

# Generalizing phylogenetics to infer patterns of shared evolutionary events

MIC-Phy 2021

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@jamoaks

**Perry L. Wood, Jr.**

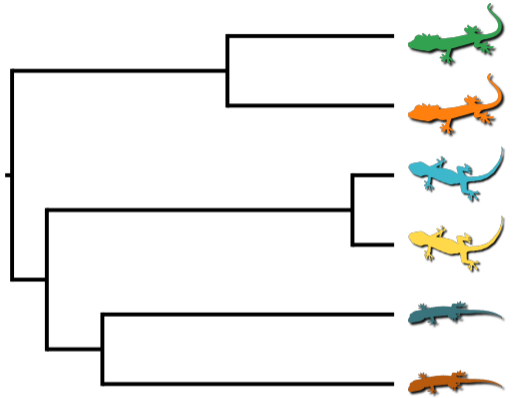
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[perryleewoodjr.com](http://perryleewoodjr.com)

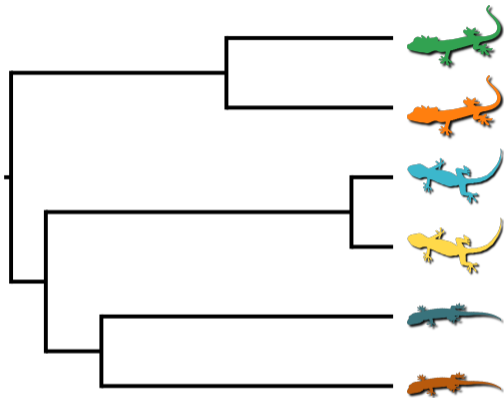
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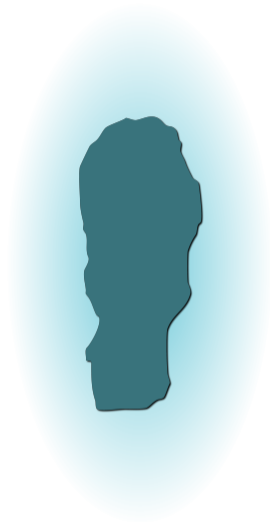
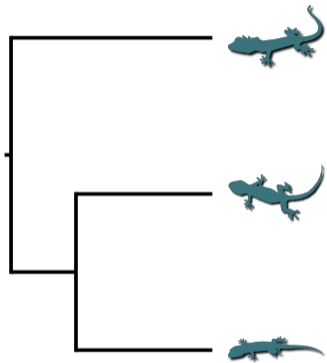


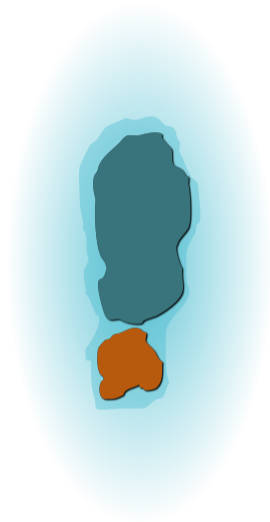
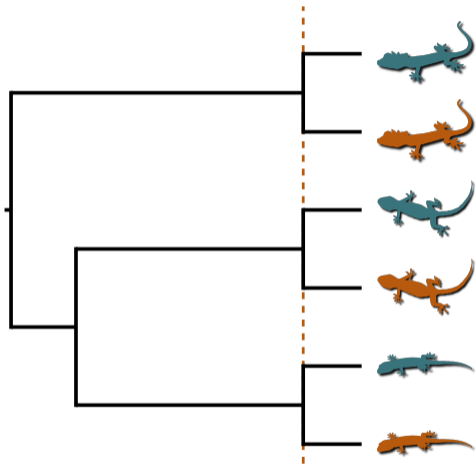
Thanks to MIC-Phy organizers!

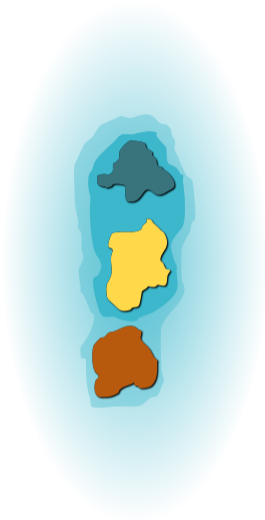
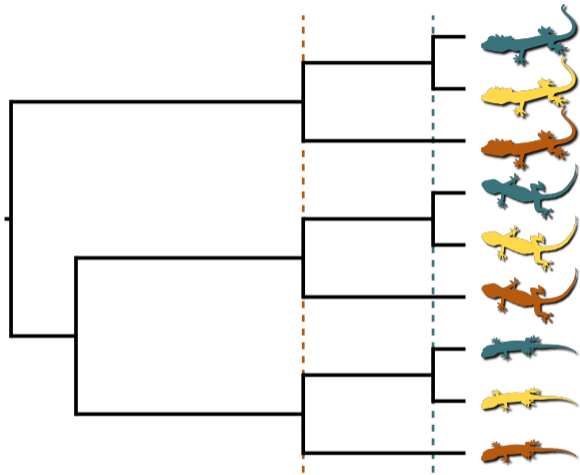


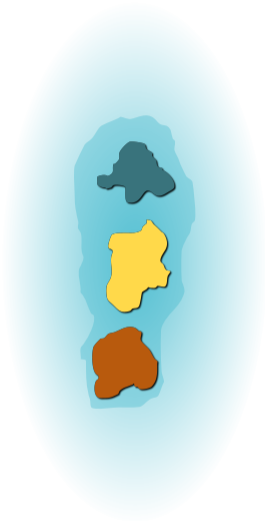
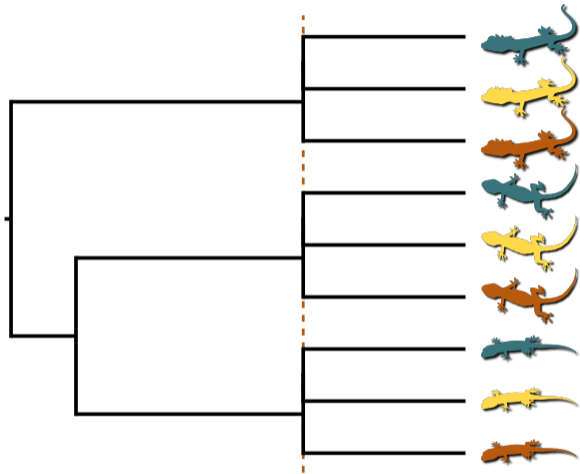
- ▶ **Assumption:** All processes of diversification affect each lineage independently and only cause bifurcating divergences.





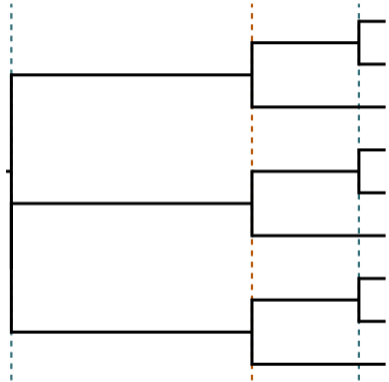






## Biogeography

- ▶ Environmental changes that affect whole communities of species



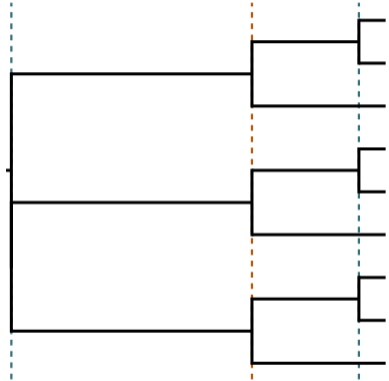


## Biogeography

- ▶ Environmental changes that affect whole communities of species

## Gene family evolution

- ▶ Chromosomal duplications



## Biogeography

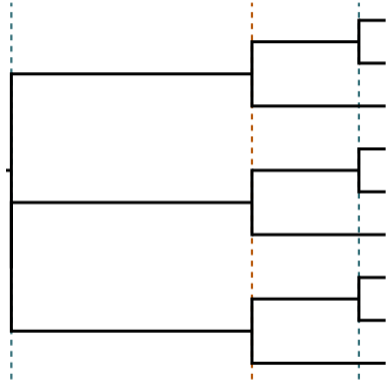
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## Epidemiology

- ▶ E.g., transmission at social gatherings



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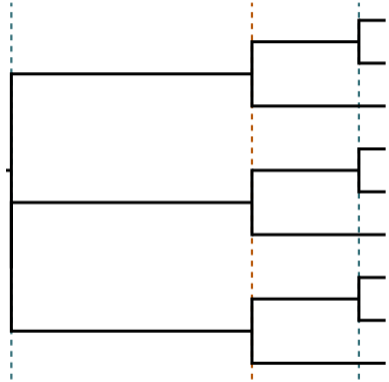
- ▶ Chromosomal duplications

## Epidemiology

- ▶ E.g., transmission at social gatherings

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

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



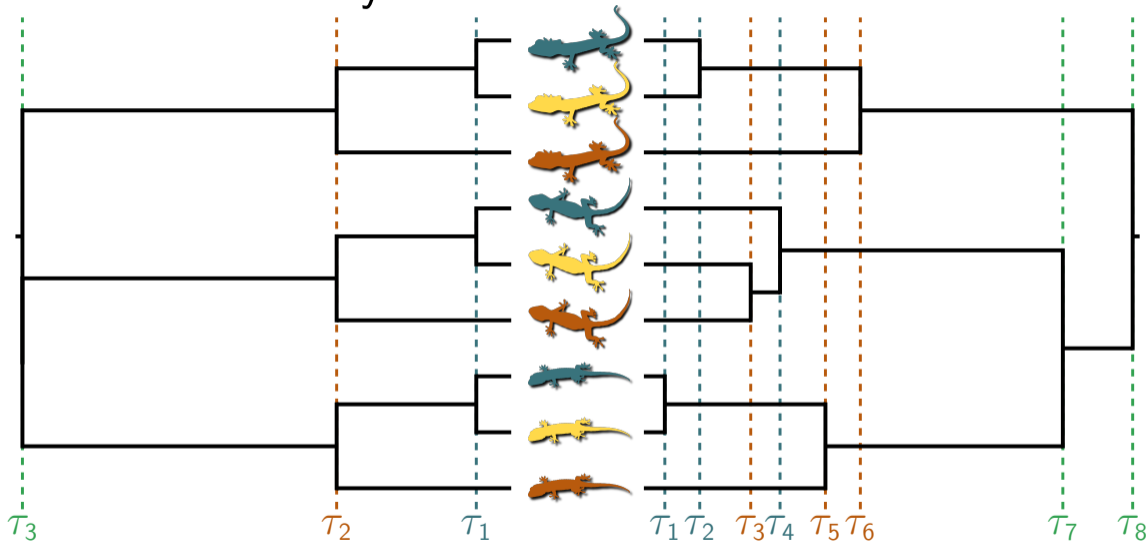
# Why account for shared divergences?

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1. Improve inference

# True history

# Current tree model



# 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

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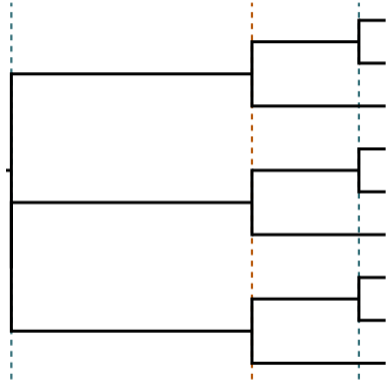
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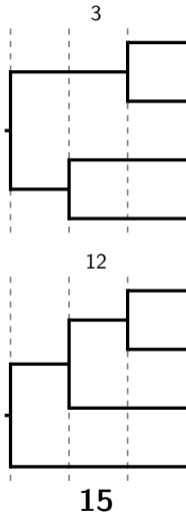
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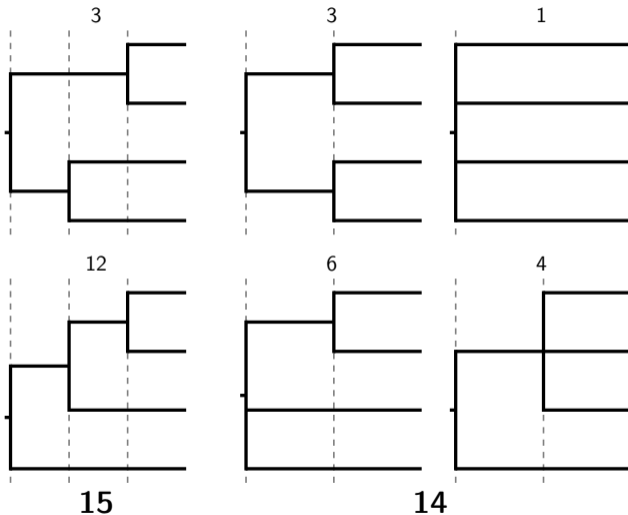


# Generalizing tree space



P. O. Lewis et al. (2005). *Systematic Biology* 54: 241–253

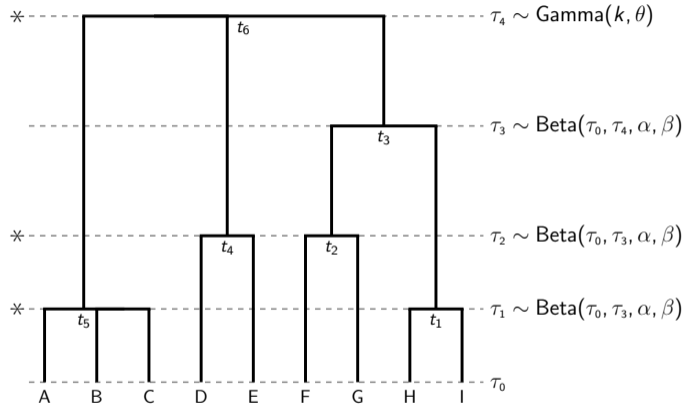
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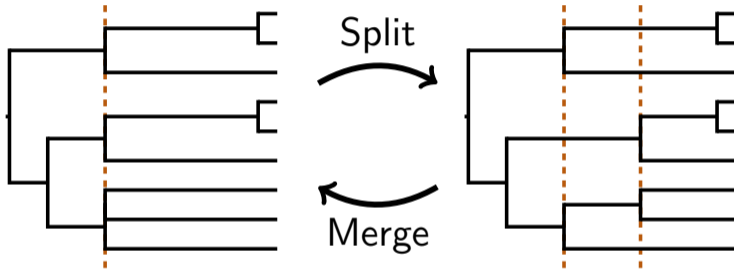
P. O. Lewis et al. (2005). *Systematic Biology* 54: 241–253

# Generalized tree distribution

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

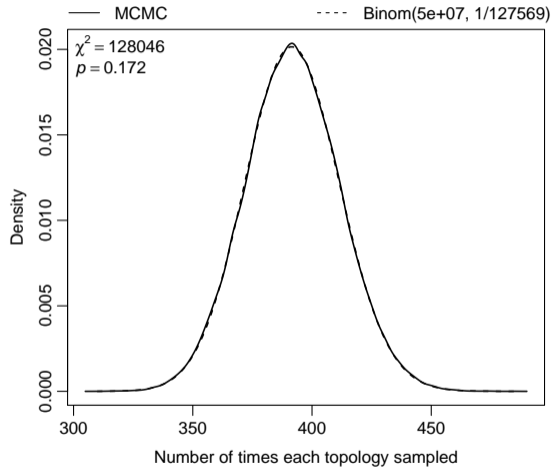


# Bayesian model averaging



Reversible-jump MCMC

# Validating rjMCMC with 7-leaf tree



The rjMCMC algorithms sample the expected generalized tree distribution

# Phycoeval (part of **Ecoevolity**<sup>2</sup>)

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

<sup>2</sup> J. R. Oaks (2019). *Systematic Biology* 68: 371–395

# Phycoeval (part of **Ecoevolity**<sup>2</sup>)

- ▶ CTMC model of characters evolving along genealogies
- ▶ Infer species trees by analytically integrate over genealogies<sup>1</sup>
- ▶ rjMCMC sampling of generalized tree distribution

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- ▶ *Goal: Co-estimation of phylogeny and shared divergences from genomic data*

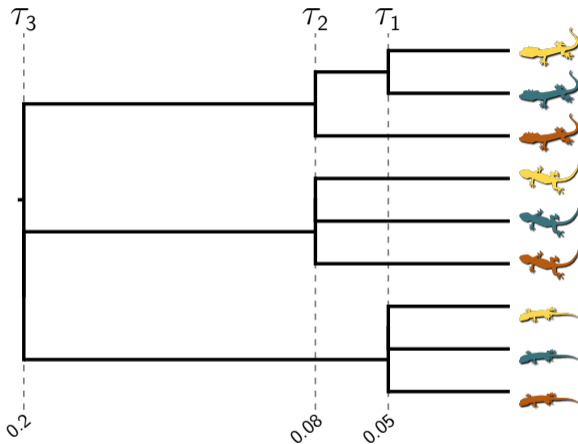
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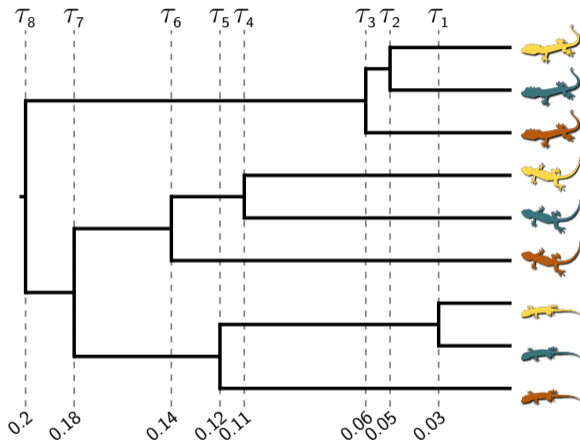
# Methods: Simulations

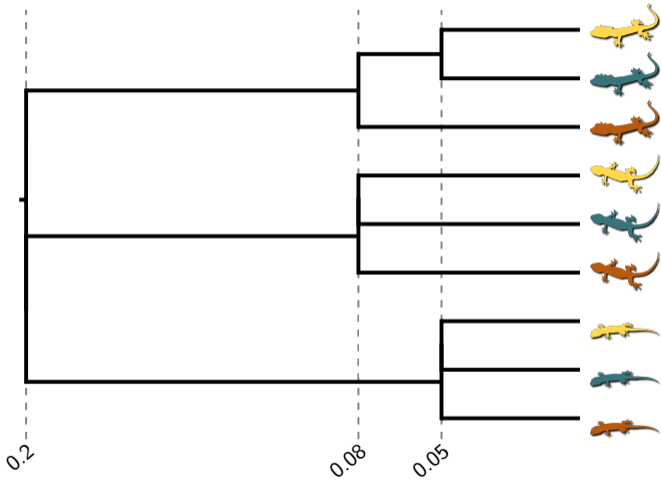
- ▶ Simulated 100 datasets with 50,000 characters
- ▶ Strict clock
- ▶ One population size
- ▶ We also did simulations where topology and div times drawn from prior

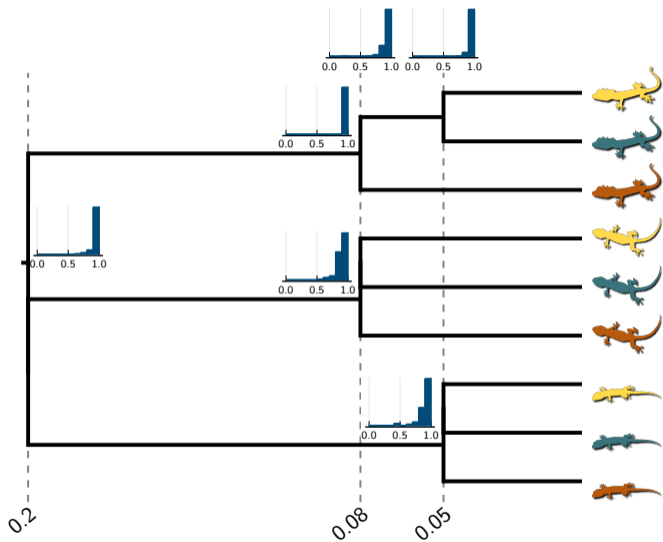


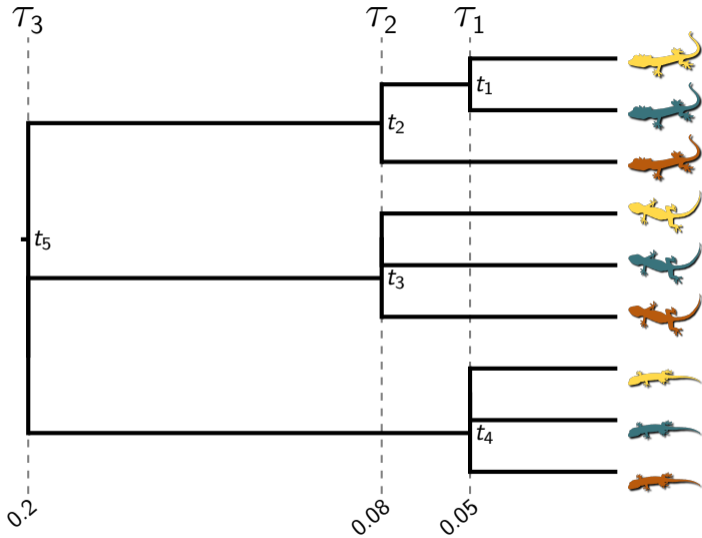
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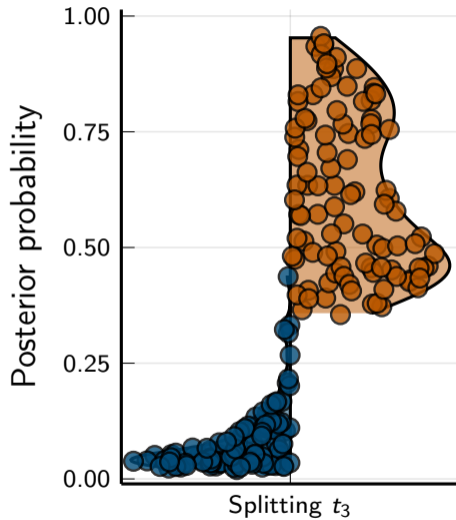
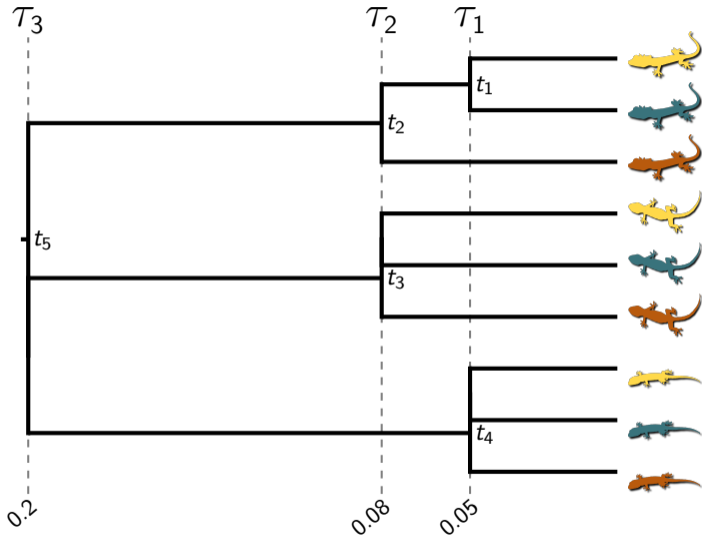




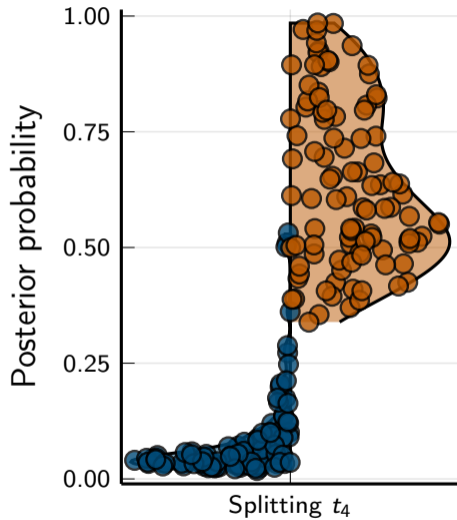
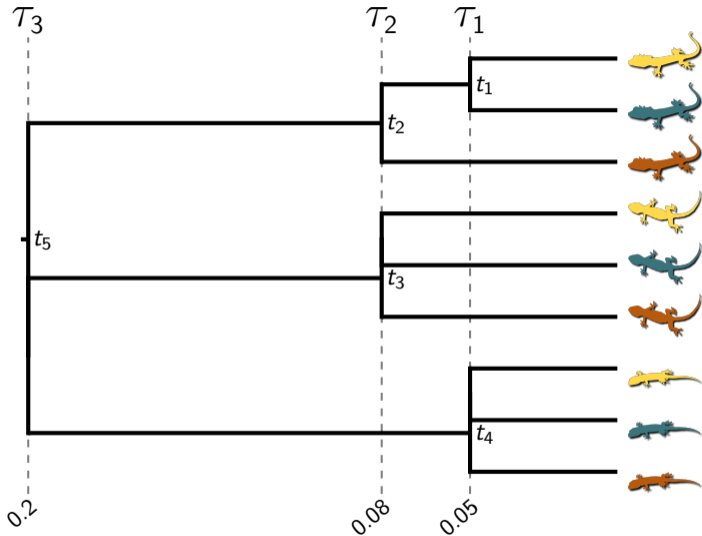




● Generalized ● Bifurcating

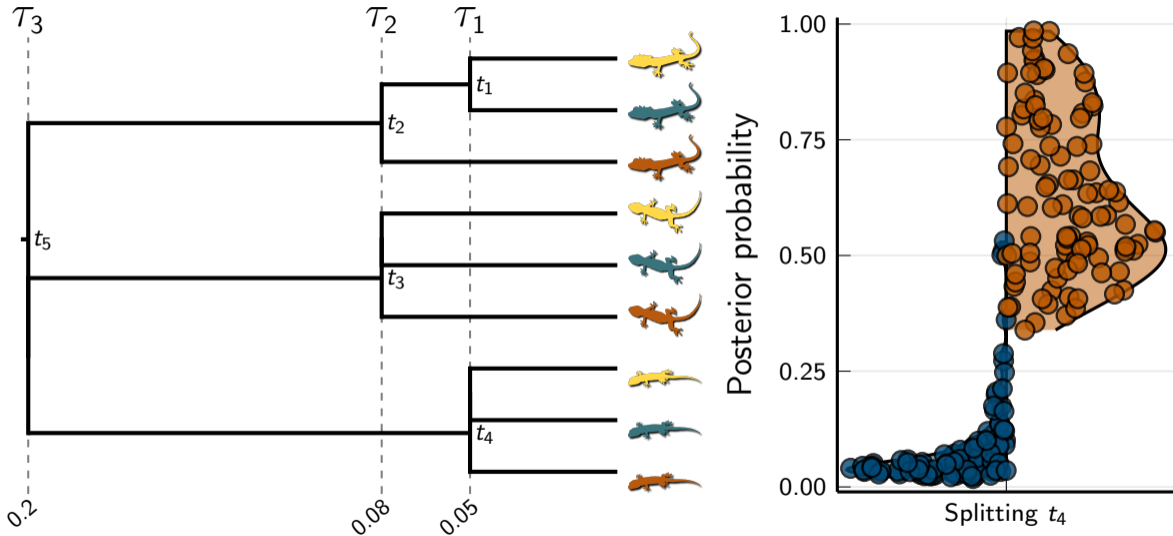


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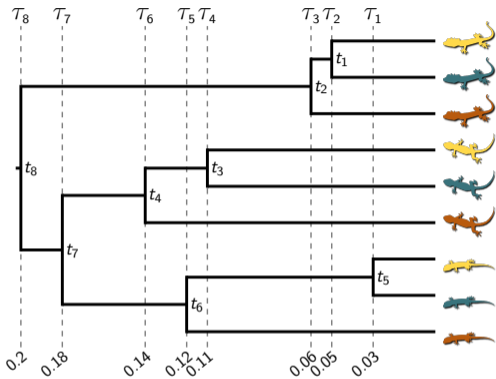


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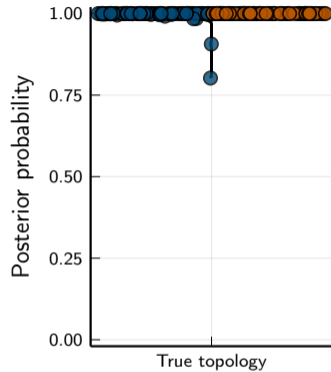
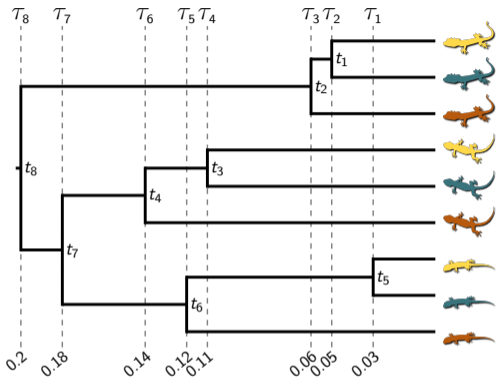


New method avoids spurious support for non-existent branches

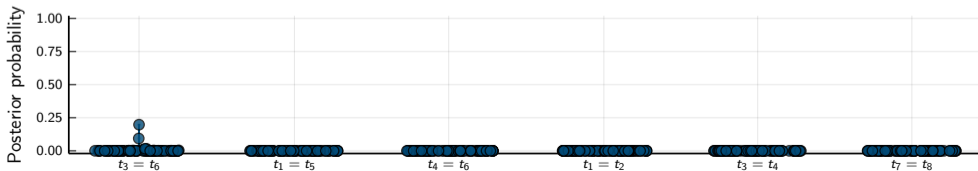
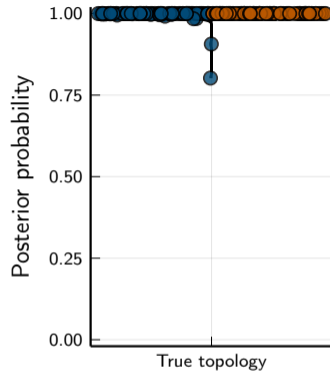
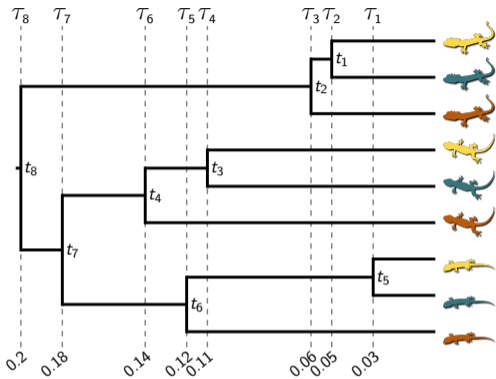
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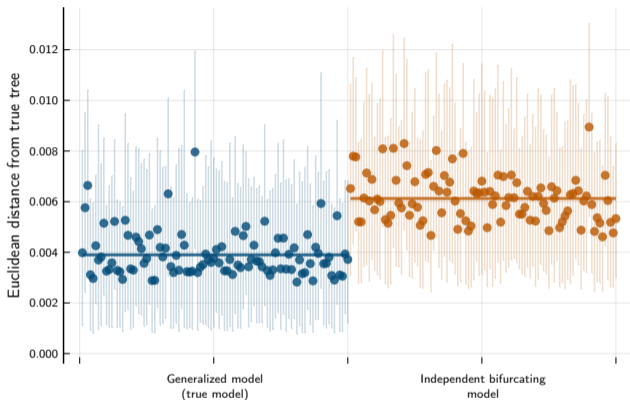
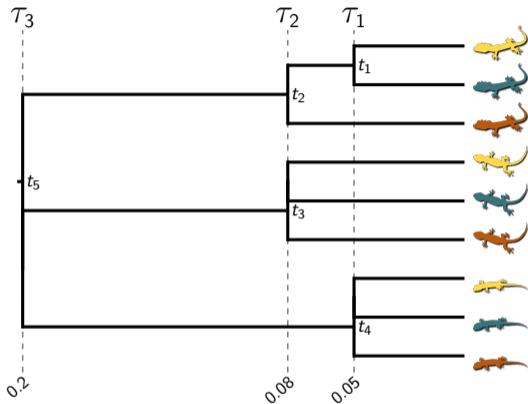
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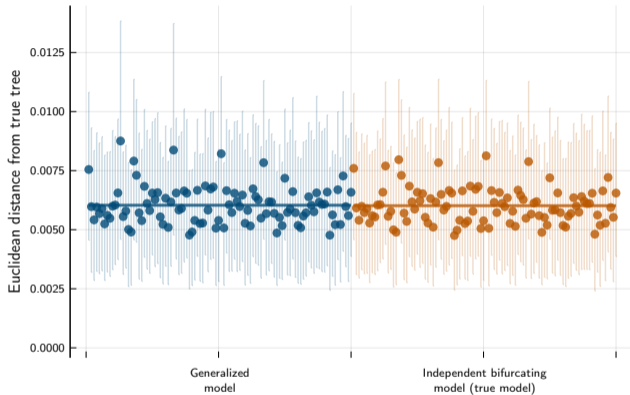
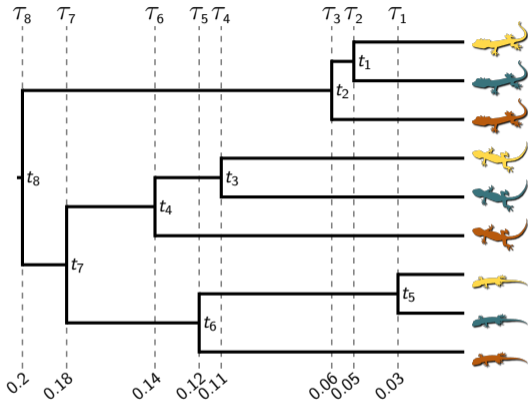


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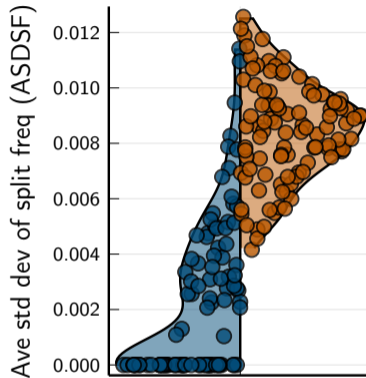
Wilcoxon signed-rank test P-value =  $4.08e^{-18}$

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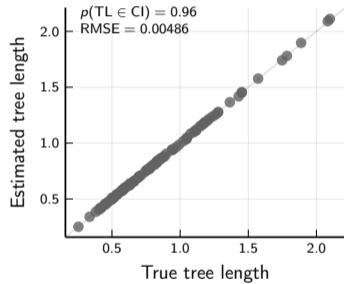
Wilcoxon signed-rank test P-value = 0.36

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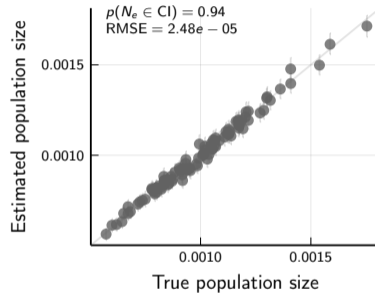
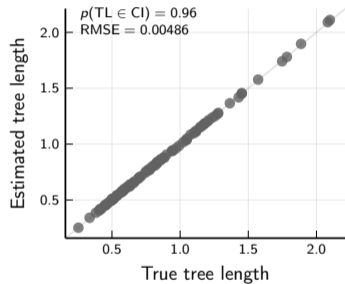
New method improves MCMC convergence and mixing

# Tree-varying simulation results

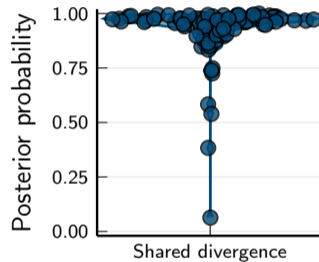
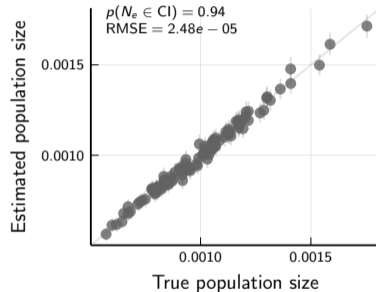
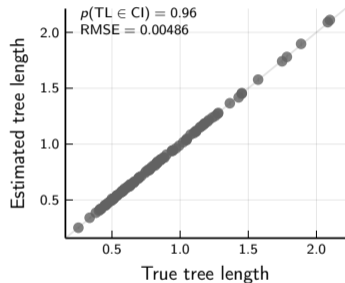




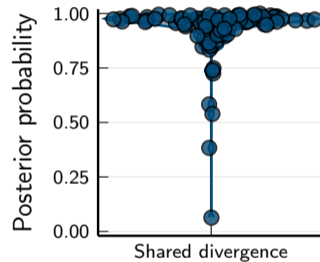
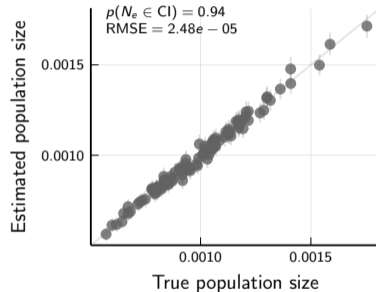
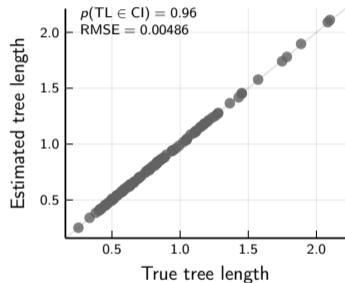
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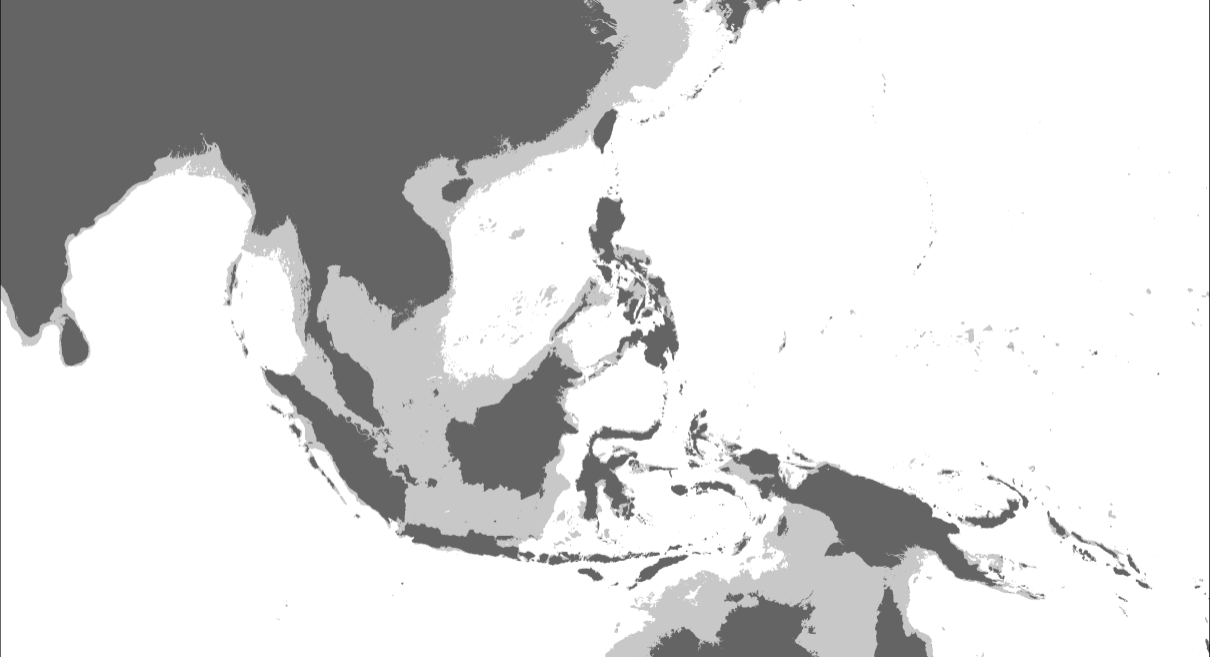


# Tree-varying simulation results



New method perform well with data simulated on random trees







**Did fragmentation of islands  
promote diversification?**



**Did fragmentation of islands  
promote diversification?**



Scan for sea-level animation



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J. R. Oaks et al. (2019). *Evolution* 73: 1151–1167





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- ▶ Sampled individuals from 27 and 26 populations across Philippines for *Cyrtodactylus* and *Gekko*, respectively



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J. R. Oaks et al. (2019). *Evolution* 73: 1151–1167



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- ▶ Sampled individuals from 27 and 26 populations across Philippines for *Cyrtodactylus* and *Gekko*, respectively
- ▶ Collected short DNA sequences (RADseq) from across genome of each individual
  - ▶ *Cyrtodactylus*: 1702 loci & 155,887 sites
  - ▶ *Gekko*: 1033 loci & 94,813 sites

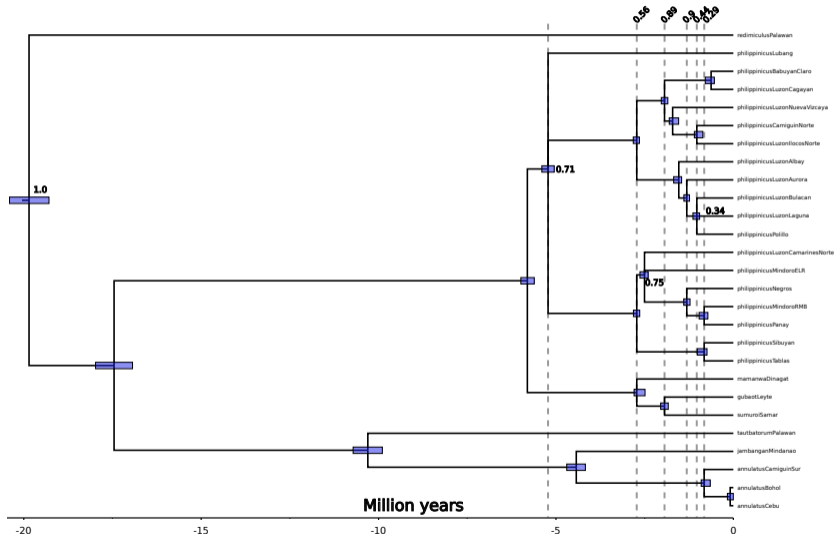


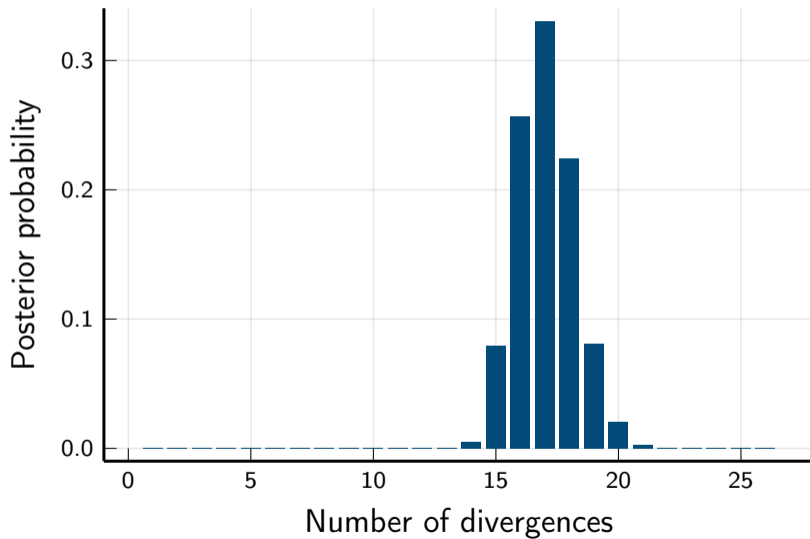
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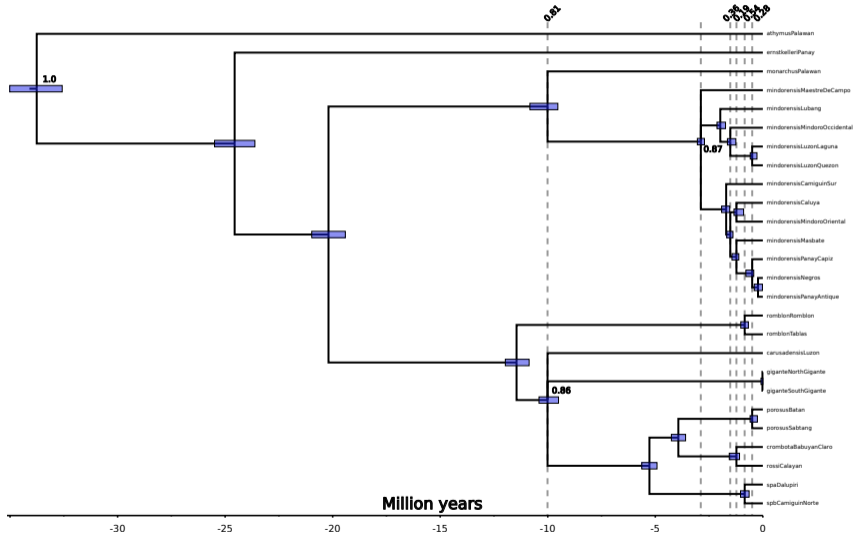
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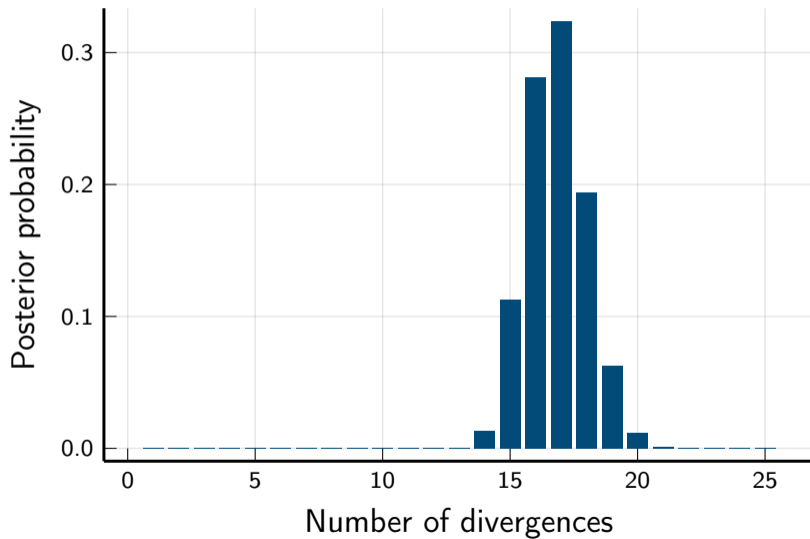
# Cyrtodactylus





# Gekko





# Take-home points

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

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- ▶ We can accurately infer phylogenies with shared divergences with moderately sized genomic data sets
- ▶ Generalizing tree space can avoid spurious support and improve MCMC mixing
- ▶ We found support for shared divergences among Philippine gekkonids

# So much to do...

- ▶ Theory on generalized tree space
- ▶ Better algorithms to take advantage of new ways to explore this space
- ▶ Port generalized tree prior to RevBayes to couple with other data models, relaxed-clock models, biogeographic models, etc.
- ▶ Couple with paleogeographically explicit model of range evolution
- ▶ Develop process-based priors

# Everything is on GitHub...

## Software:

- ▶ Phycoeval: <https://github.com/phyletica/ecoevolity>

## Open-Science Notebooks:

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

# Acknowledgments

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

## Computation:

- ▶ Alabama Supercomputer Authority
- ▶ Auburn University Hopper Cluster

## Funding:



DEB 1656004

## Photo credits:

- ▶ Rafe Brown
- ▶ [PhyloPic](#)

Thanks to the organizers of MIC-Phy!

# Questions?

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