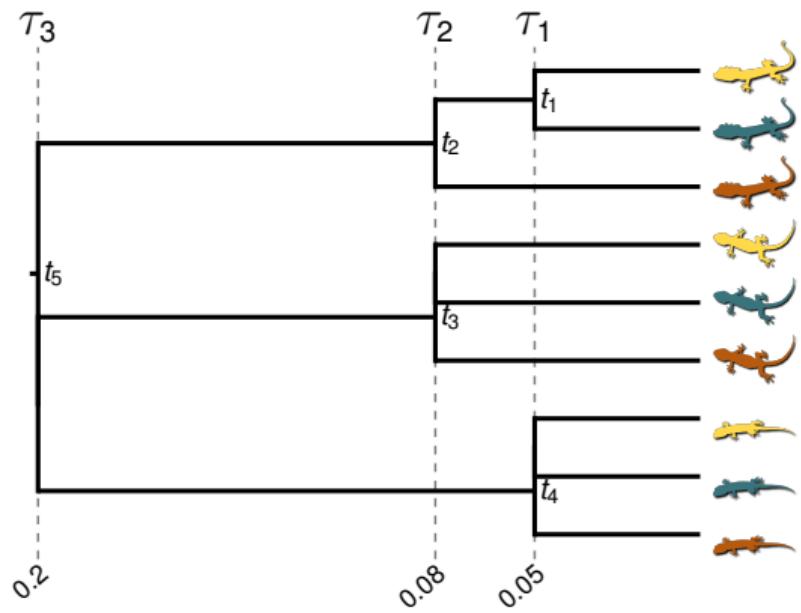
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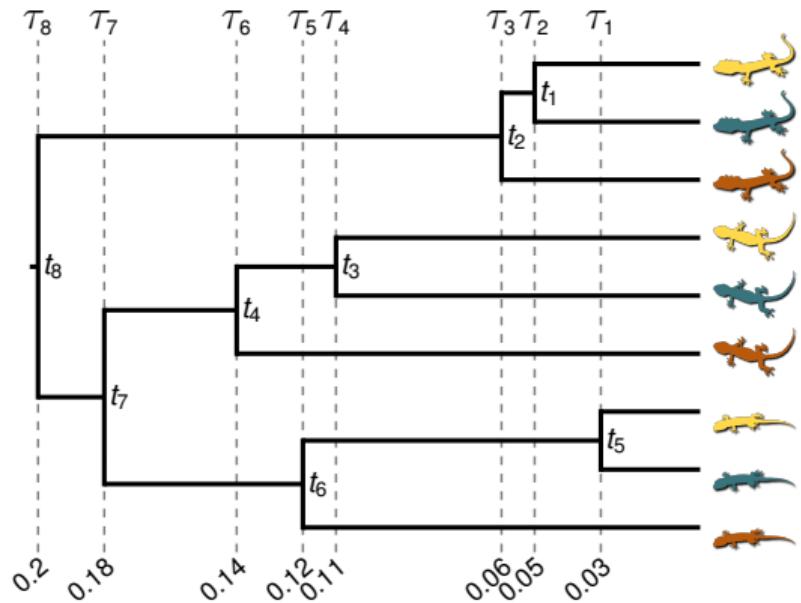
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M_G significantly better at inferring trees with shared divergences

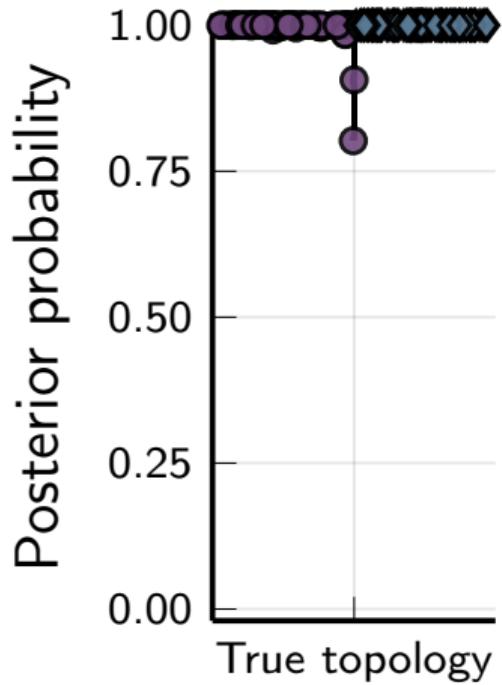
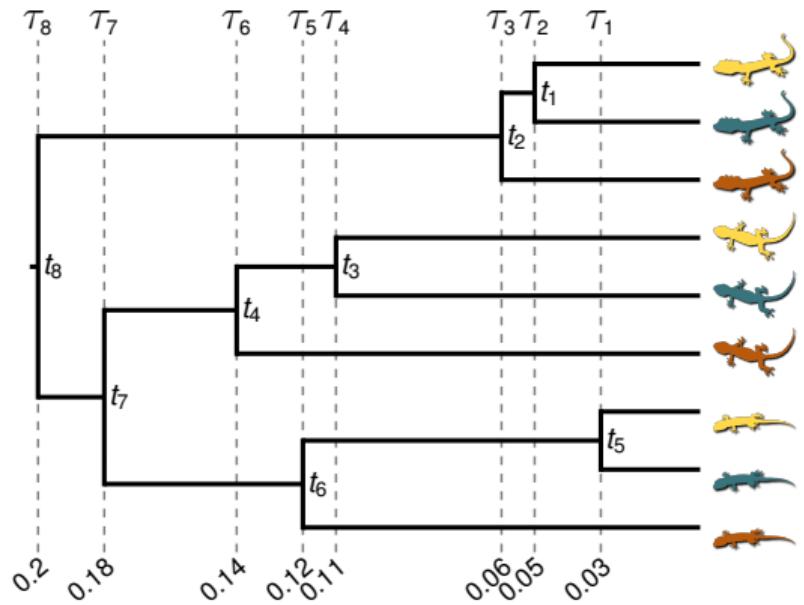
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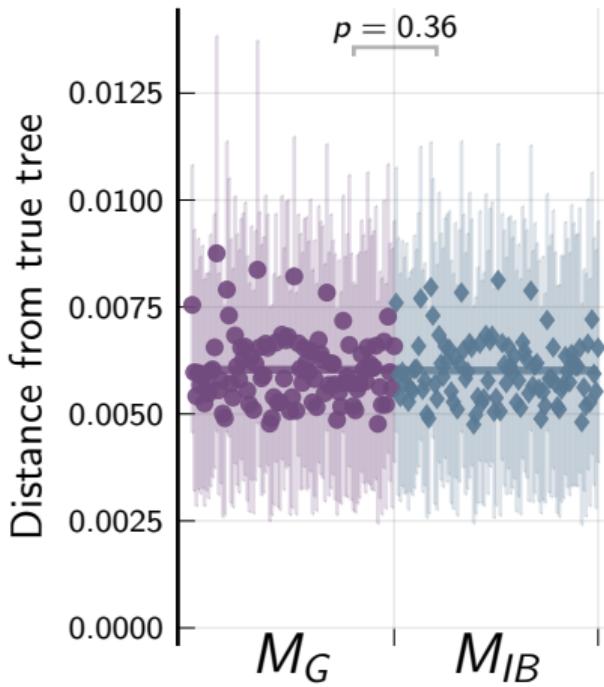
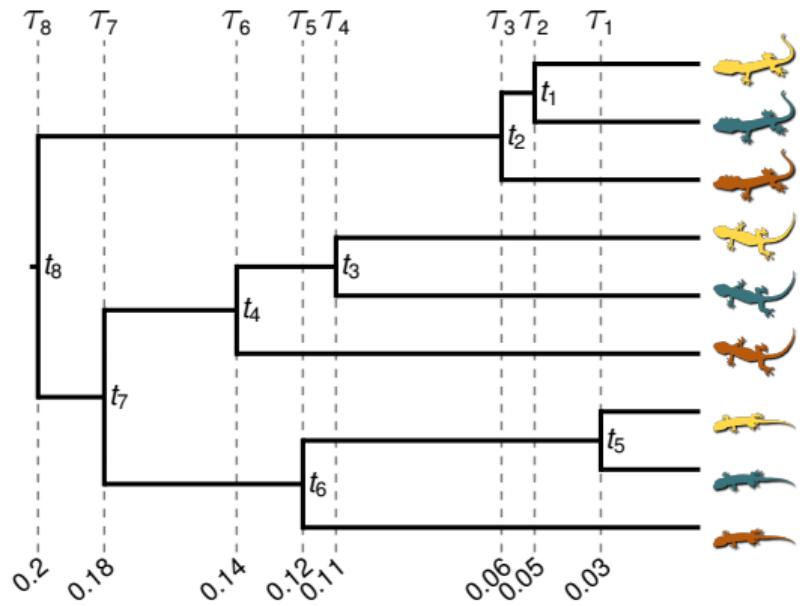
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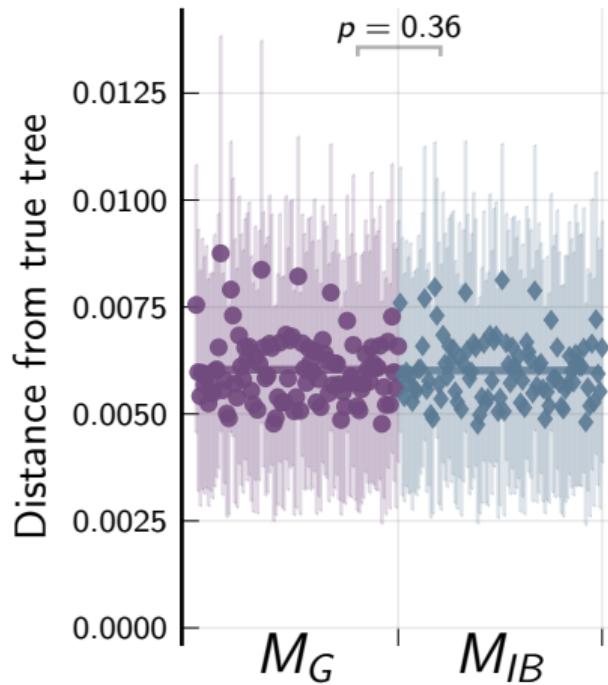
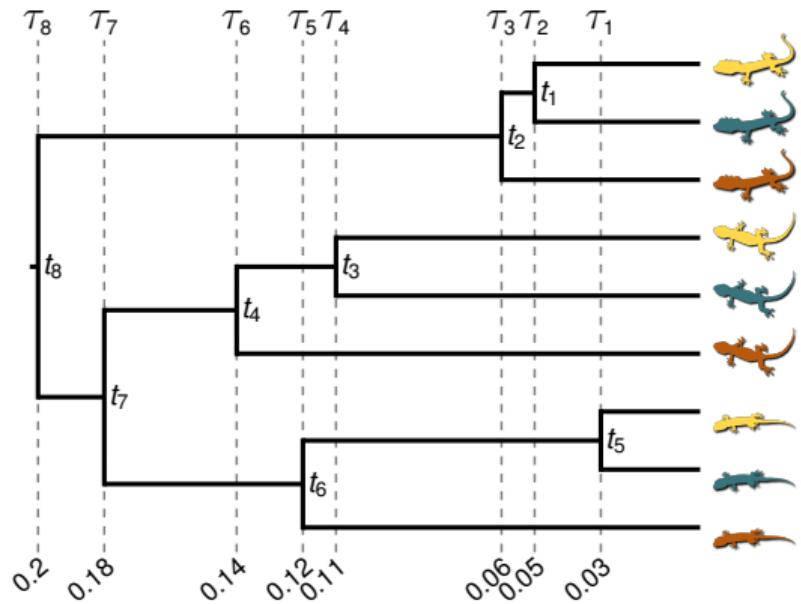
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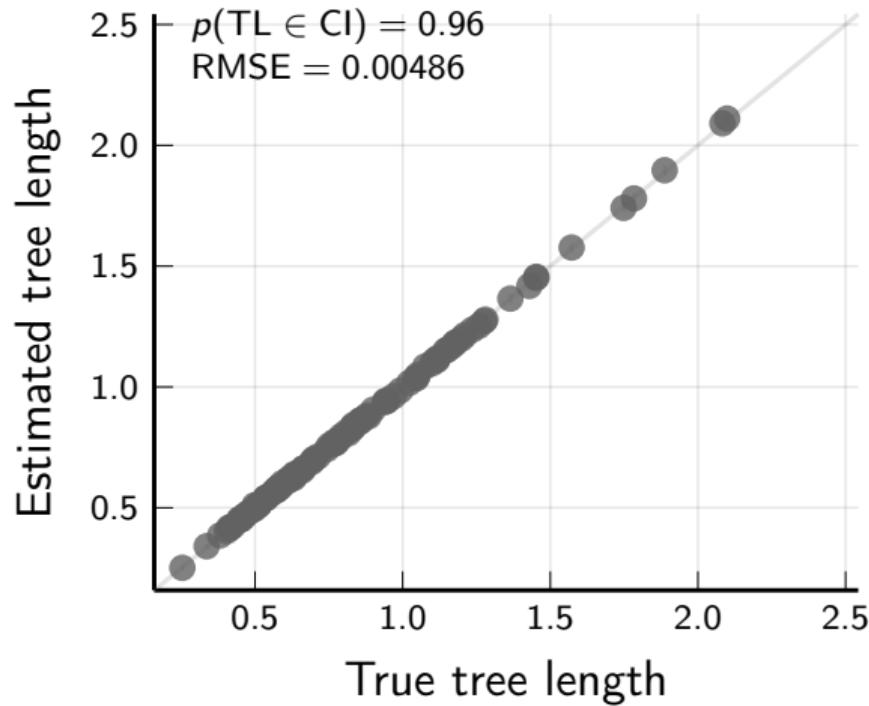
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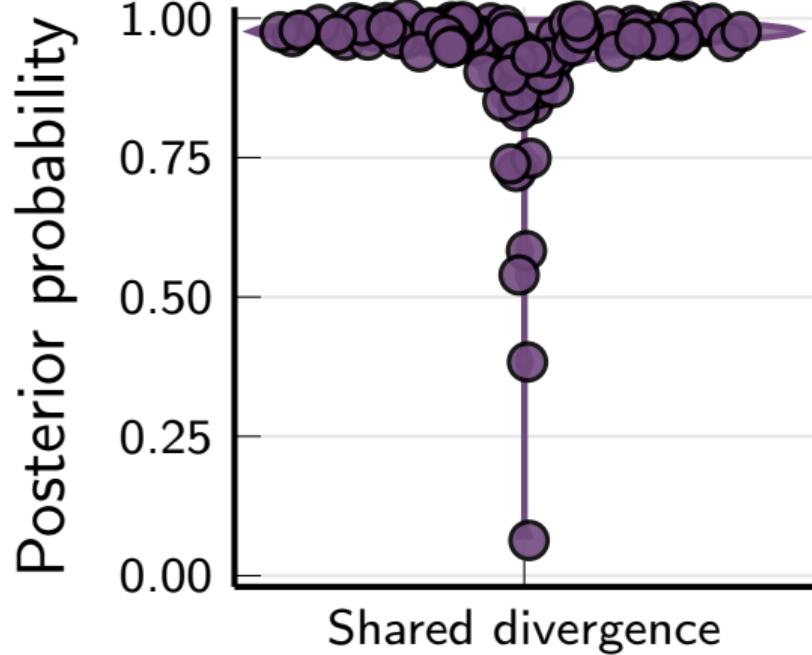
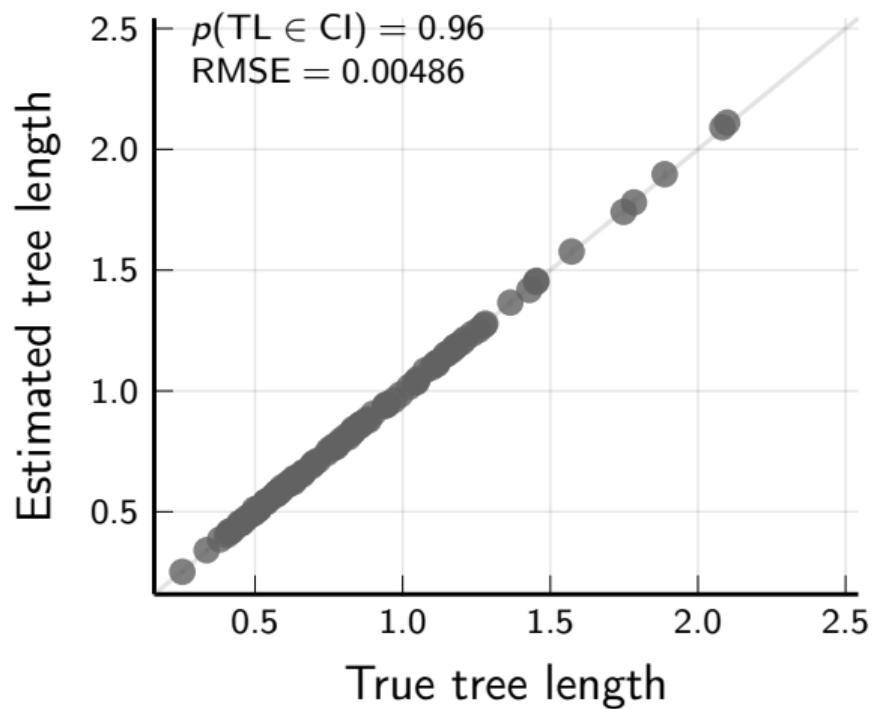


M_G performs as well as true model when divergences are independent

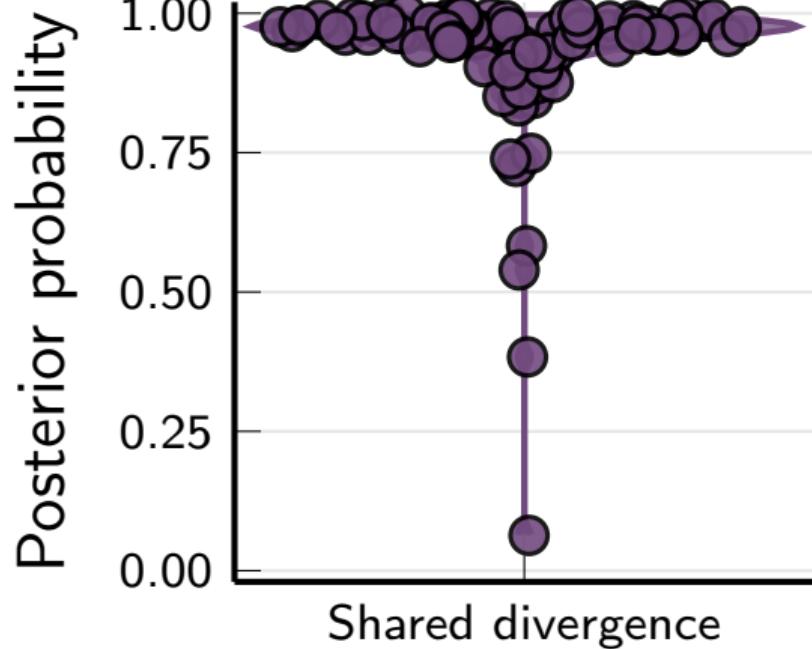
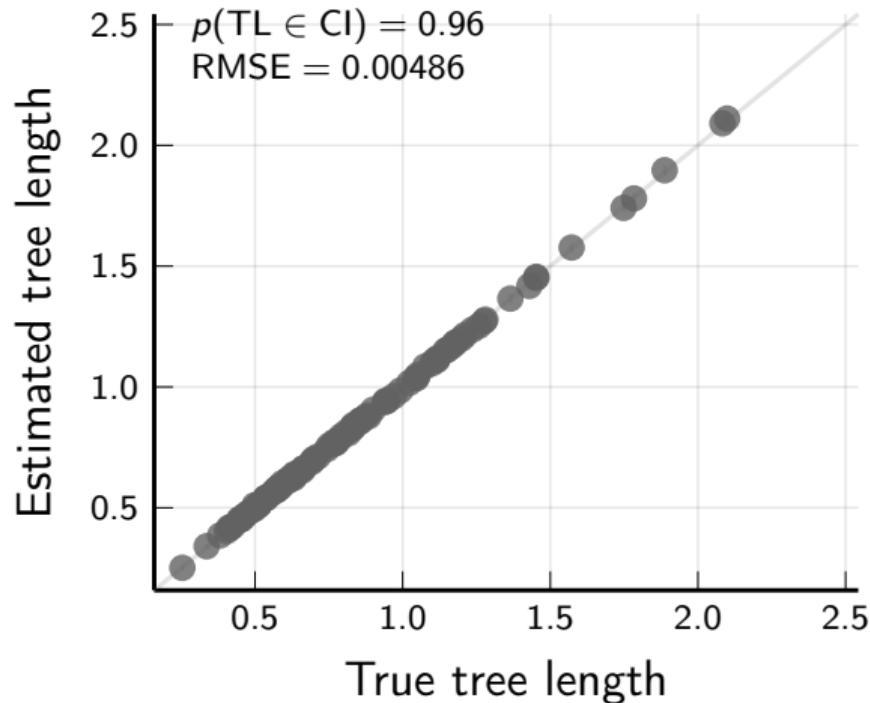
Results: random M_G trees



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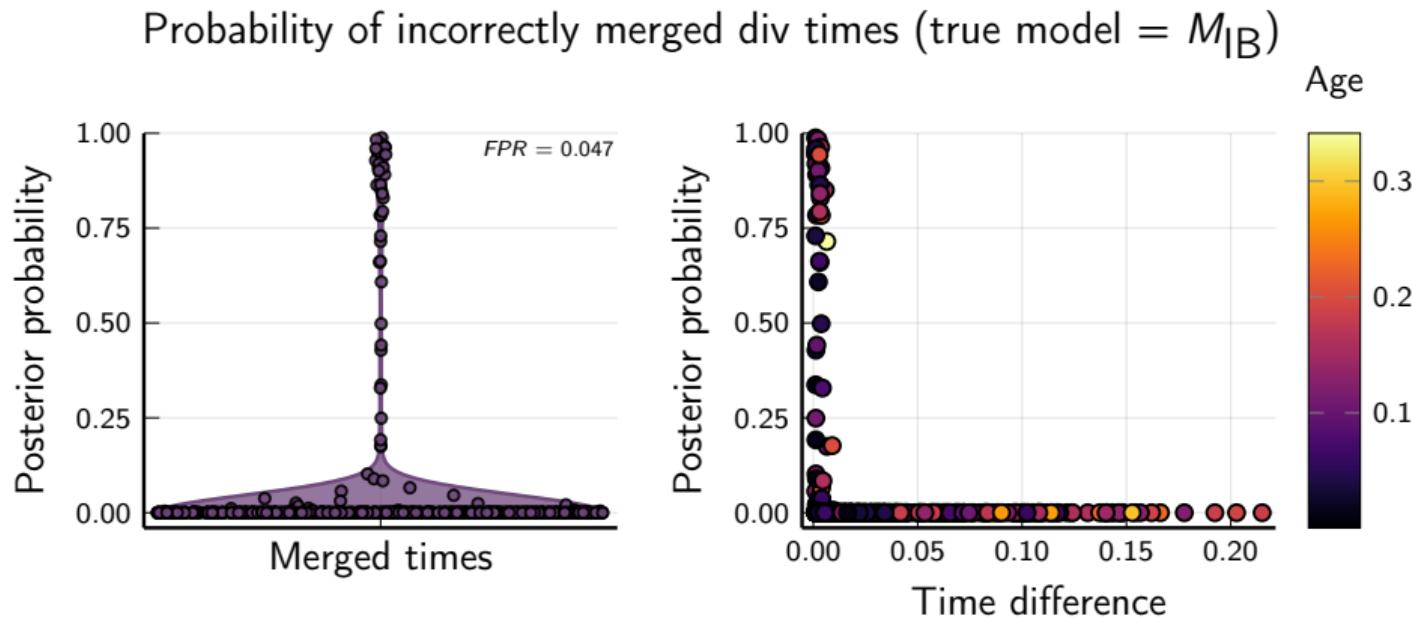


Results: random M_G trees

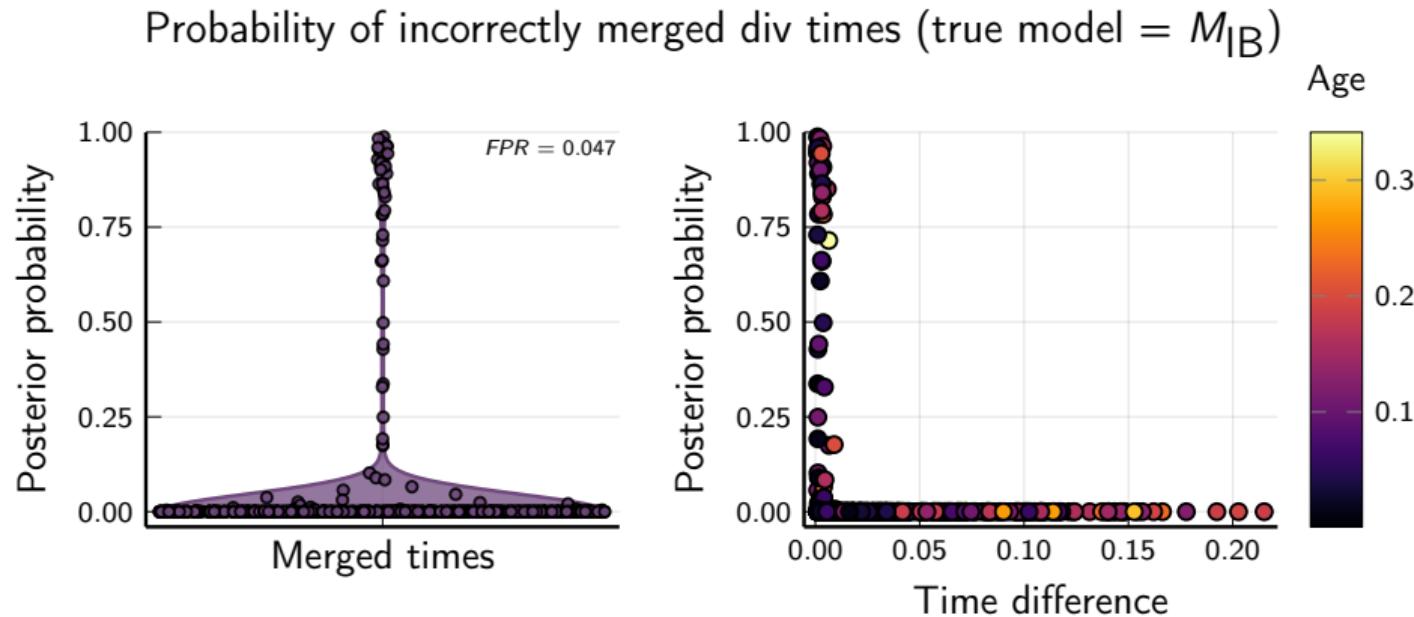


M_G performs well with data simulated on random trees with shared divergences

Results: random M_{IB} trees



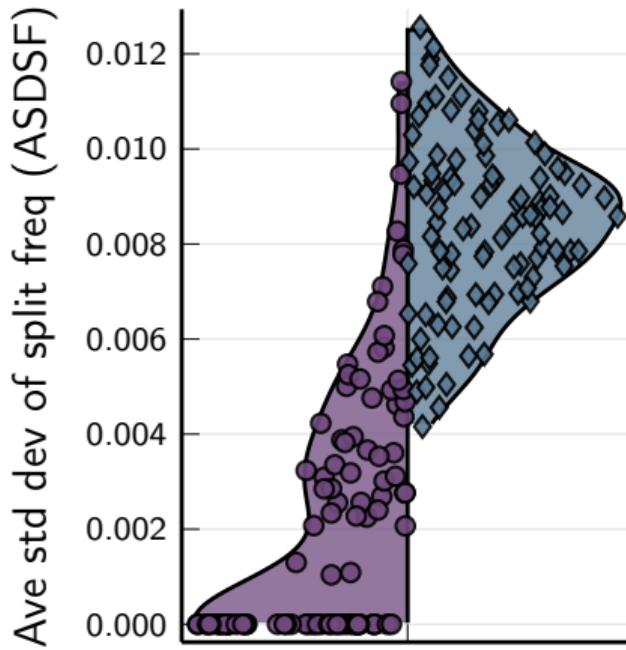
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M_G has low false positive rate

● M_G = Generalized model

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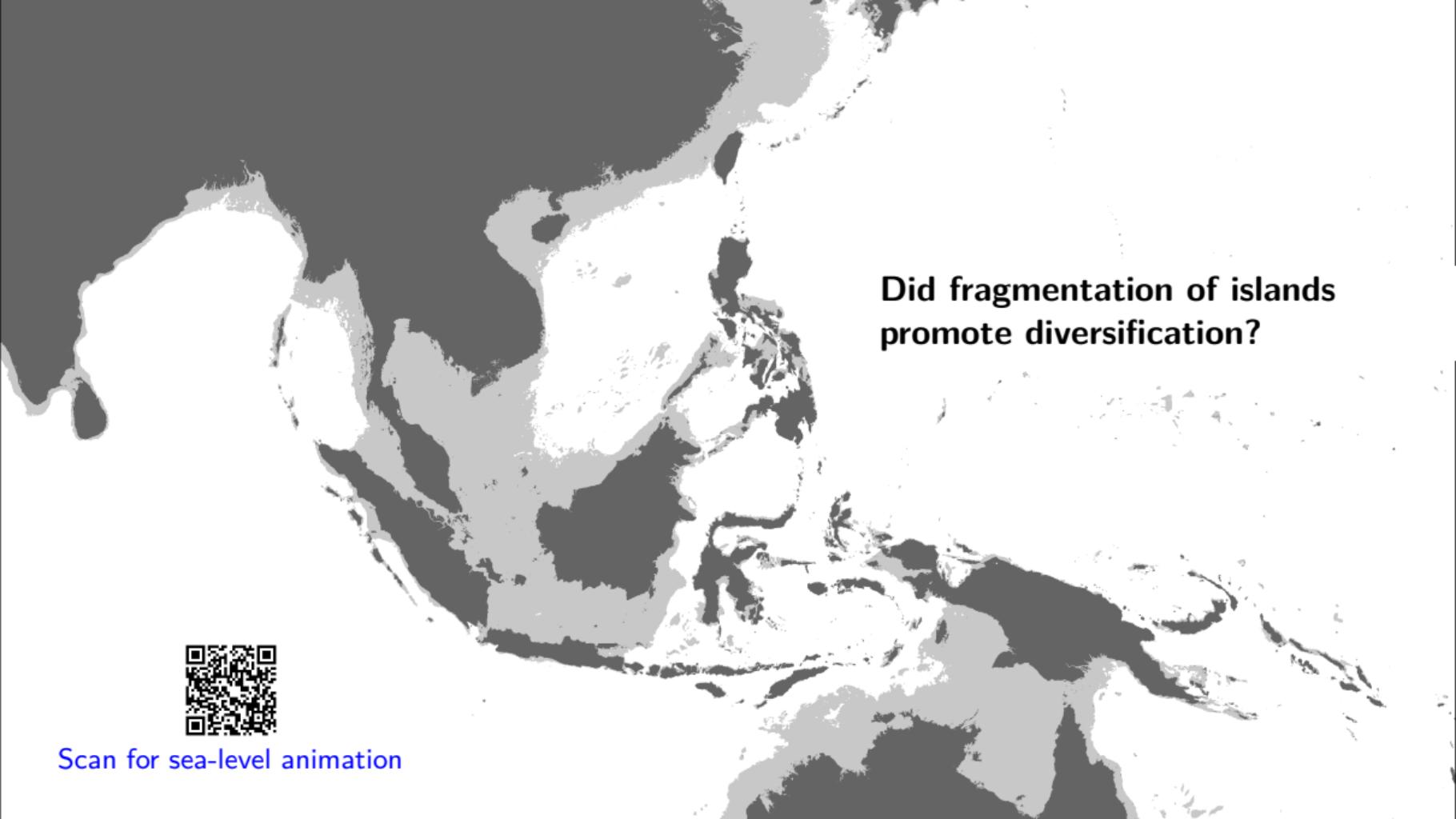
Generalizing tree space improves MCMC convergence and mixing



Scan for sea-level animation



Scan for sea-level animation

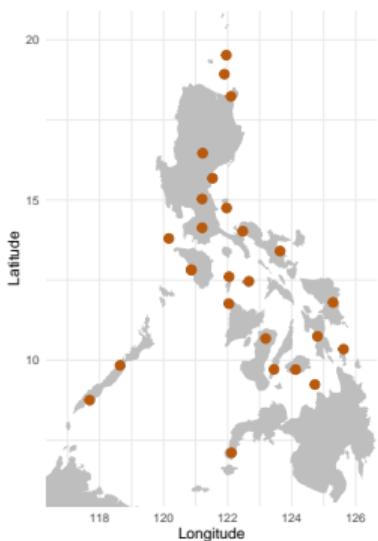


**Did fragmentation of islands
promote diversification?**



Scan for sea-level animation

Cyrtodactylus



©Rafe M. Brown

Gekko



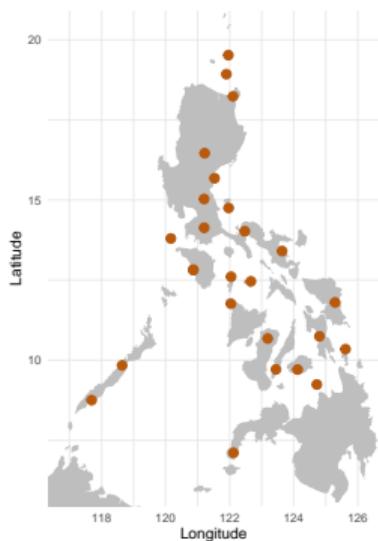
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Cyrtodactylus



©Rafe M. Brown

1702 loci
155,887 sites



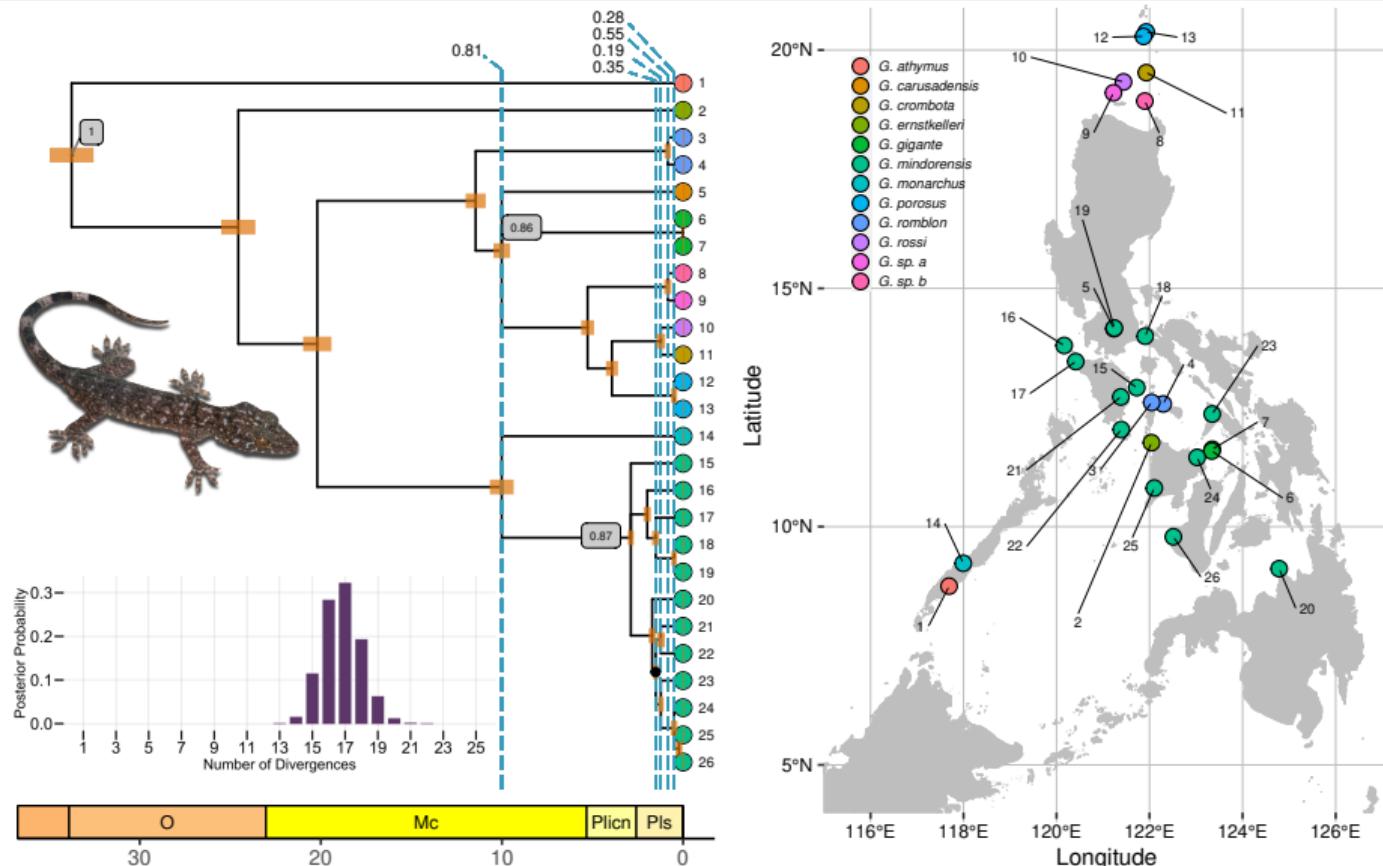
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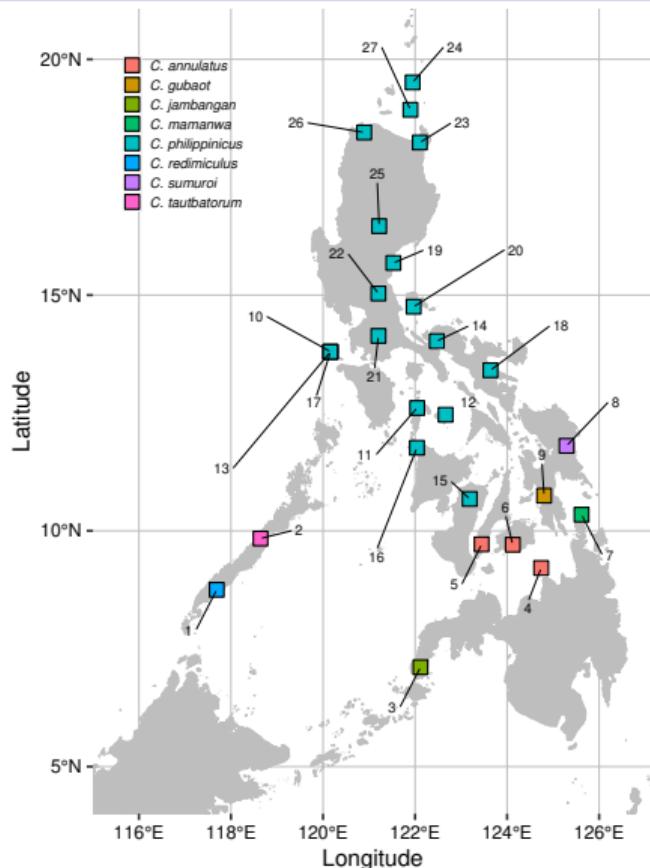
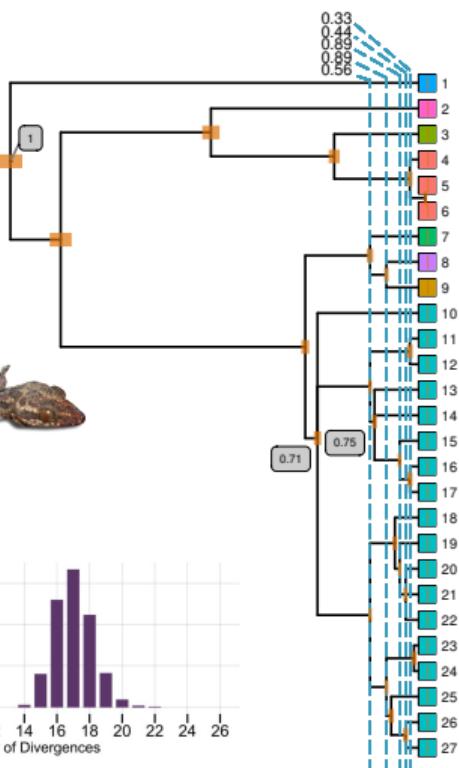
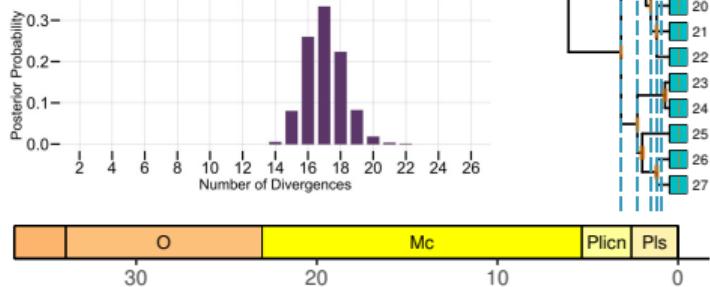
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1033 loci
94,813 sites

Gekko



Cyrtodactylus



Take-home points

- ▶ We can accurately infer phylogenies with shared divergences with moderately sized data sets

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- ▶ Generalizing tree space avoids spurious support and improves MCMC mixing
- ▶ Among Philippine gekkonids, we found support for shared divergences predicted by sea-level changes

Open science: everything is available...

Software:

- ▶ Phycoeval:
<https://github.com/phyletica/ecoevolity>
(release coming soon)

Open-Science Notebooks:

- ▶ Phycoeval analyses: <https://github.com/phyletica/phycoeval-experiments>
- ▶ Gecko RADseq:
<https://github.com/phyletica/gekgo>



phyletica.org/codiv-sanger-bake-off

Vision for LIB position

Phylogenetic theory/methods

- ▶ Develop process-based and trait-dependent distributions over the space of generalized trees

Empirical work

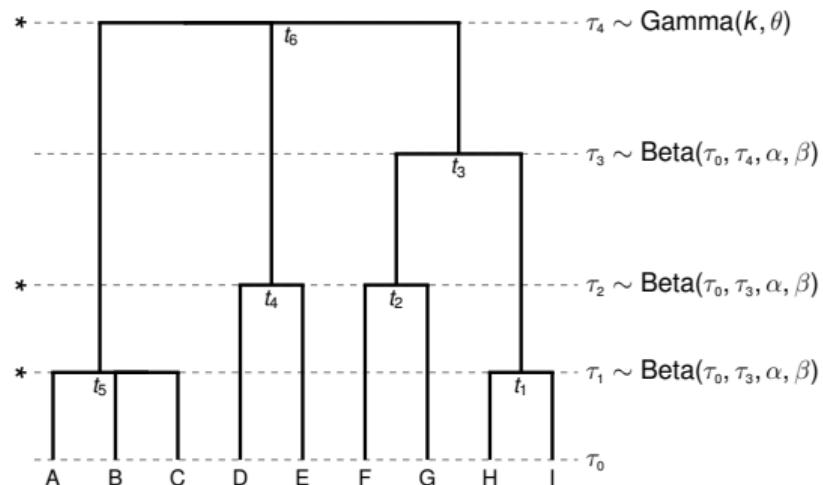
- ▶ Did the evolution of habitat preference affect the diversification of bent-toed geckos?
- ▶ Epidemiological dynamics of “super-spreading” events during the COVID-19 pandemic

Teaching

- ▶ Coding to learn evolution

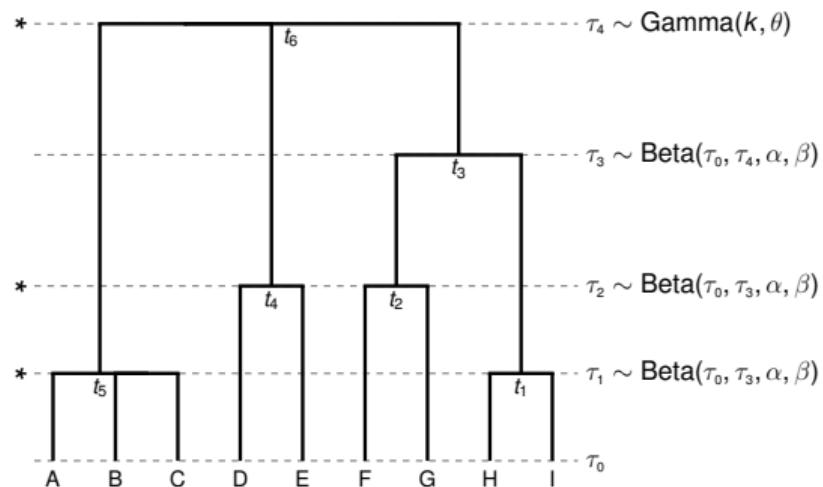
Generalized tree distribution

- ▶ Our current distribution over trees is motivated by mathematical convenience



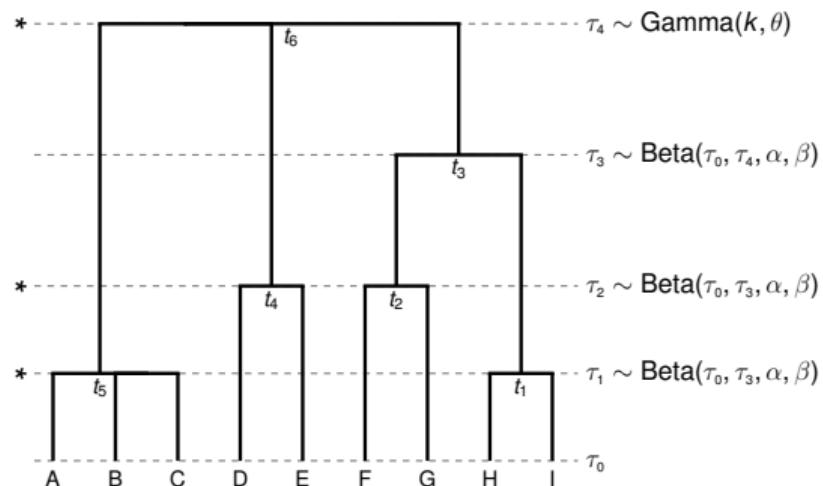
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- ▶ Goal: port M_G algorithms to RevBayes and develop generalized birth-death model

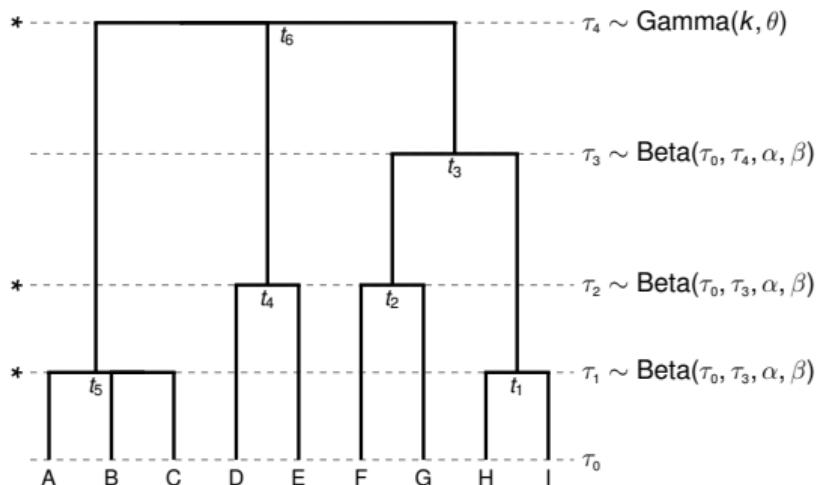


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Sebastian Höhna
LMU Munich

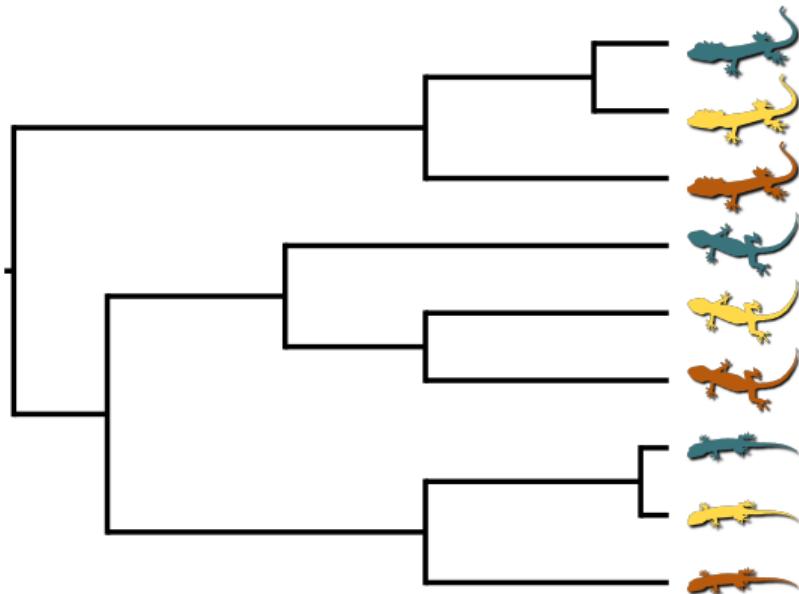


Generalizing the birth-death process

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Birth-death basics:

- ▶ Lineages speciate at rate λ
- ▶ Lineages go extinct at rate μ
- ▶ We sample extant lineages with probability ρ



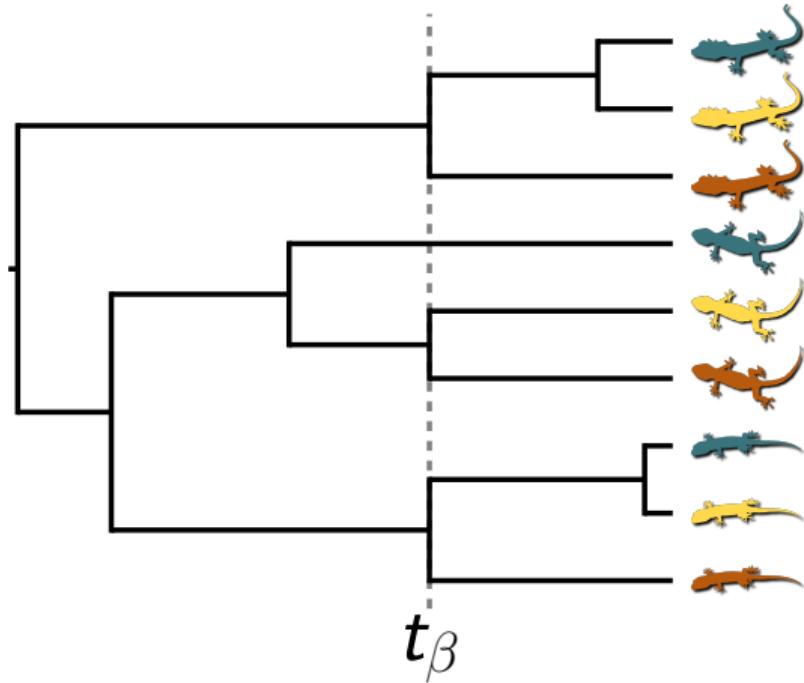
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“Birth-death-burst” (BDB) process:

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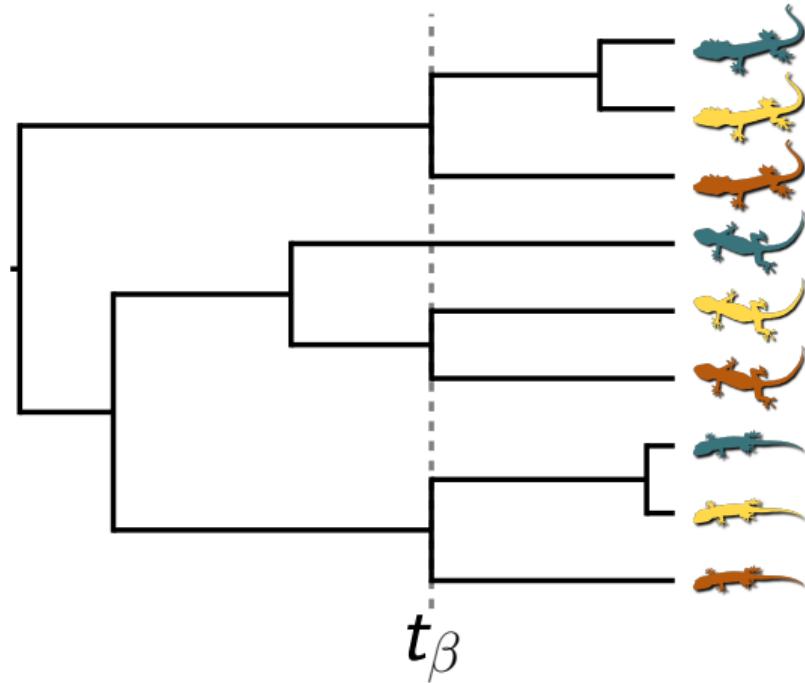
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- ▶ Allow λ , μ , λ_β , & β to vary depending on the traits of lineages across the tree



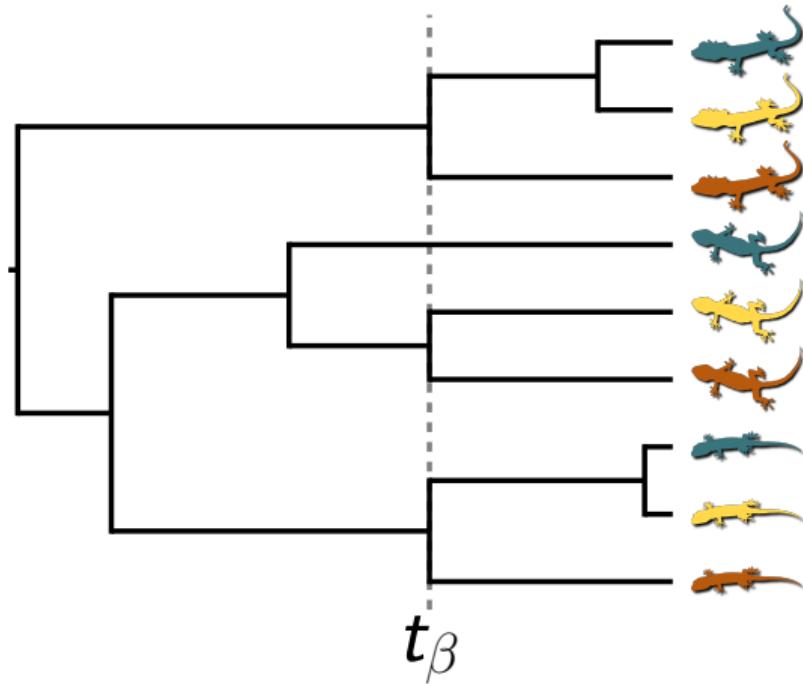
Generalizing the birth-death process

Birth-death basics:

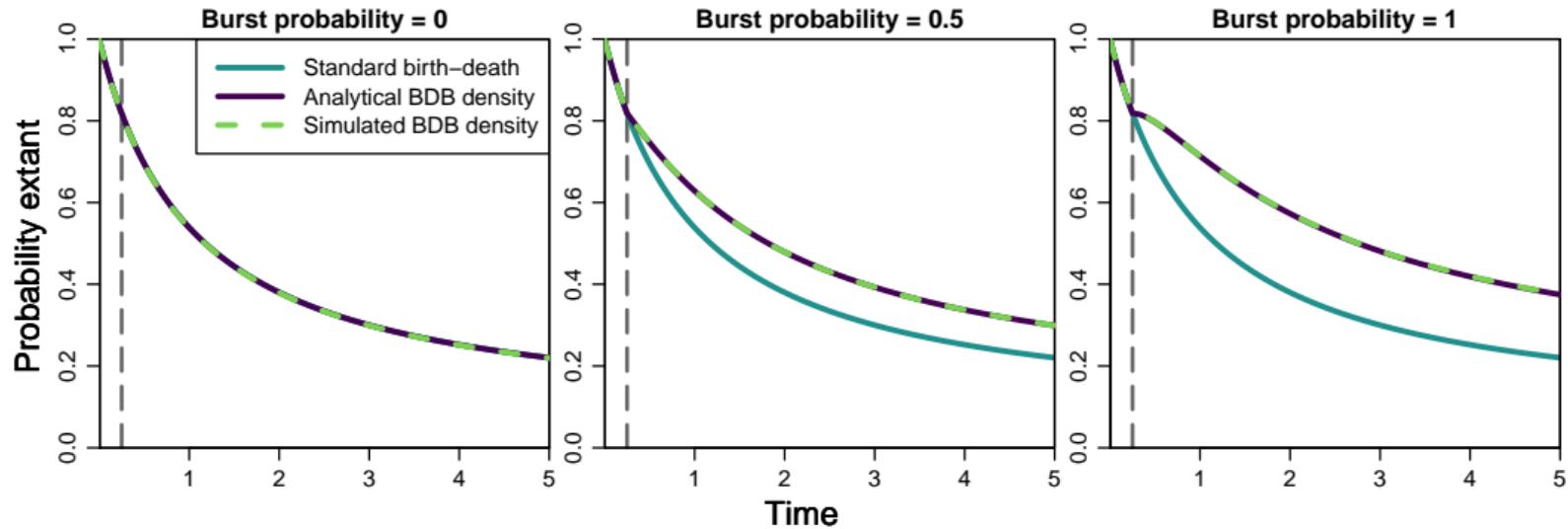
- ▶ Lineages speciate at rate λ
- ▶ Lineages go extinct at rate μ
- ▶ We sample extant lineages with probability ρ

“Birth-death-burst” (BDB) process:

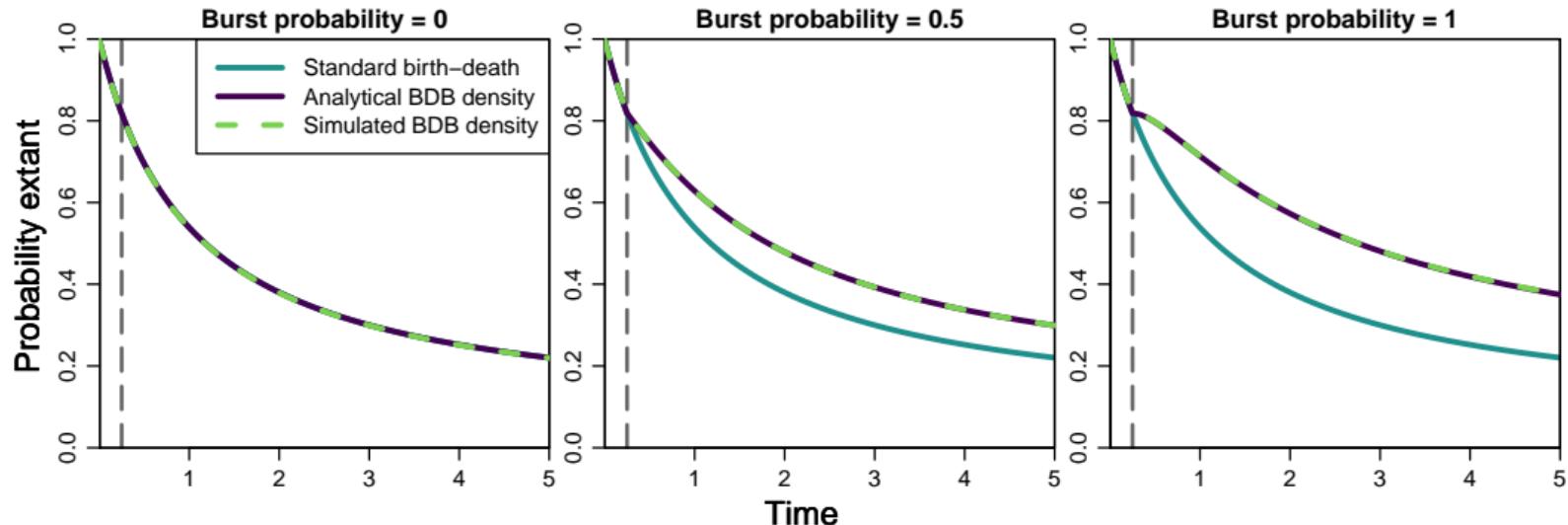
- ▶ Include “burst events” that occur at rate λ_β
- ▶ Each lineage diverges with probability β
- ▶ Allow λ , μ , λ_β , & β to vary depending on the traits of lineages across the tree
- ▶ Bayesian model-averaging to infer set of trait-dependent BDB models that best explain data



Birth-death-burst validation

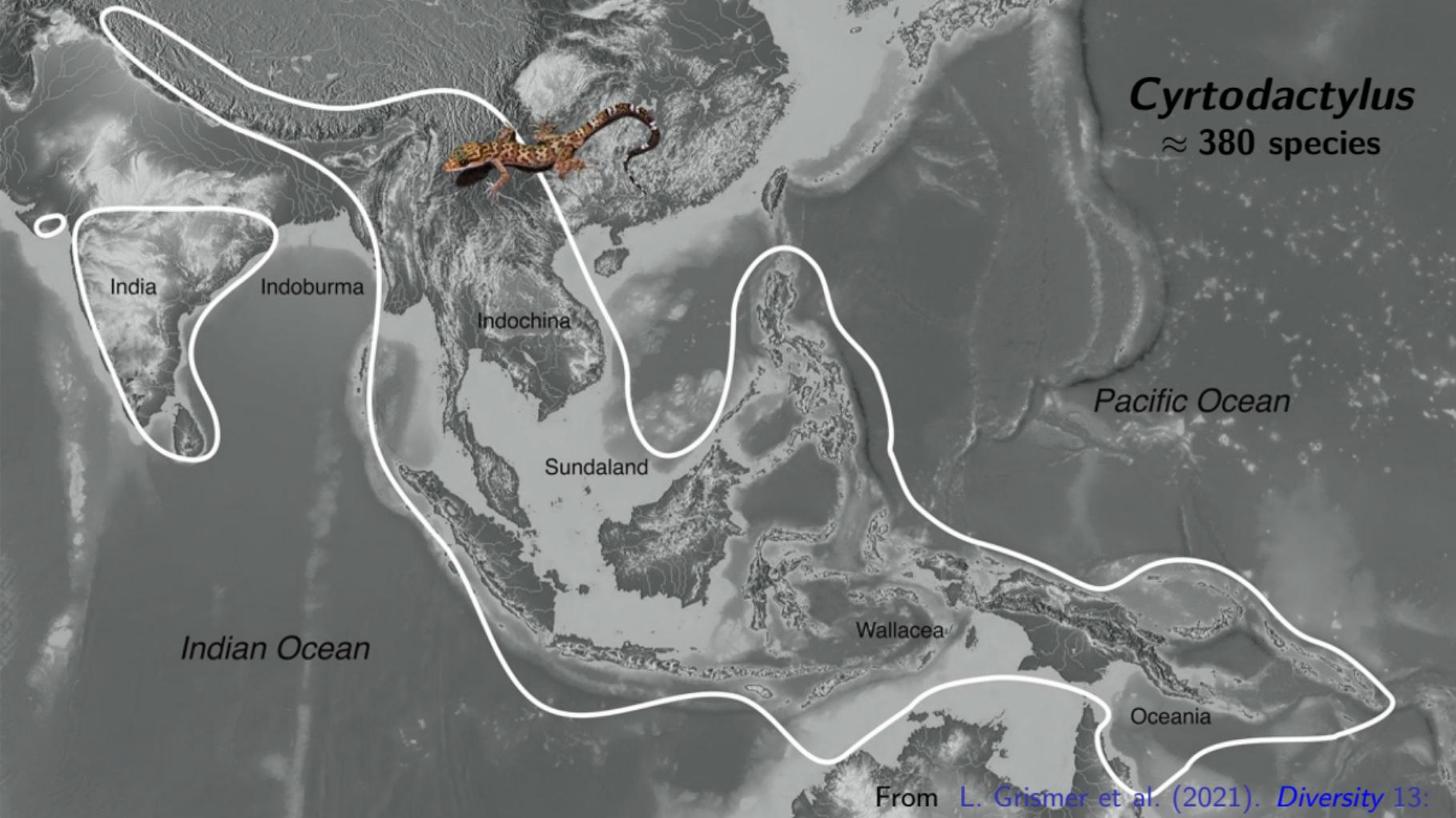


Birth-death-burst validation



We have correctly derived the likelihood of trees under the BDB model

Cyrtodactylus
≈ 380 species



Indian Ocean

India

Indoburma

Indochina

Sundaland

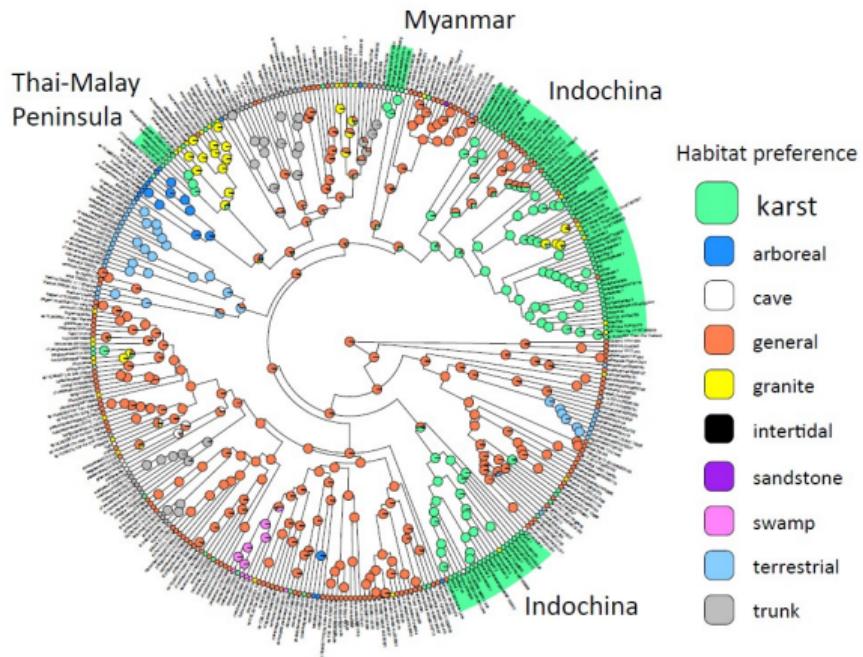
Pacific Ocean

Wallacea

Oceania

Karst endemism in *Cyrtodactylus*

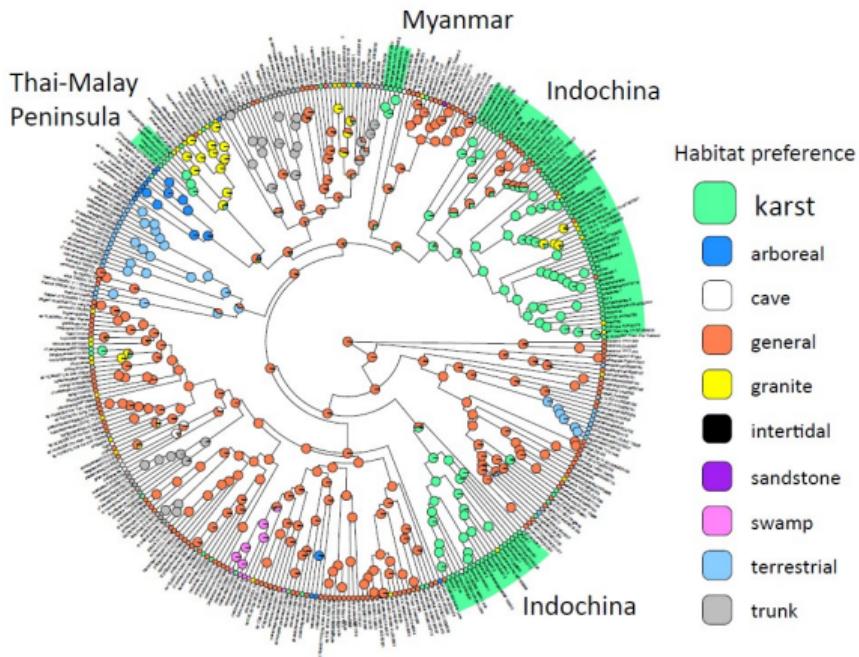
- ▶ *Cyrtodactylus* are ecologically diverse, ranging from generalists to microhabitat specialists



L. Grismer et al. (2021). *Diversity* 13:

Karst endemism in *Cyrtodactylus*

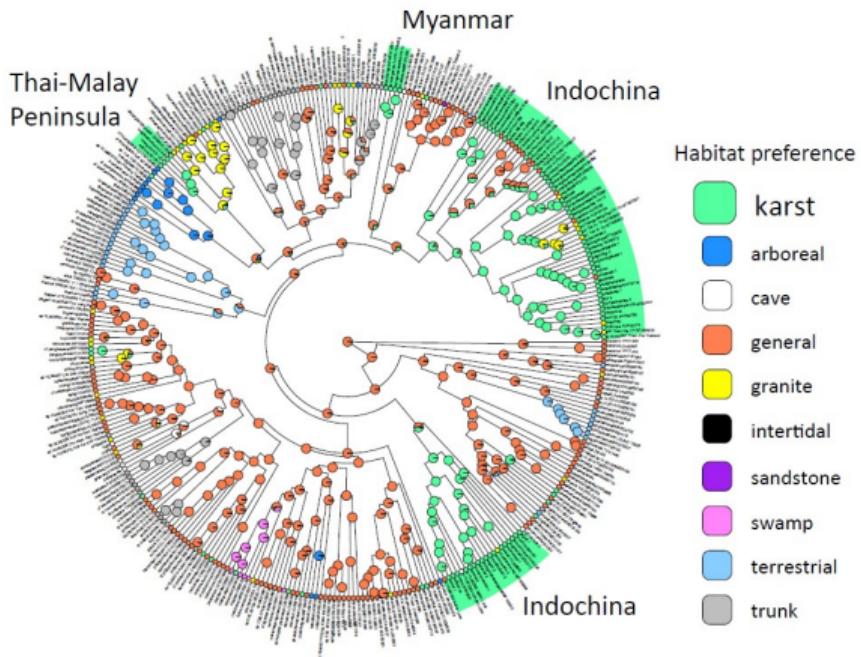
- ▶ *Cyrtodactylus* are ecologically diverse, ranging from generalists to microhabitat specialists
- ▶ Karst-specificity evolved 24 times



L. Grismer et al. (2021). *Diversity* 13:

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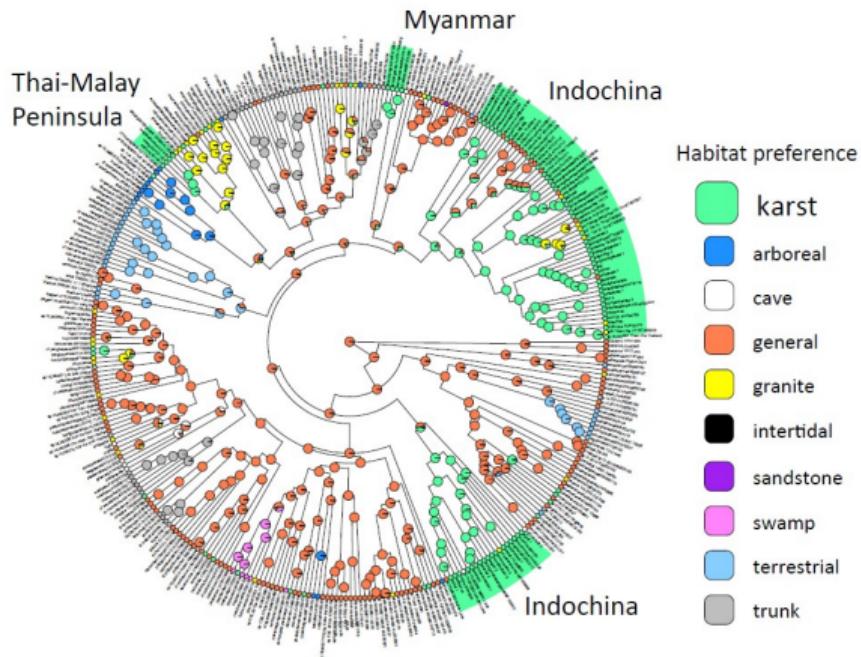
- ▶ *Cyrtodactylus* are ecologically diverse, ranging from generalists to microhabitat specialists
- ▶ Karst-specificity evolved 24 times
- ▶ Comprise 25% of species despite tiny fraction of landscape being karst



L. Grismer et al. (2021). *Diversity* 13:

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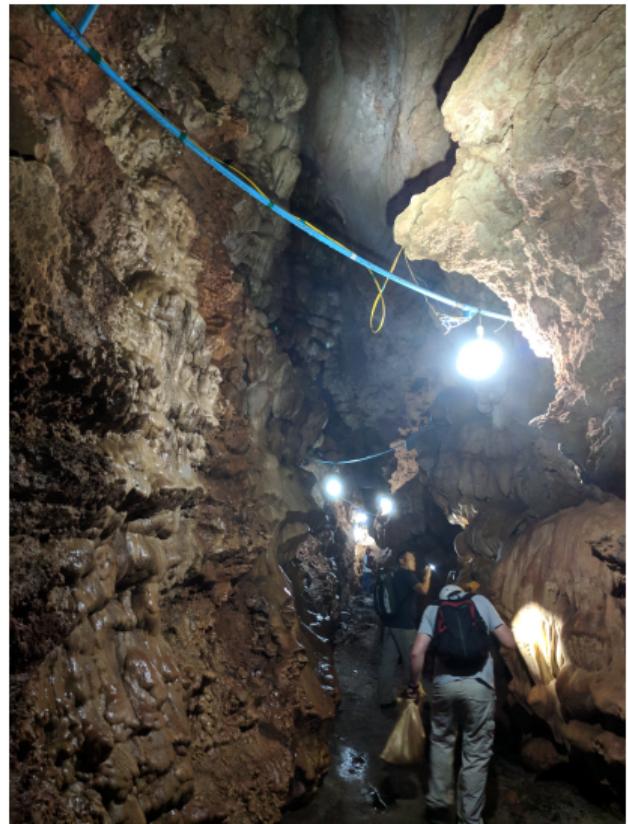
- ▶ *Cyrtodactylus* are ecologically diverse, ranging from generalists to microhabitat specialists
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- ▶ Comprise 25% of species despite tiny fraction of landscape being karst
- ▶ Karst-specific species show remarkable levels of micro-endemism



L. Grismer et al. (2021). *Diversity* 13:





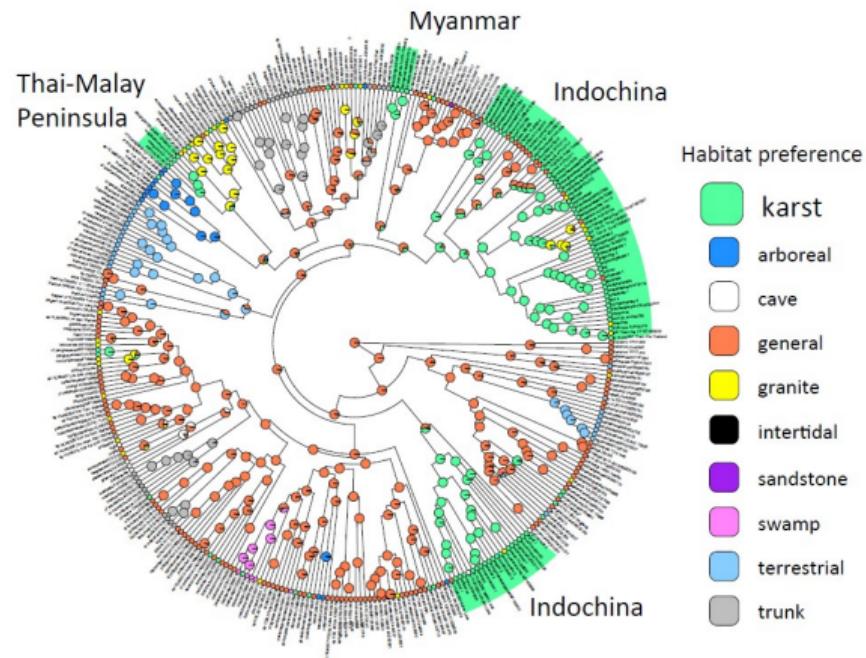




©Perry Wood, Jr.

Why high levels of diversity and endemism on karst?

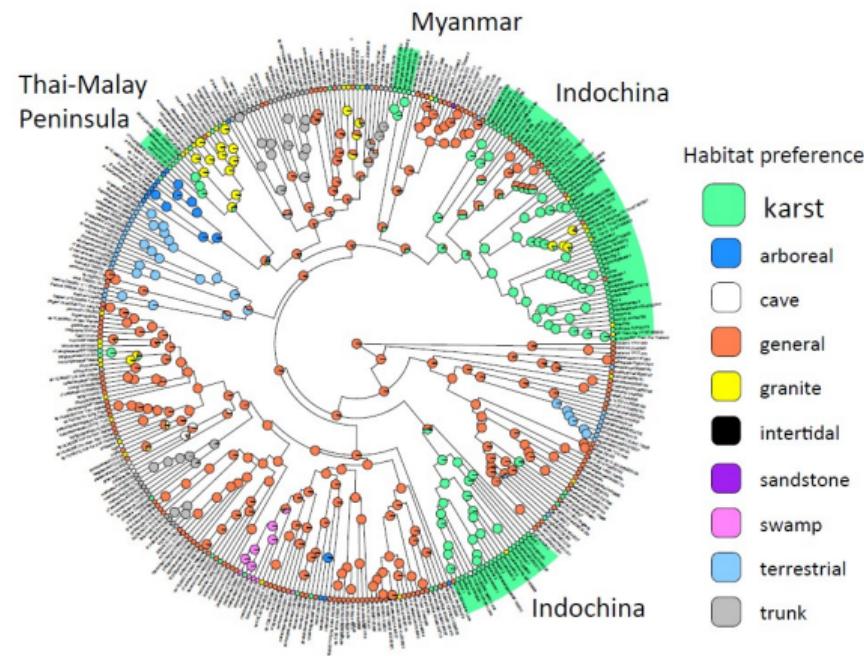
- ▶ “Rapid” fragmentation of karst habitat caused by the uplift and subsequent erosion of limestone sediment over the last 30my



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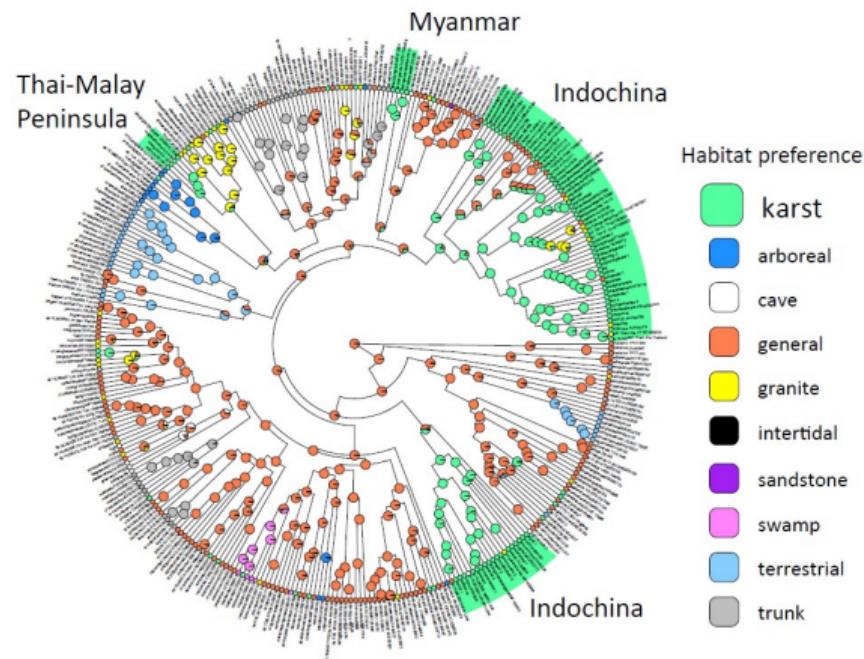
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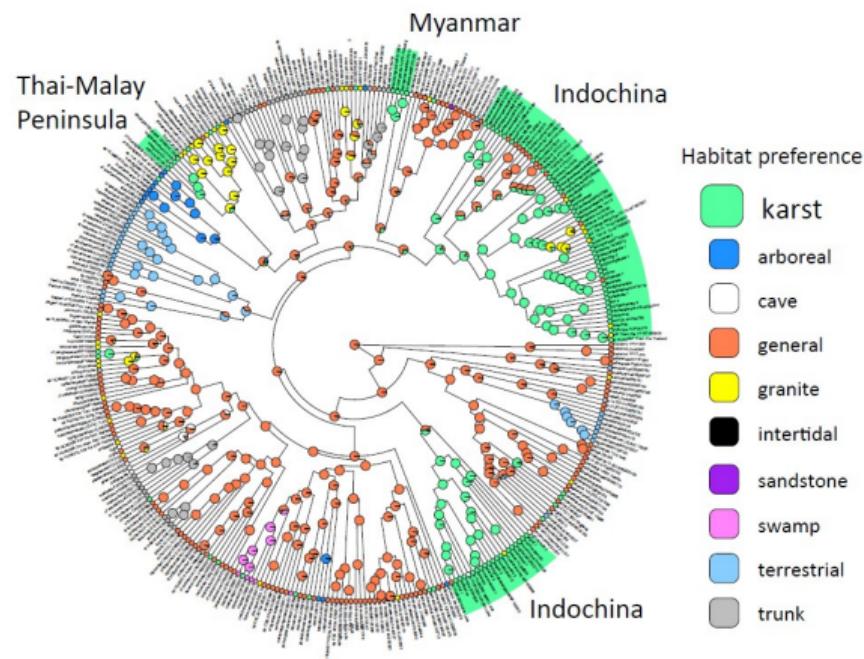
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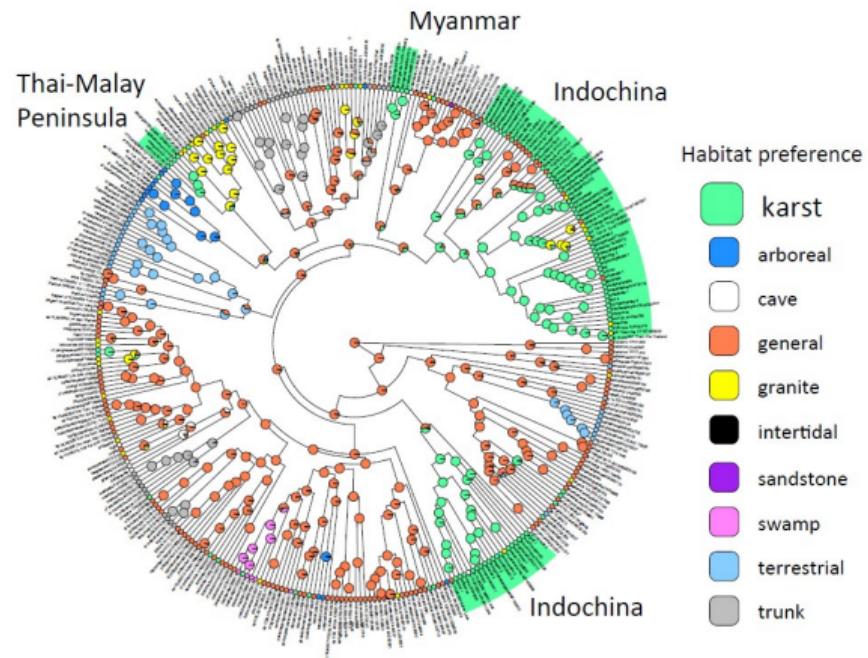
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L. Grismer et al. (2021). *Diversity* 13:

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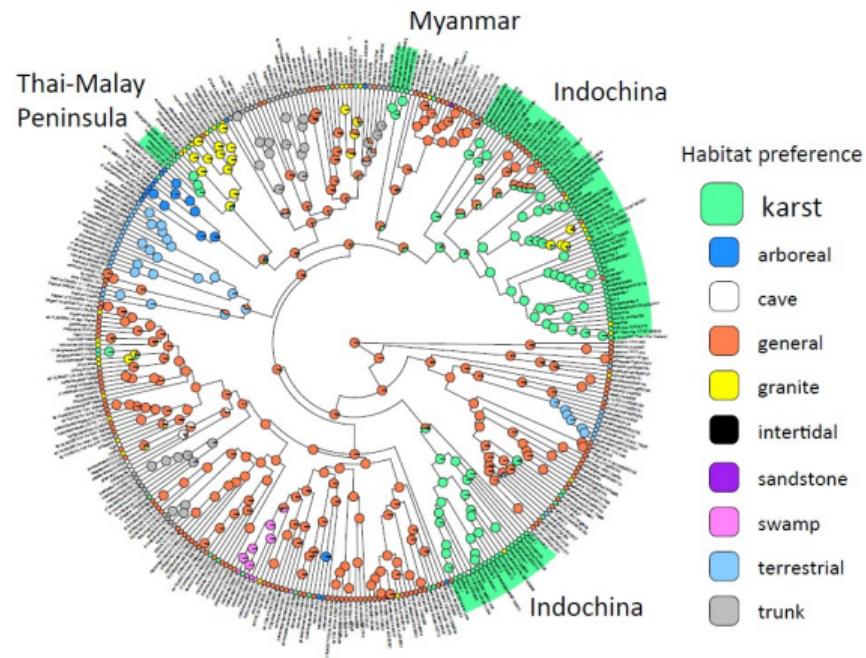
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Plan:

- ▶ Access to tissue samples of 368 of the 380 *Cyrtodactylus* species



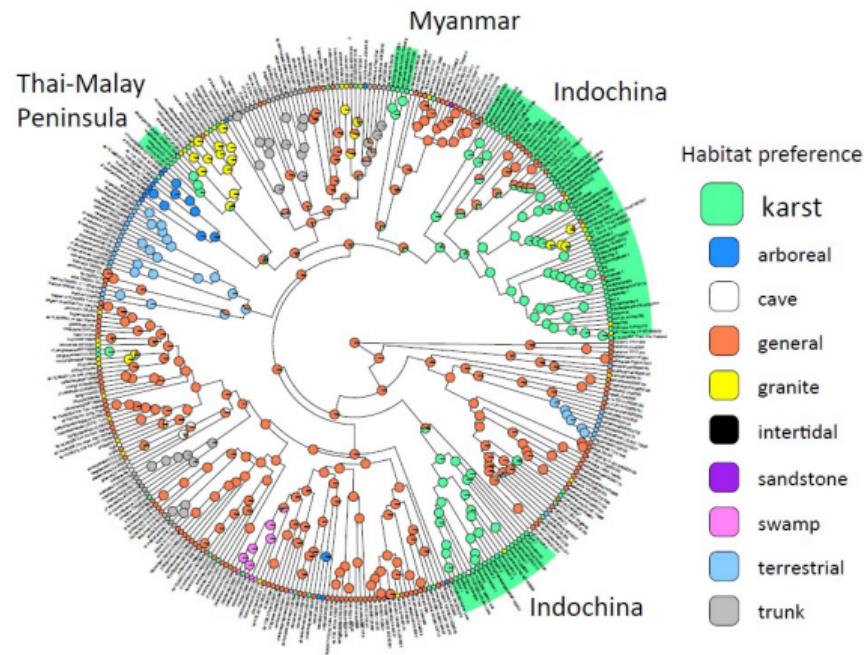
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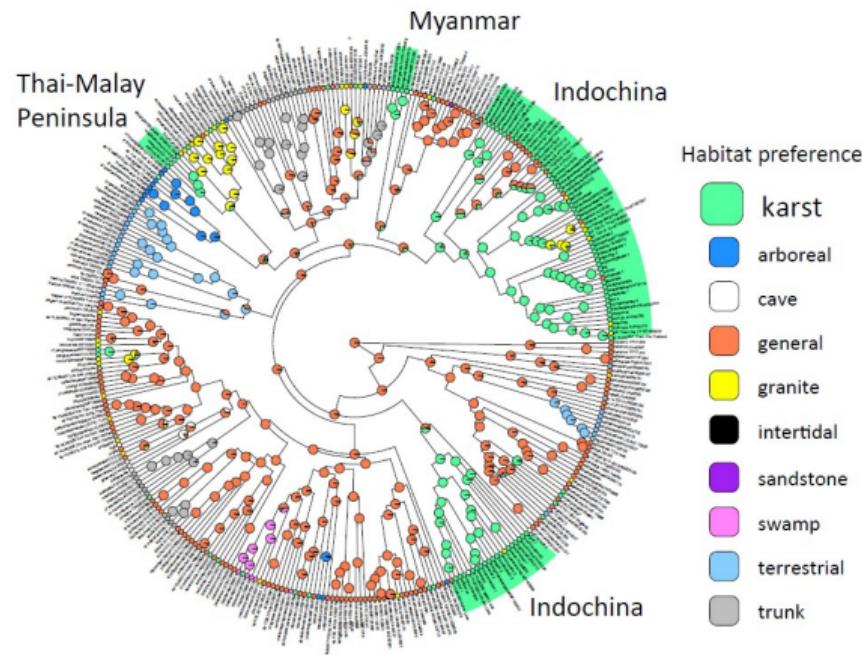
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Model averaging to infer the posterior set of state-dependent models



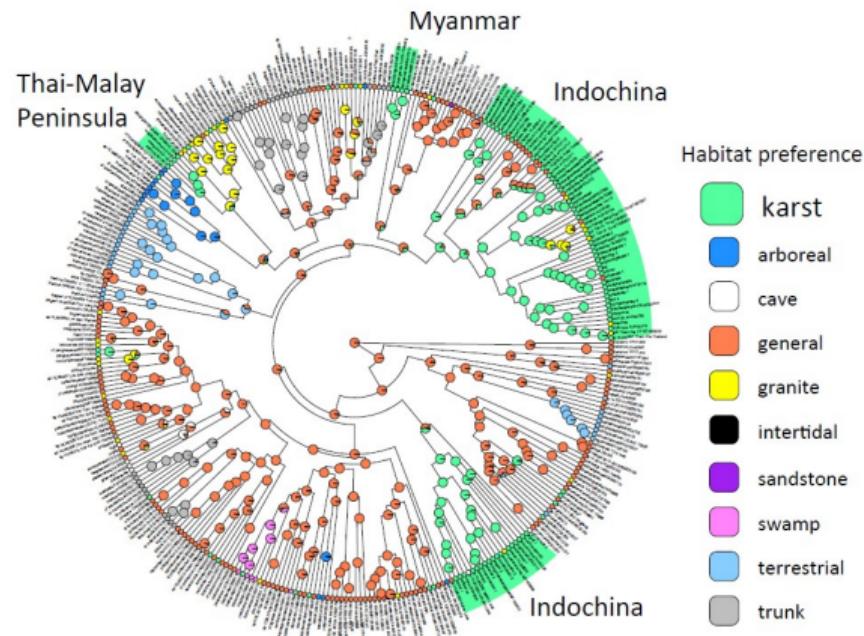
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- ▶ Approximate posterior probability that karst-specific lineages have higher rate of shared divergences (λ_β)

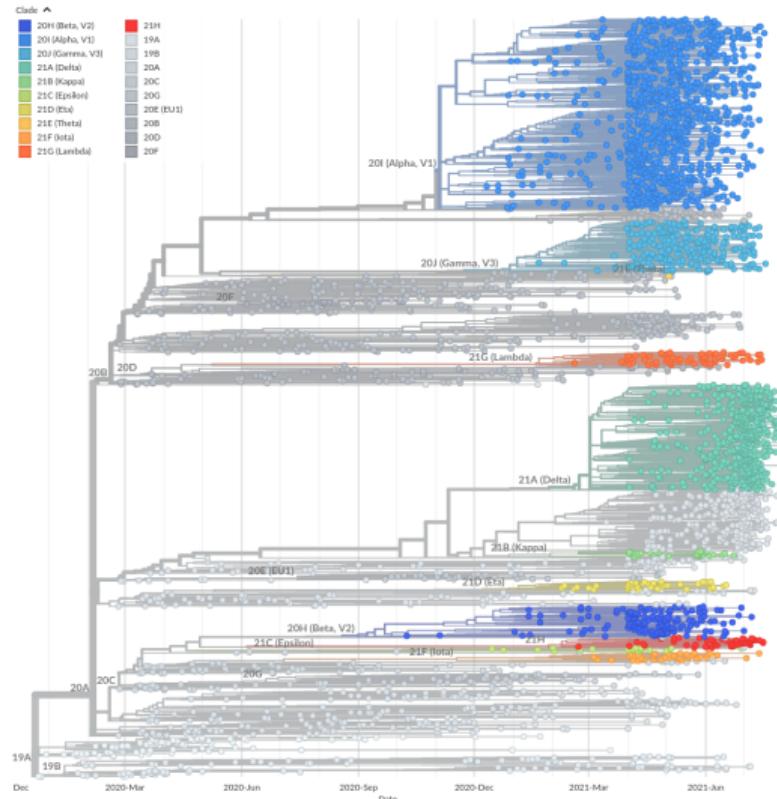


L. Grismer et al. (2021). *Diversity* 13:

Epidemiological dynamics of COVID-19 pandemic

Questions:

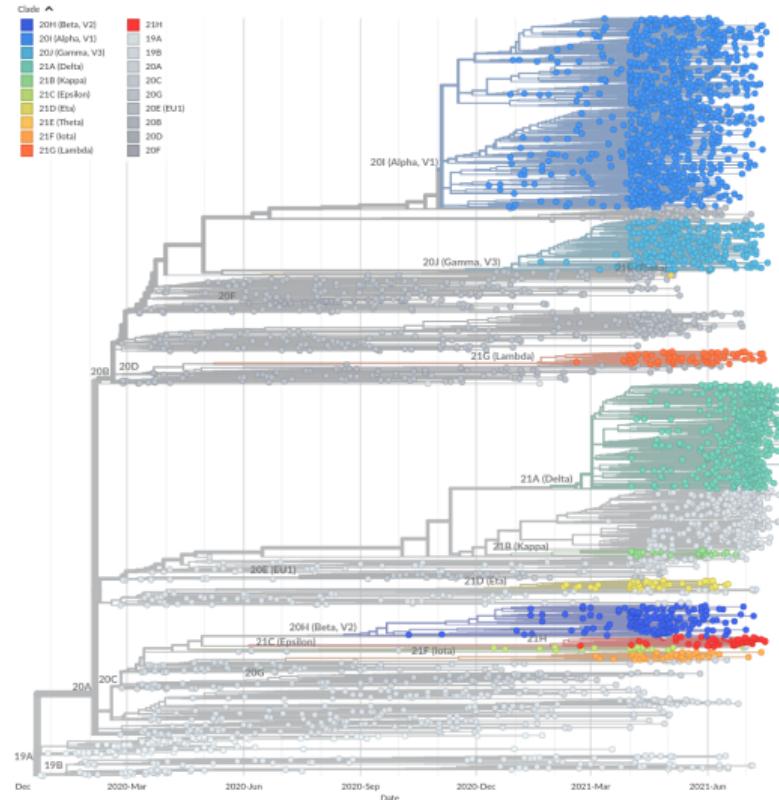
- ▶ What is the relative contribution of social gatherings to the spread of SARS-CoV-2?



Epidemiological dynamics of COVID-19 pandemic

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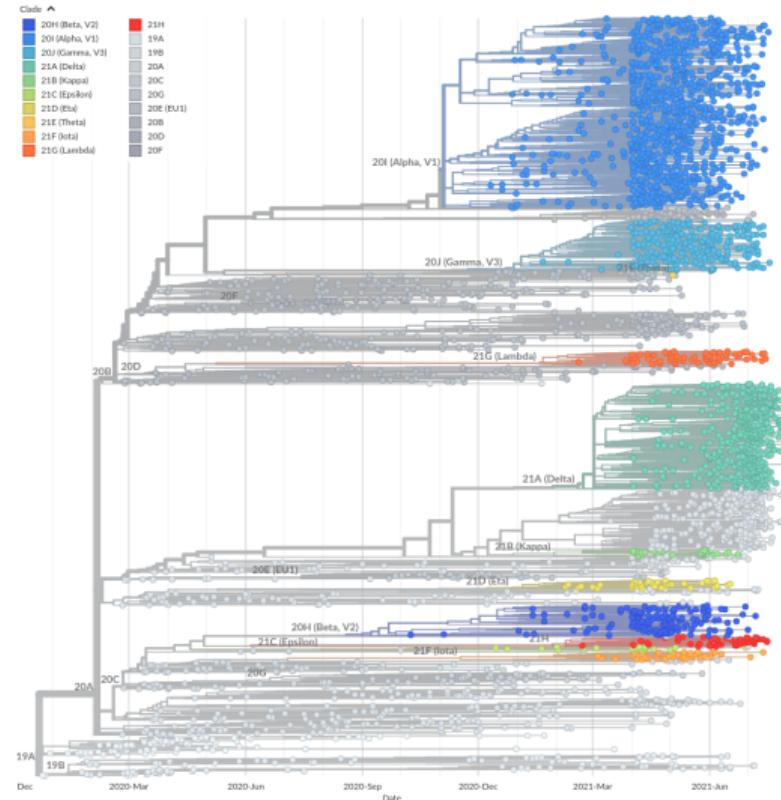
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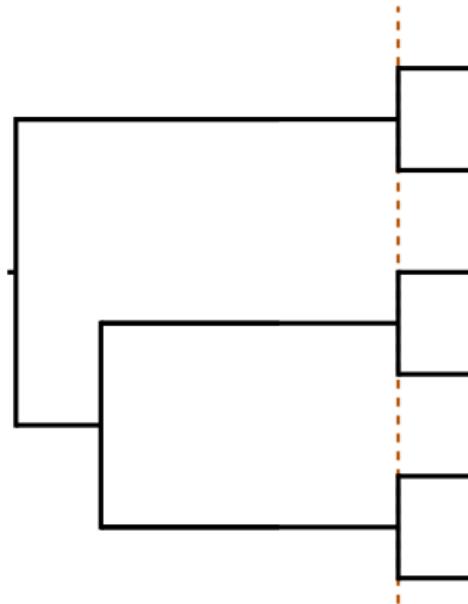
- ▶ What is the relative contribution of social gatherings to the spread of SARS-CoV-2?
- ▶ To what degree does this vary among variants of the virus?
- ▶ To what degree does this increase during holidays?



Divergence patterns predicted by gatherings

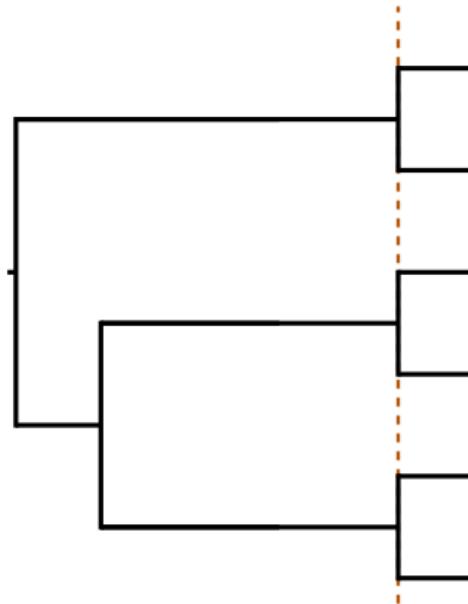
Divergence patterns predicted by gatherings

- ▶ Multiple infected people spreading SARS-CoV-2 at a gathering will create shared divergences across “transmission tree”



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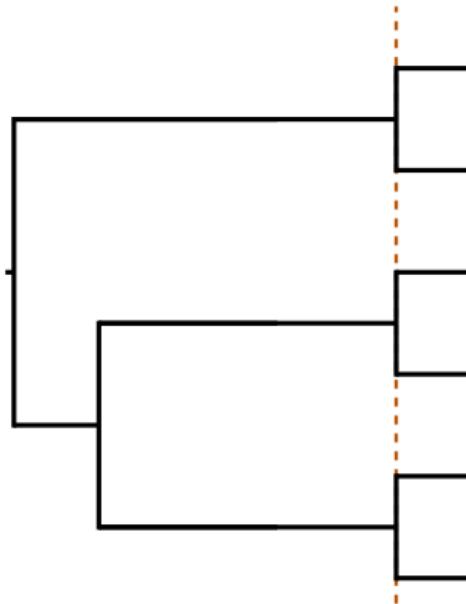
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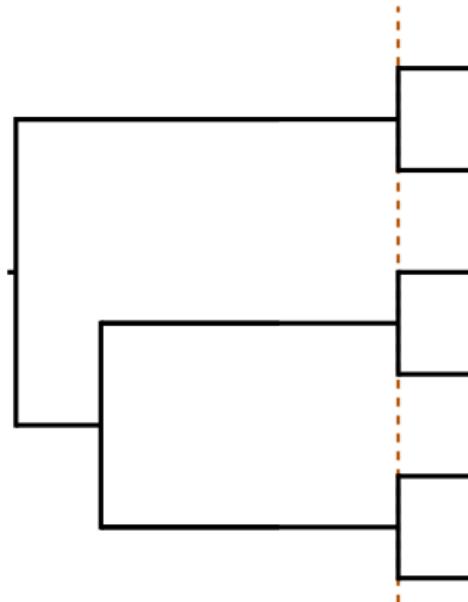


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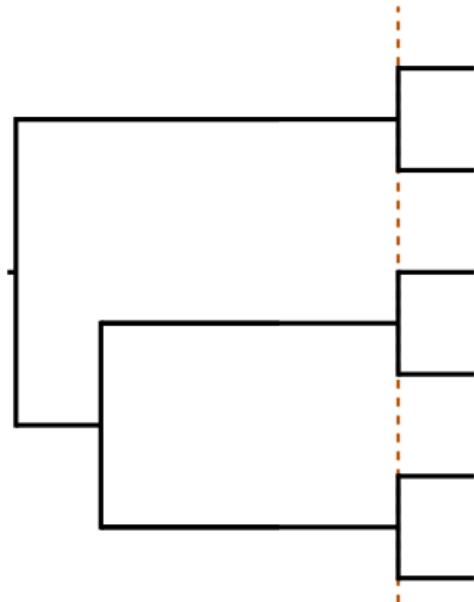


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Plan:

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- ▶ Estimate relative rate of shared divergences (λ_β/λ)

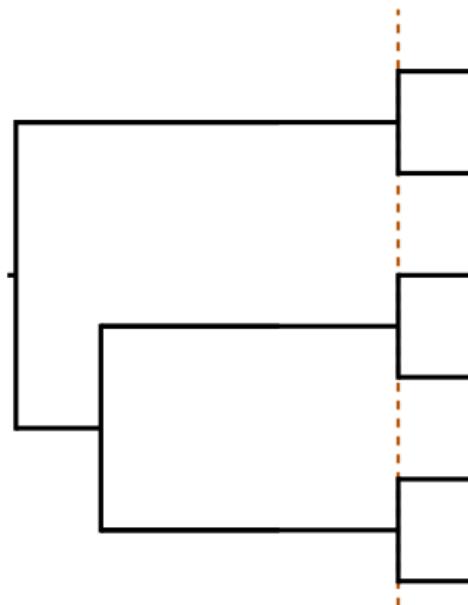


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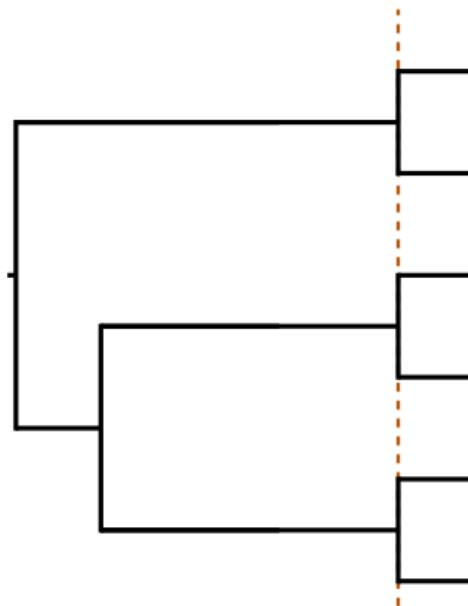


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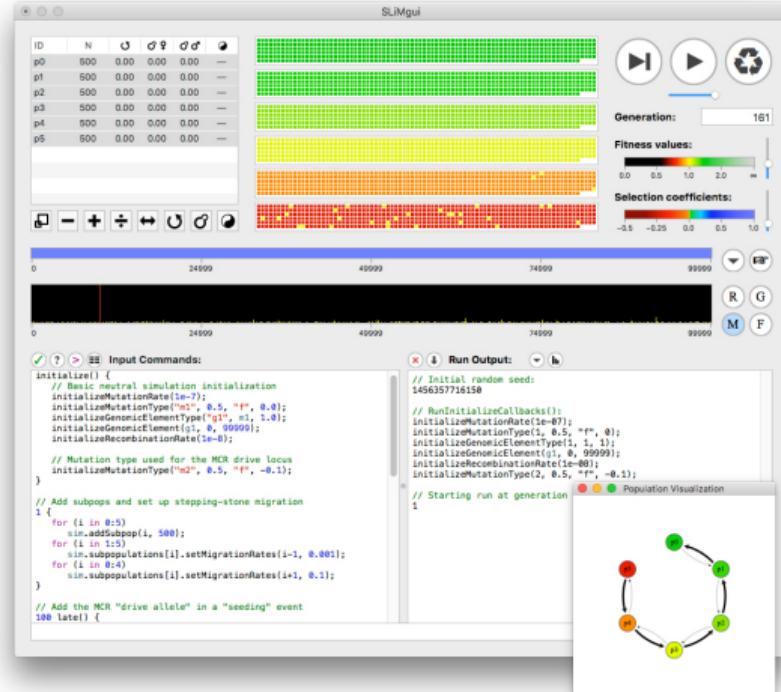
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- ▶ Summarize λ_β over time to quantify the effect of holidays



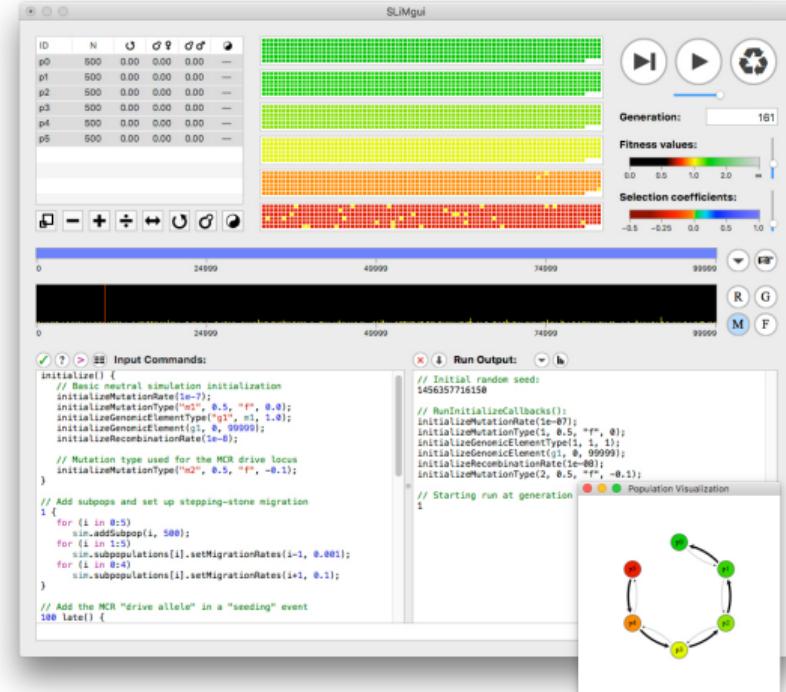
Teaching: Coding to learn evolution

- ▶ Develop coding-to-learn evolution course



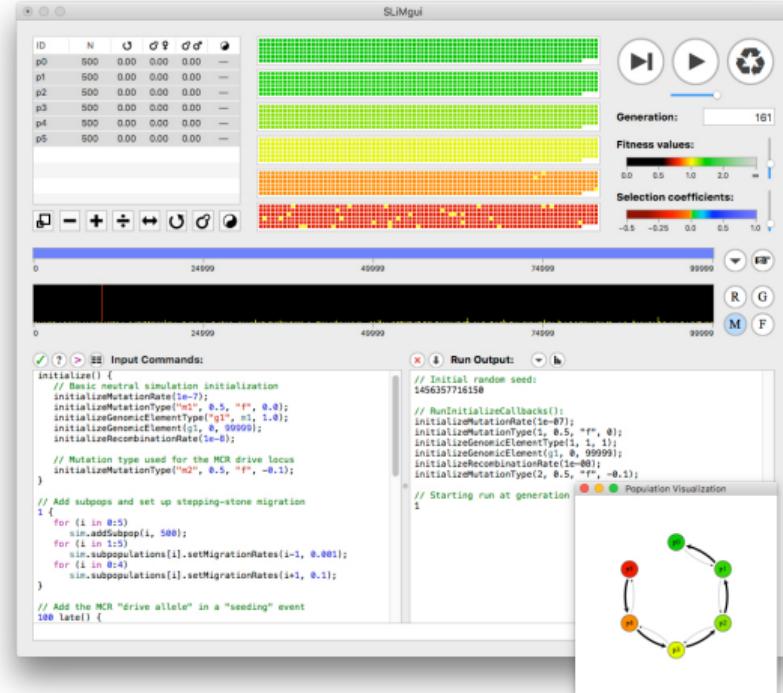
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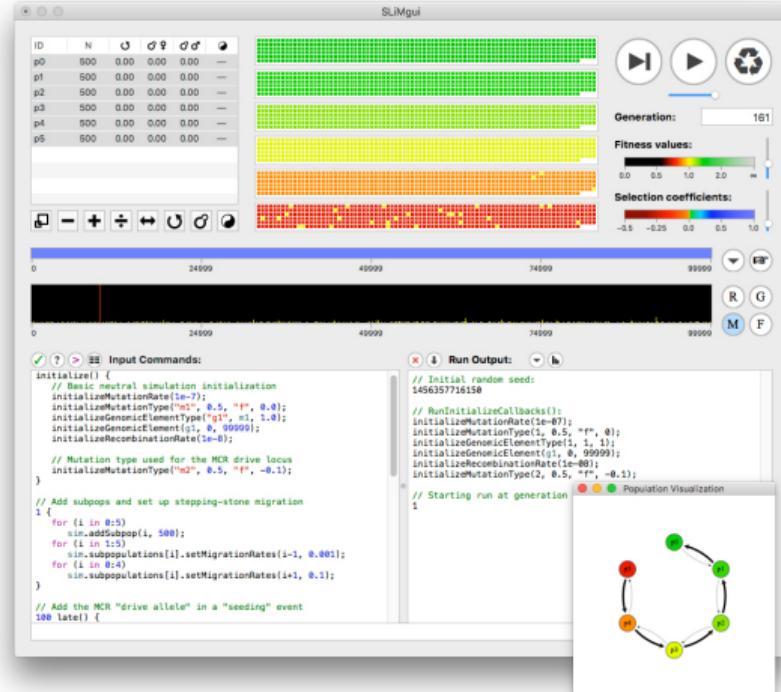
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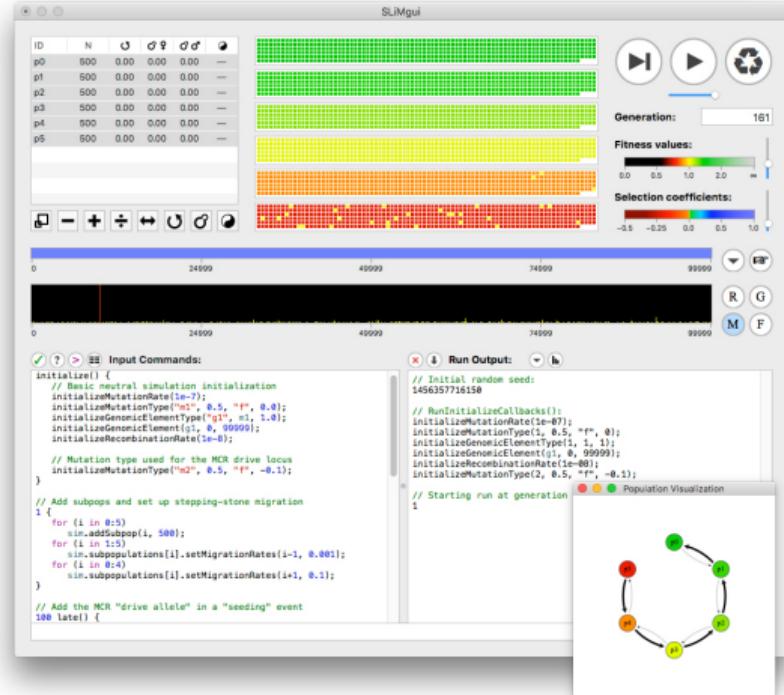
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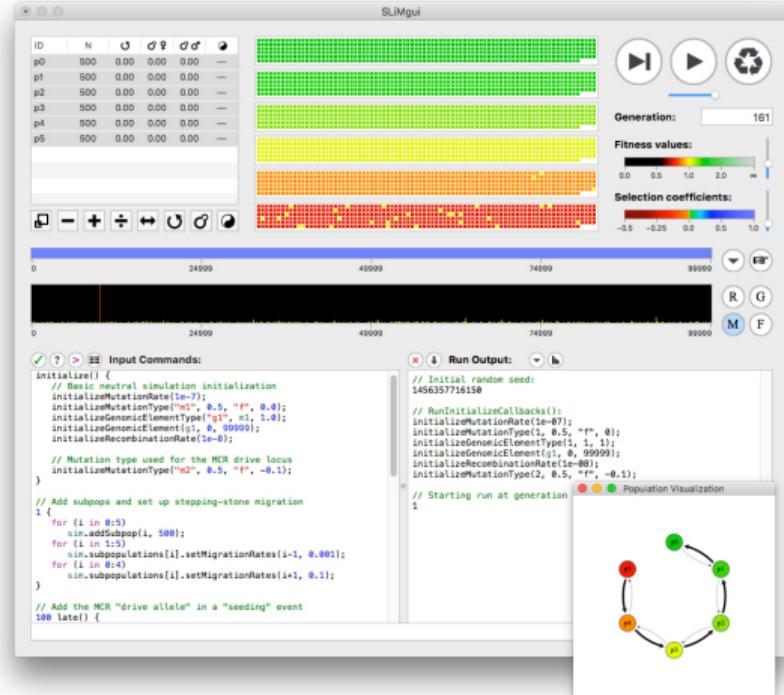
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- ▶ Students co-author paper



Acknowledgments

- ▶ Phyletica Lab (the Phyleticians)
- ▶ Mark Holder
- ▶ Rafe Brown
- ▶ Cam Siler
- ▶ Lee Grismar

Computation:

- ▶ Alabama Supercomputer Authority
- ▶ Auburn University Hopper Cluster

Funding:



DEB 1656004

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- ▶ Rafe Brown
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Questions?

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