

Bayesian statistical approaches to inferring shared evolutionary events

Jamie Oaks

Auburn University

phyletica.org

 @jamoaks

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Phyletica Lab

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Postdocs

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

Graduate students

- ▶ Tashitso Anamza
- ▶ Matt Buehler
- ▶ Kerry Cobb
- ▶ Kyle David
- ▶ Saman Jahangiri
- ▶ Randy Klabacka
- ▶ Morgan Muell
- ▶ Tanner Myers
- ▶ Claire Tracy
- ▶ Breanna 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



Generalizing Bayesian phylogenetics to infer patterns predicted by processes of diversification



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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

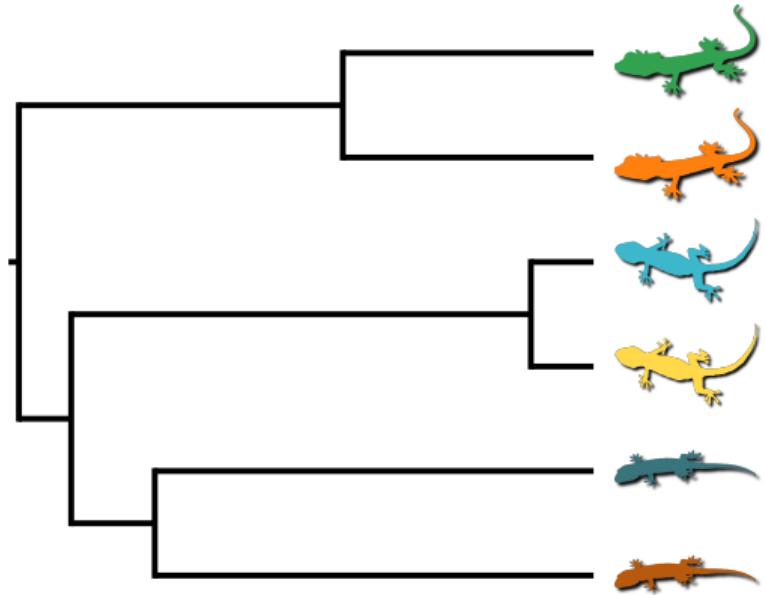


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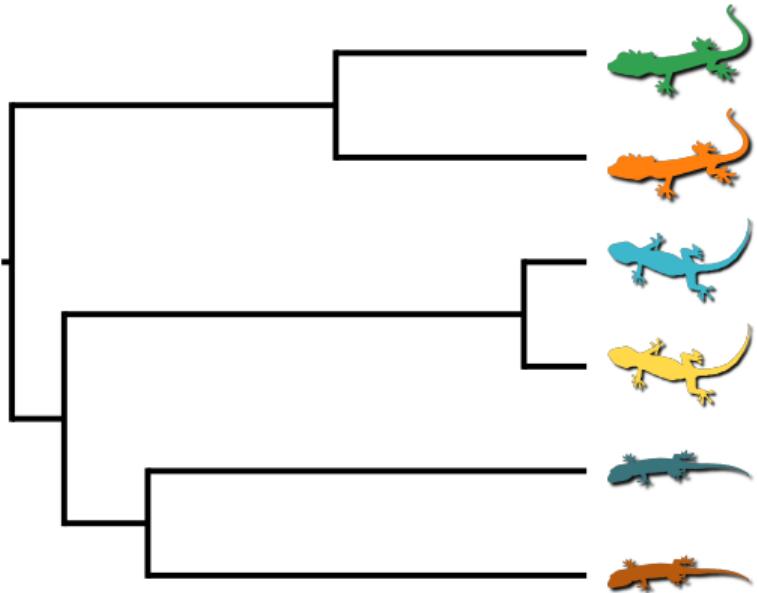
- ▶ Phylogenetics is rapidly becoming the statistical foundation of biology
- ▶ “Big data” present exciting possibilities and challenges
- ▶ Many opportunities to develop new ways to study biology in light of phylogeny

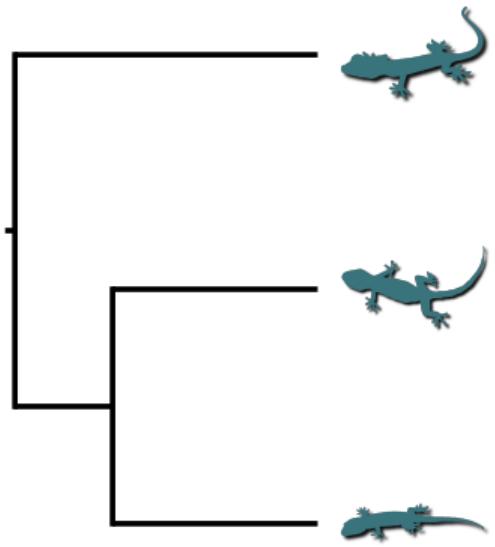


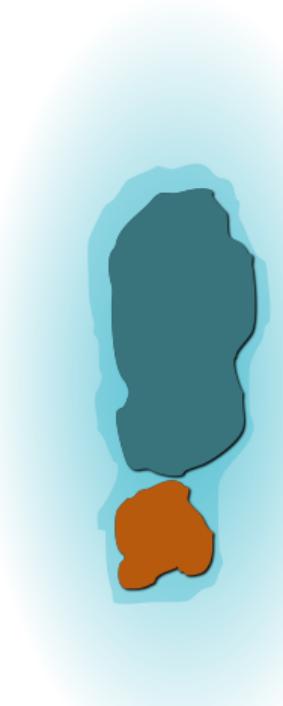
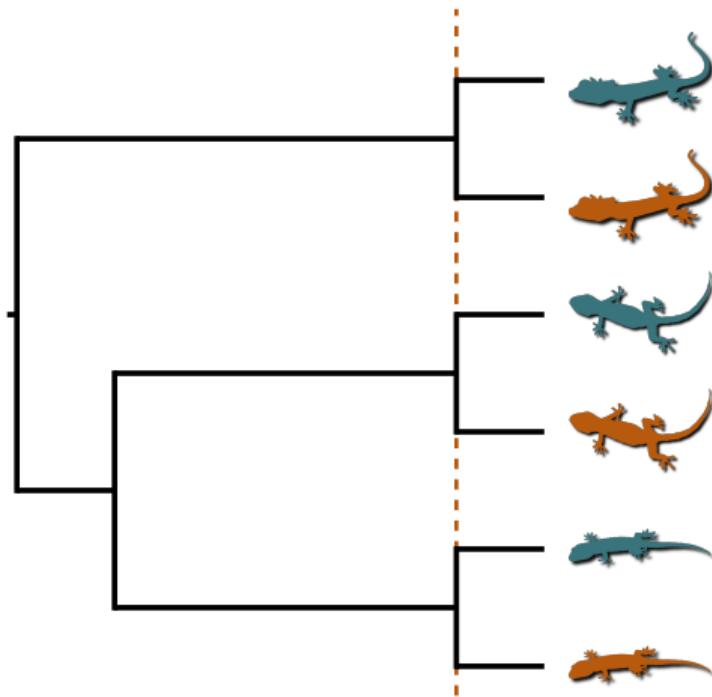
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- ▶ **Assumption:** All processes of diversification affect each lineage independently

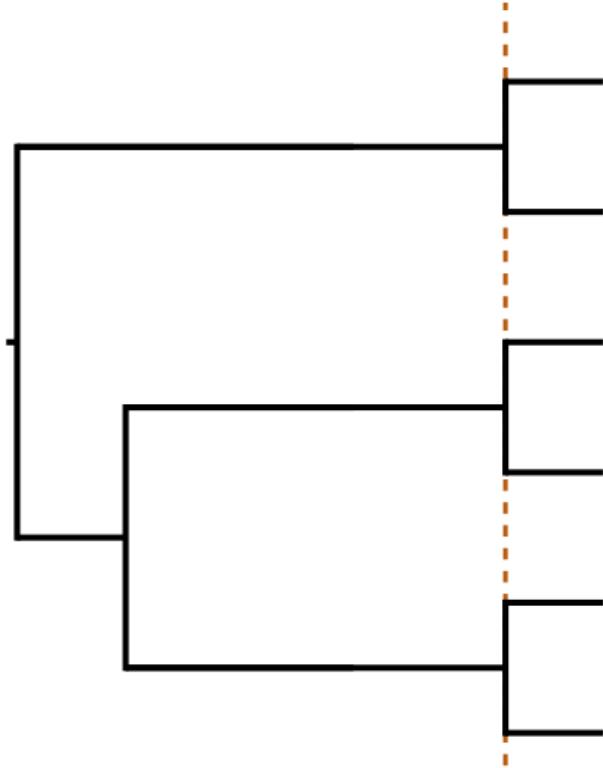






Biogeography

- ▶ Environmental changes that affect whole communities of species

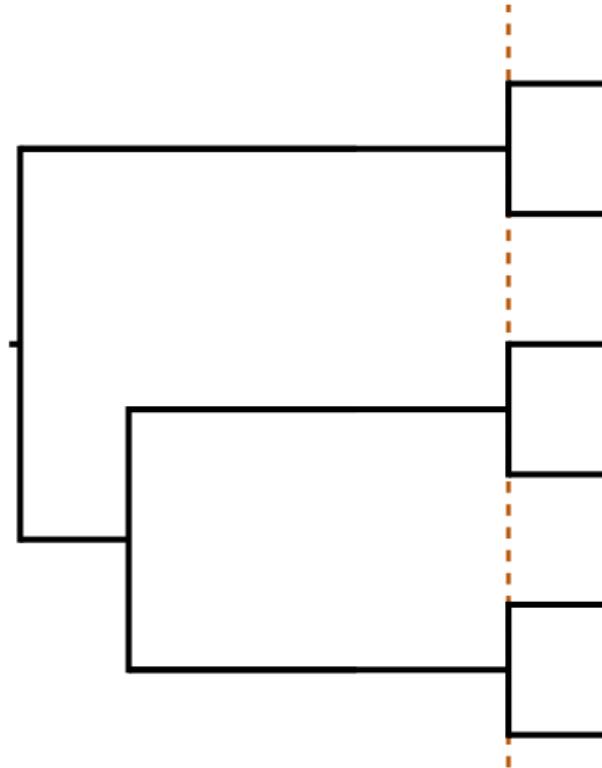


Biogeography

- ▶ Environmental changes that affect whole communities of species

Genome evolution

- ▶ Duplication of a chromosome segment harboring gene families



Biogeography

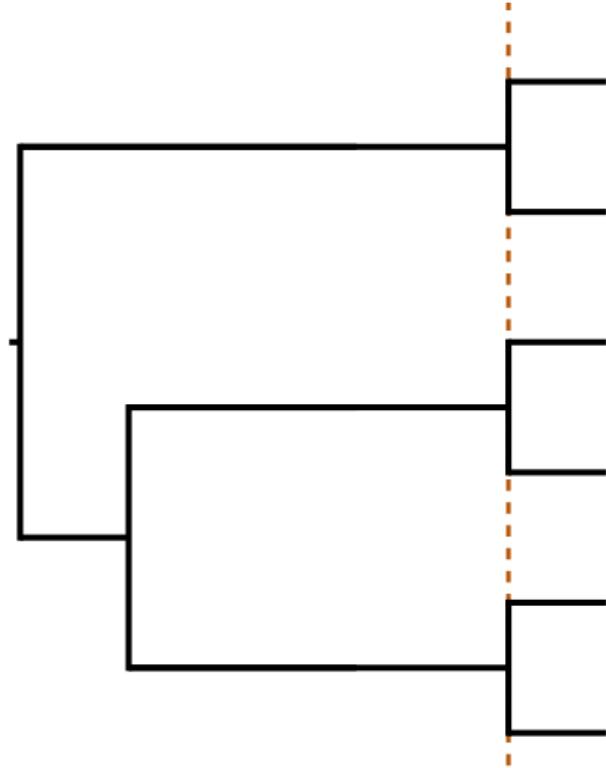
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Epidemiology

- ▶ Transmission at social gatherings



Biogeography

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Genome evolution

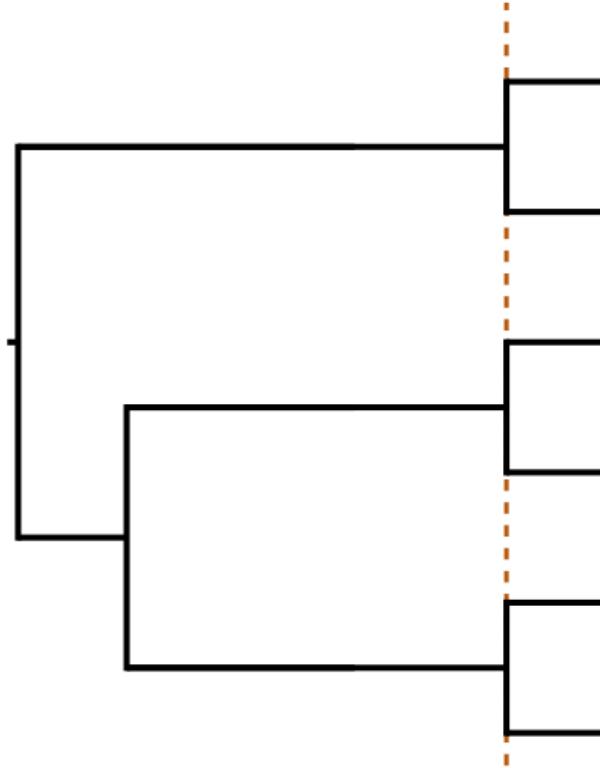
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Epidemiology

- #### ► Transmission at social gatherings

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

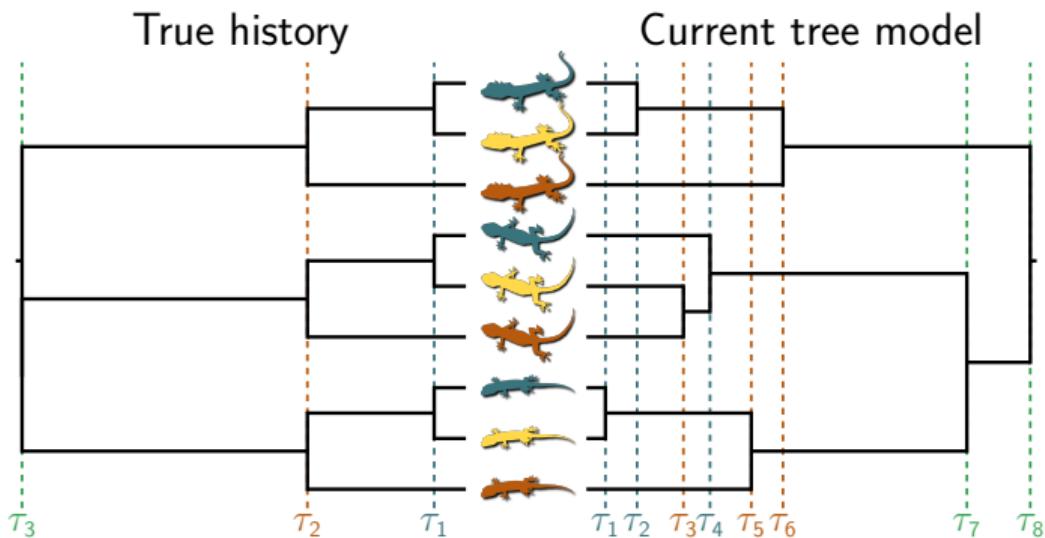
- ▶ Speciation of the host
 - ▶ Co-colonization of new host species



Why account for shared divergences?

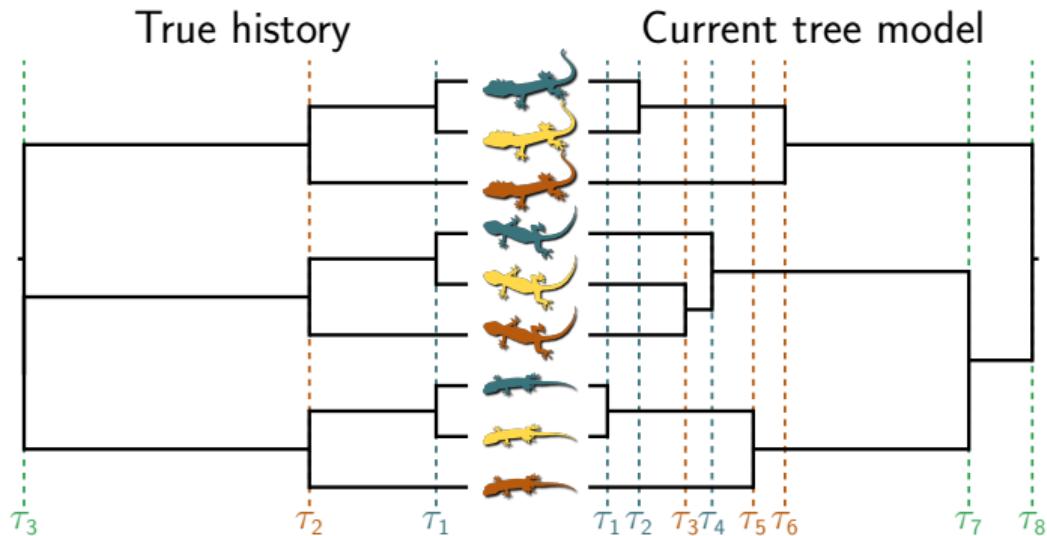
Why account for shared divergences?

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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Genome evolution

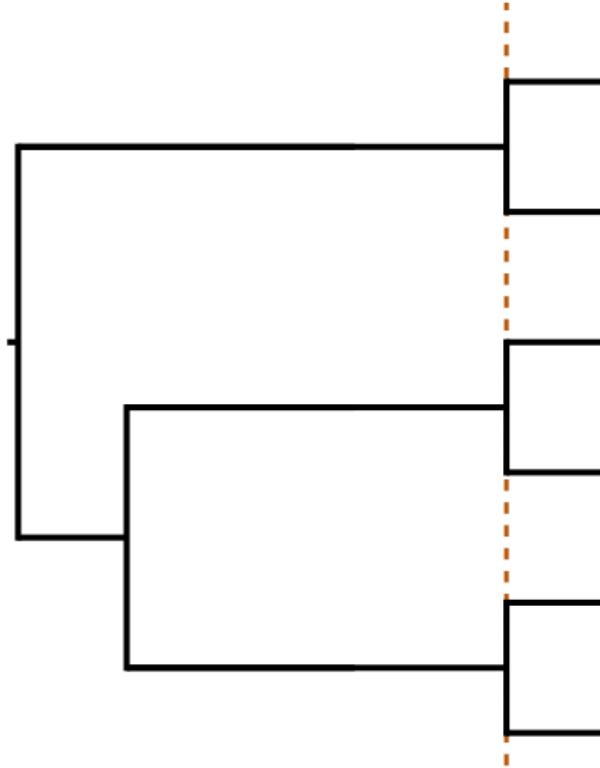
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Approaches to the problem

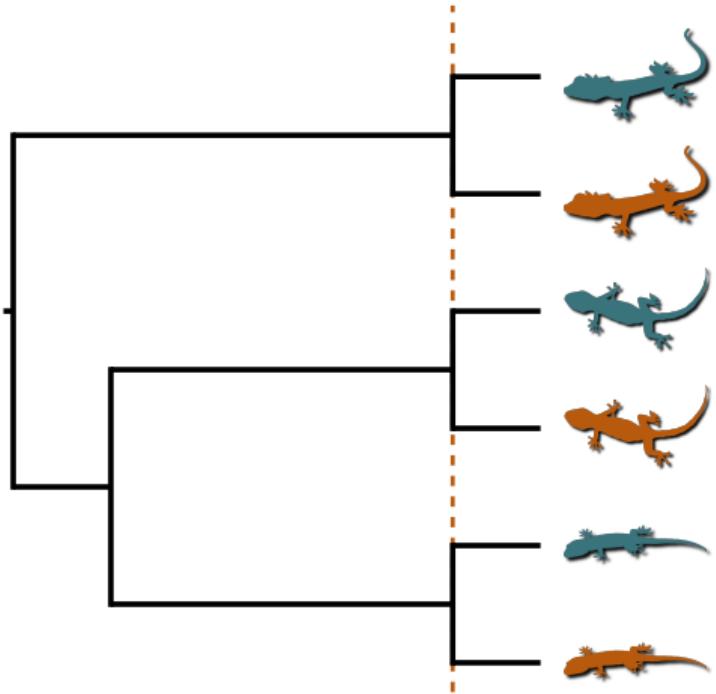
- A pairwise approach (keep it “simple”)
- A fully phylogenetic approach

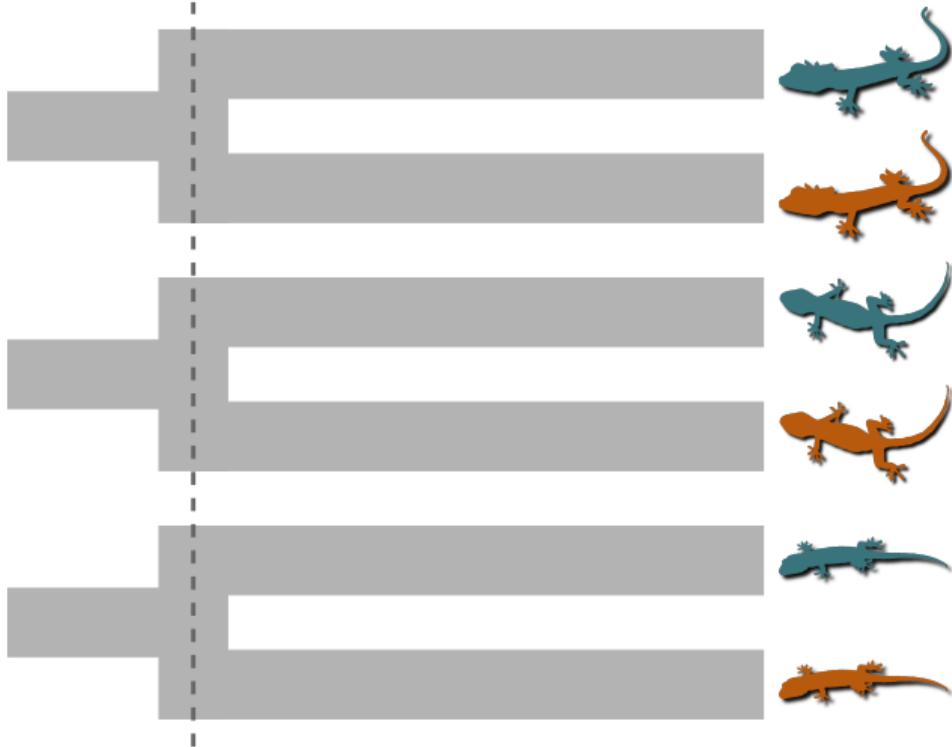
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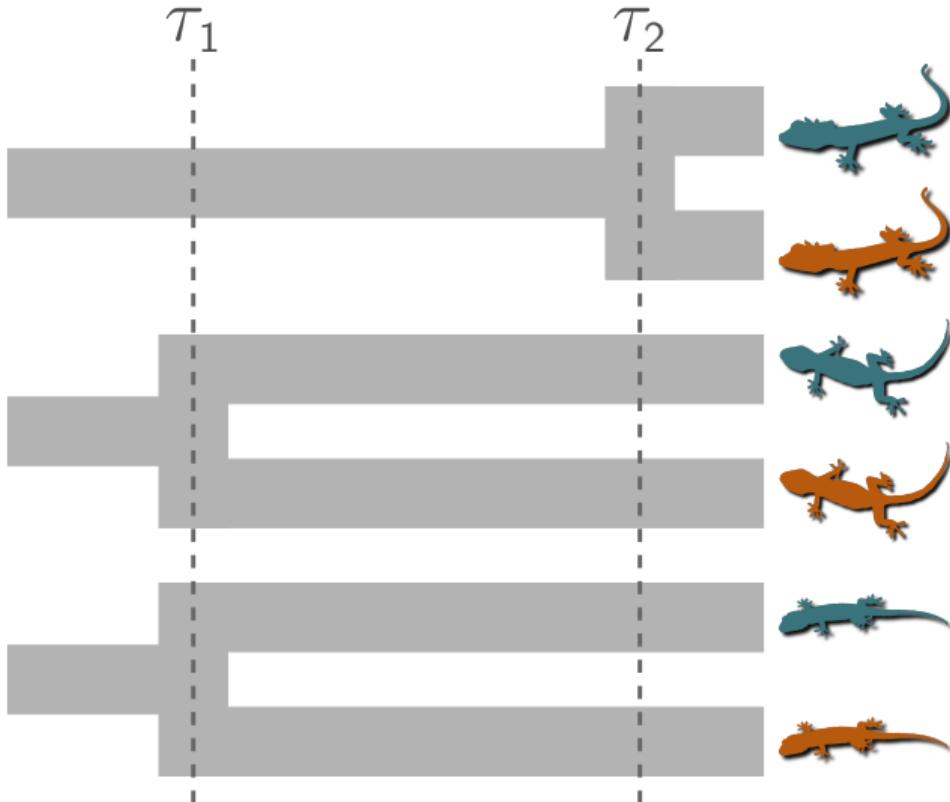
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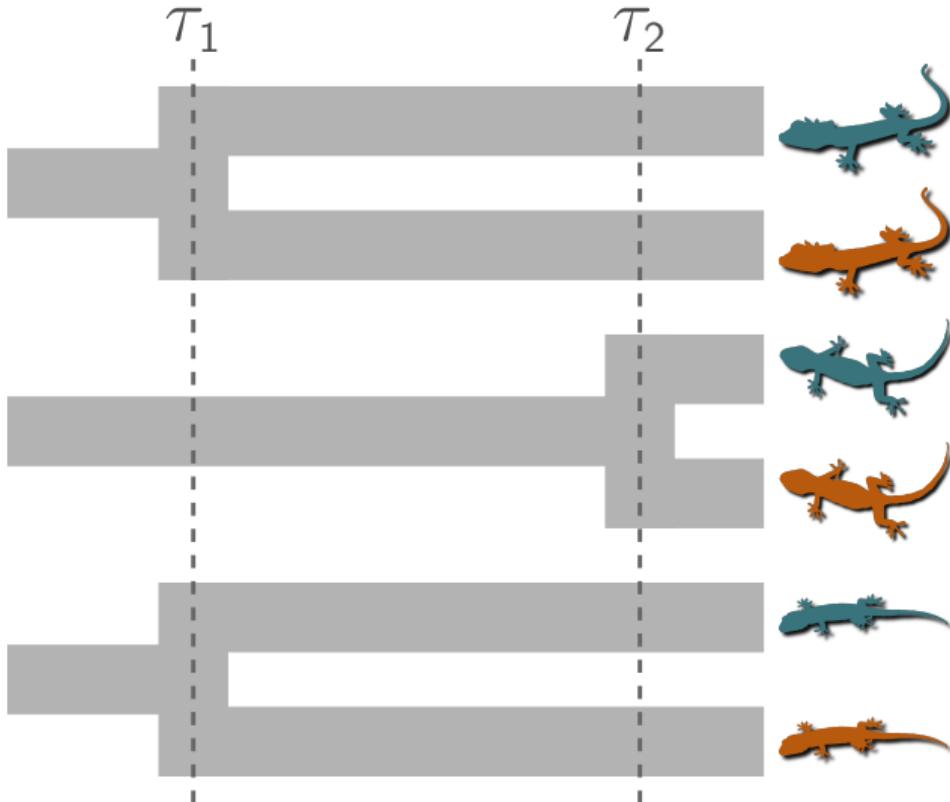
A fully phylogenetic approach

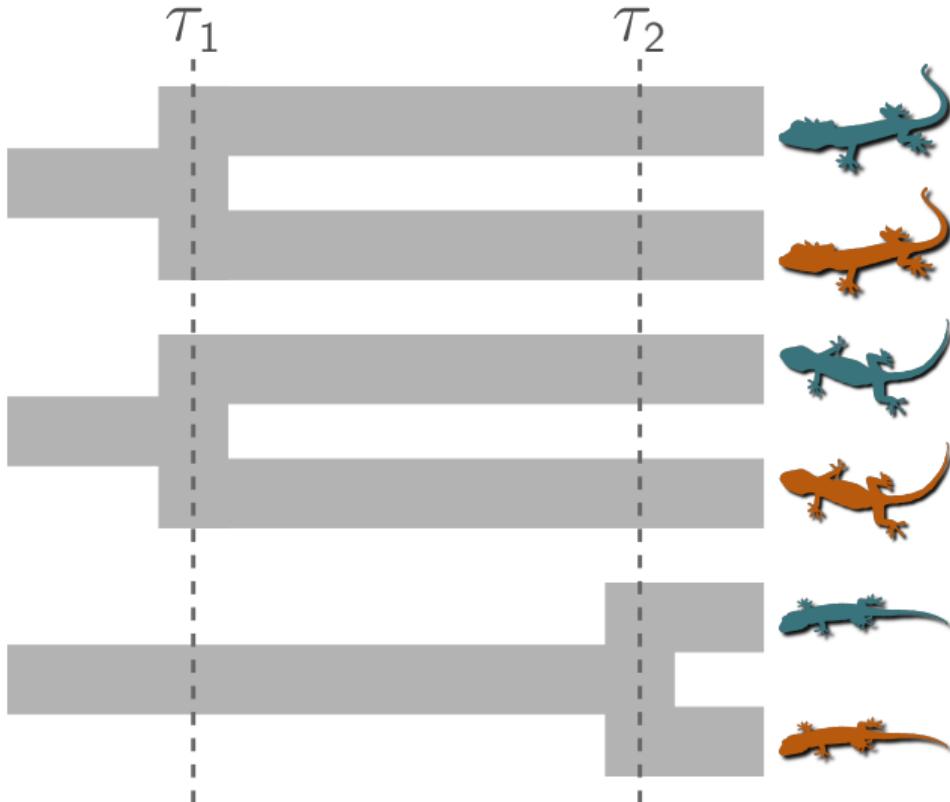


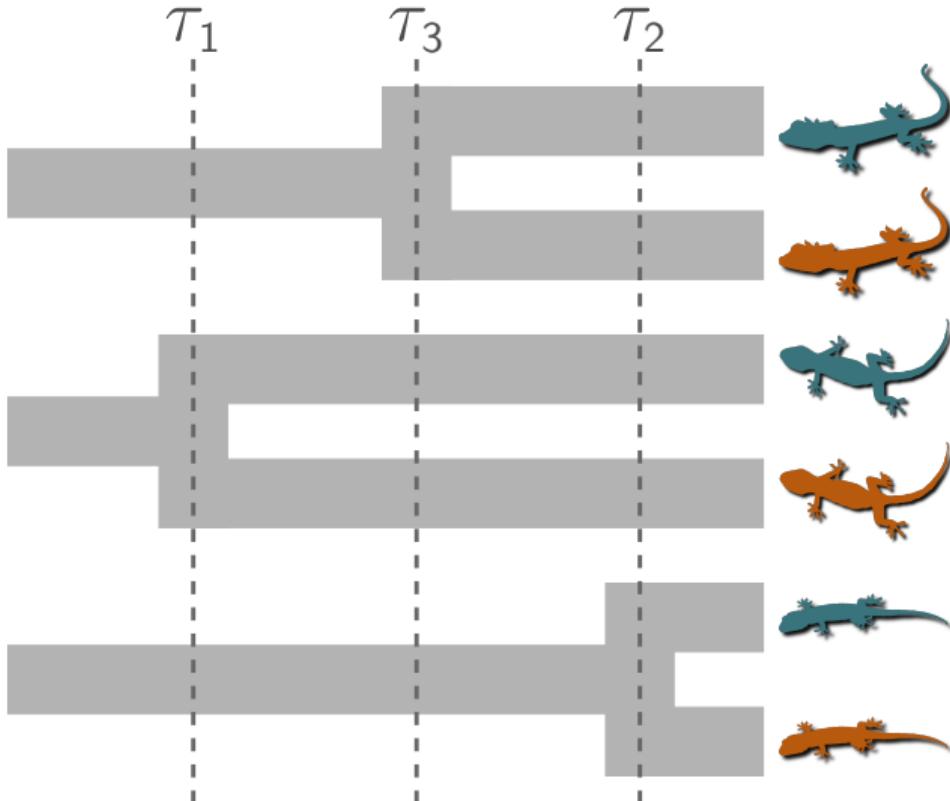


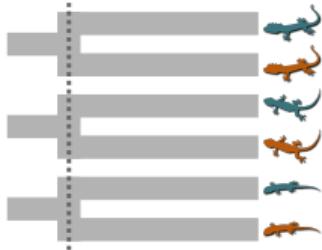
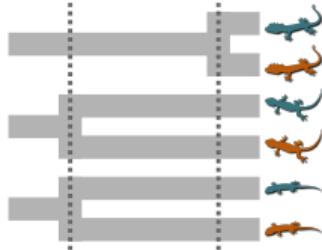
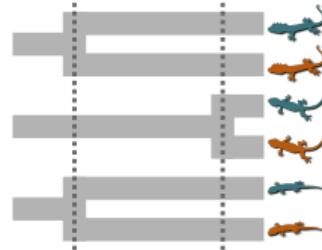
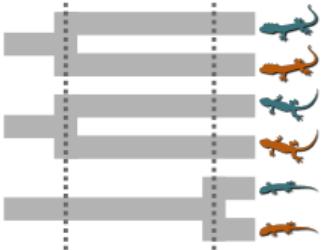
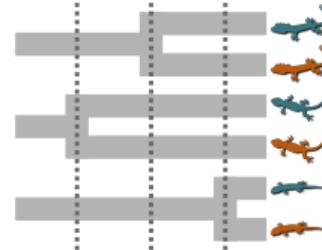
τ_1 

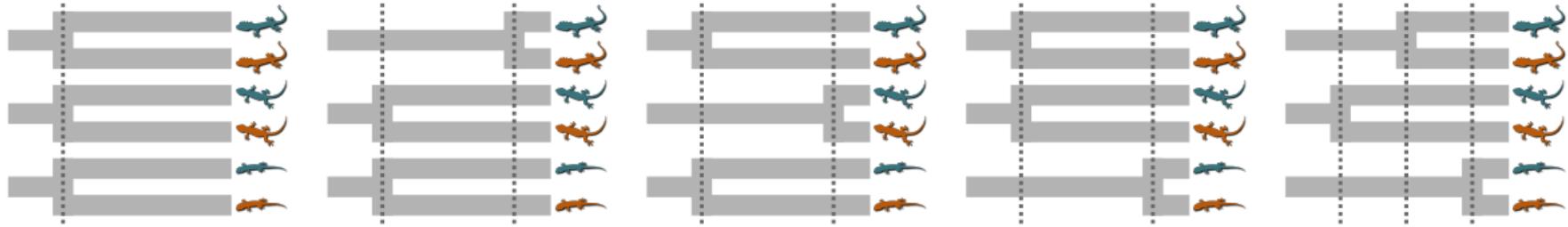








m_1  m_2  m_3  m_4  m_5 

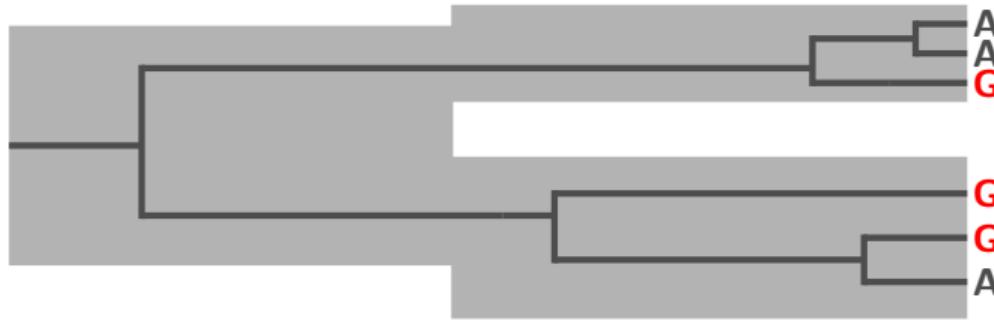
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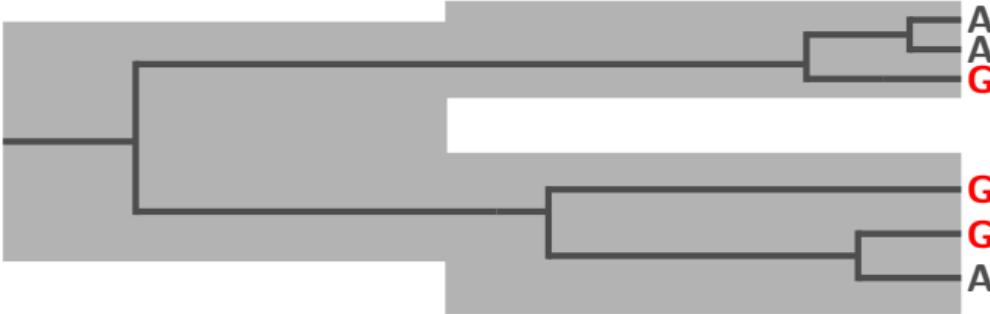
We want to infer the model and divergence times given genetic data



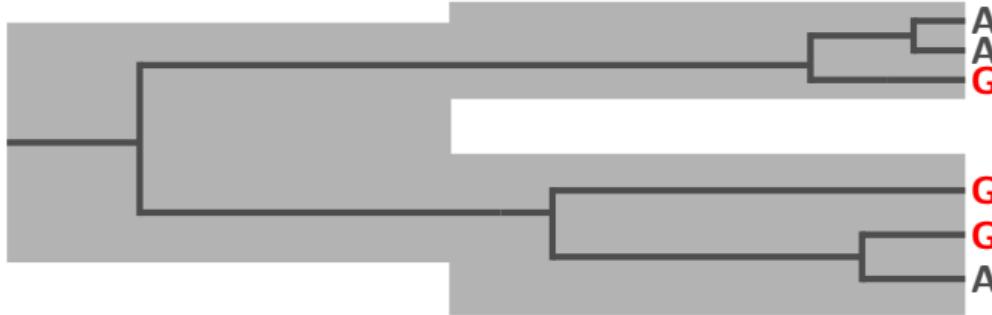
A
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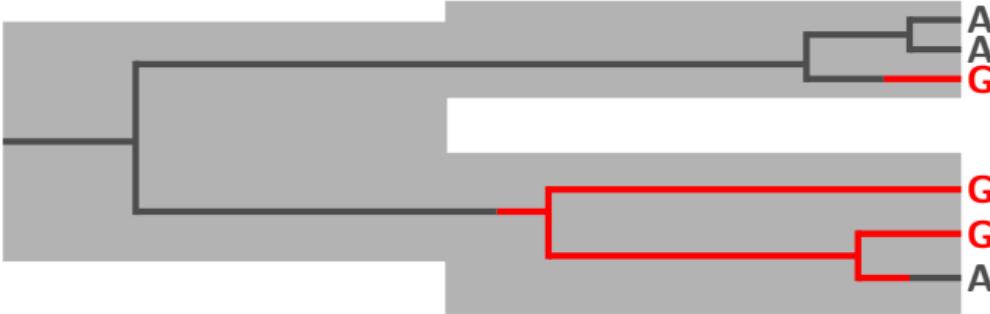
- ▶ Conditional on “population tree”, model “gene tree” using coalescent
 - ▶ Coalescent is a stochastic model of shared inheritance (continuous-time Markov chain = CTMC)



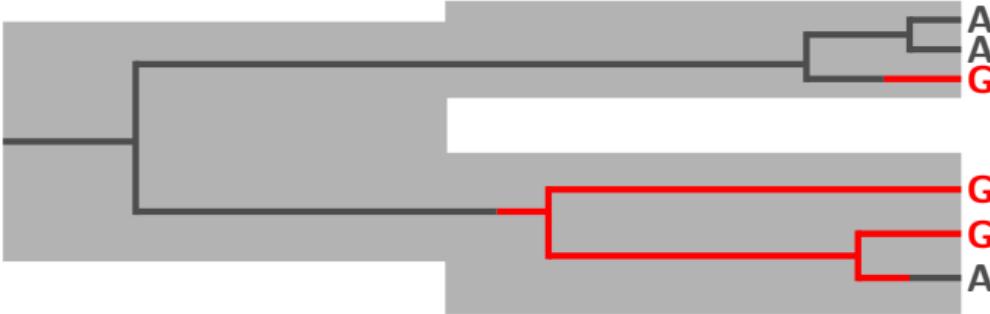
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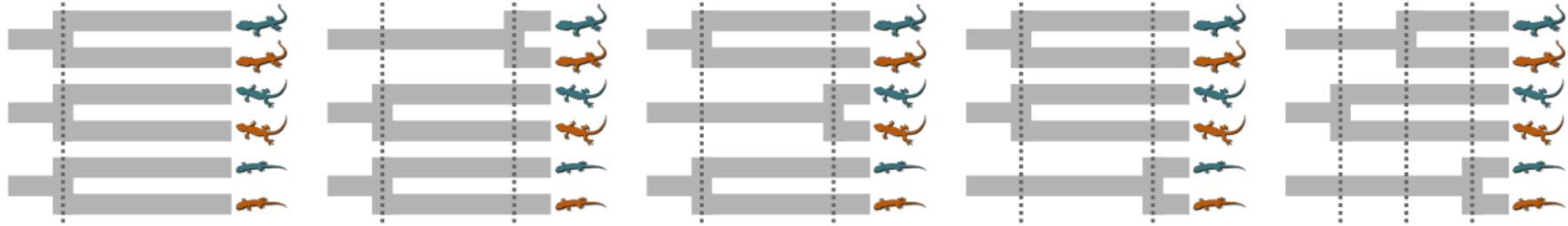
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 - ▶ Branching pattern is a function of population size
- ▶ Conditional on gene tree, model mutation as a CTMC
- ▶ Genetic characters provide information about gene trees
- ▶ Gene trees inform population tree (population sizes and divergence time)

m_1 m_2 m_3 m_4 m_5 

We want to infer the model and divergence times given genetic data

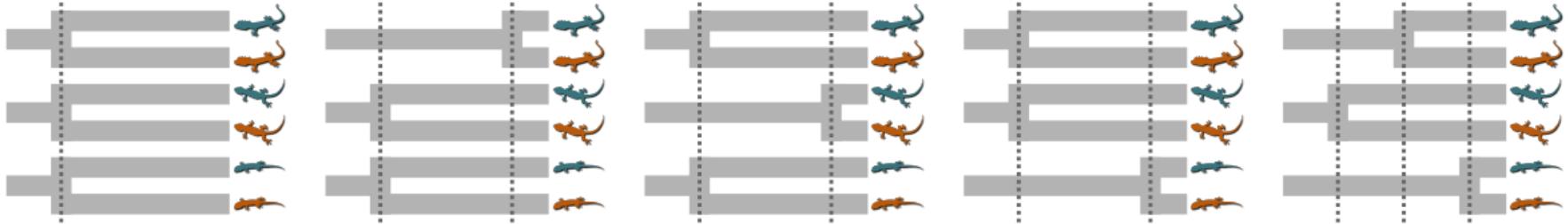
$p(m_1 | \mathbf{D})$

$p(m_2 | \mathbf{D})$

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$p(m_5 | \mathbf{D})$



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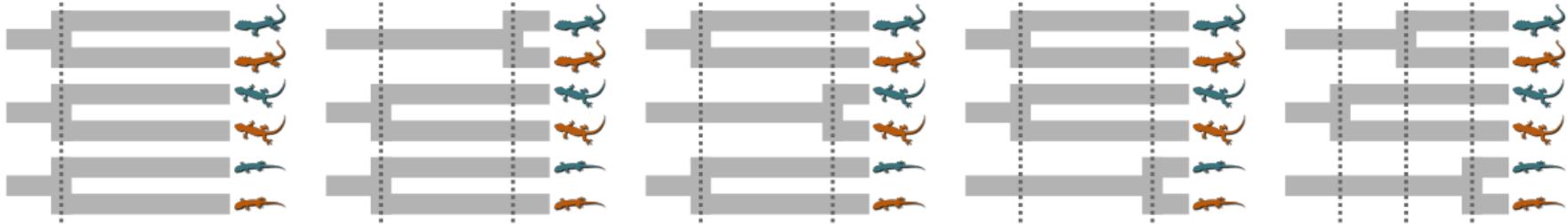
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We want to infer the model and divergence times given genetic data

$$p(m_i | \mathbf{D}) \propto p(\mathbf{D} | m_i)p(m_i)$$

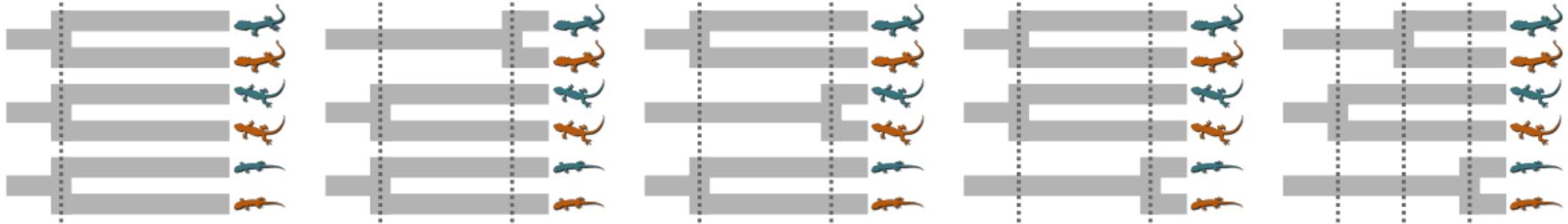
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$$p(m_i | \mathbf{D}) \propto p(\mathbf{D} | m_i) p(m_i)$$

$$p(\mathbf{D} | m_i) = \int_{\theta} p(\mathbf{D} | \theta, m_i) p(\theta | m_i) d\theta$$

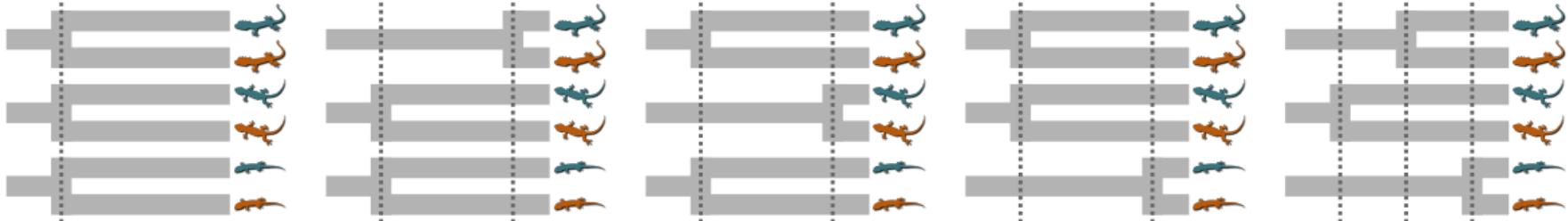
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- ▶ Divergence times
- ▶ Substitution parameters
- ▶ Gene trees
- ▶ Demographic parameters

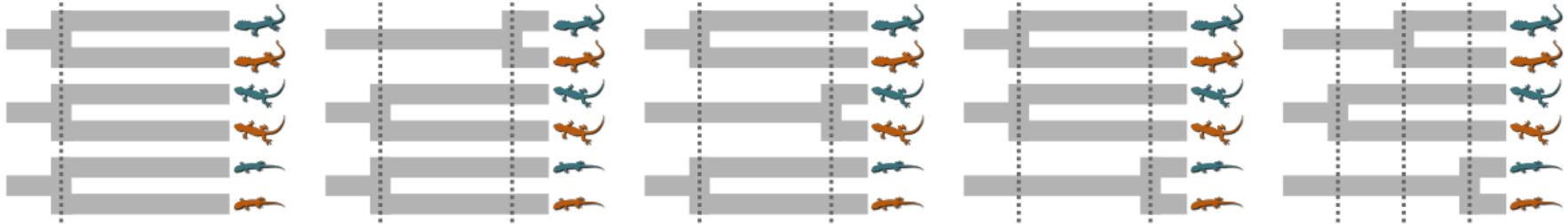
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Challenges:

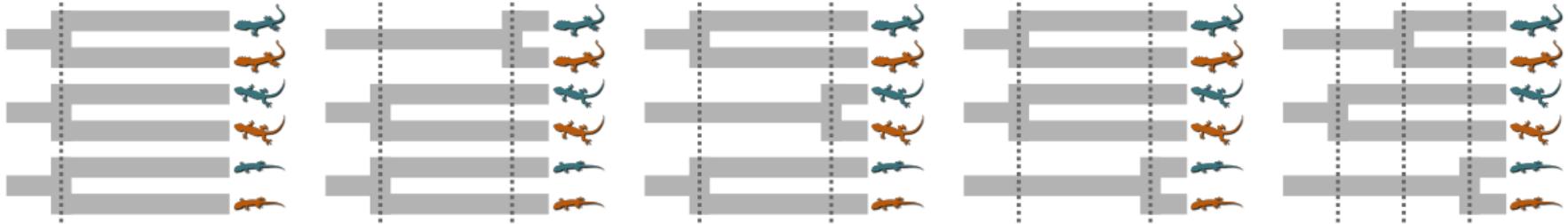
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Challenges:

1. Likelihood is tractable, but gene trees are difficult

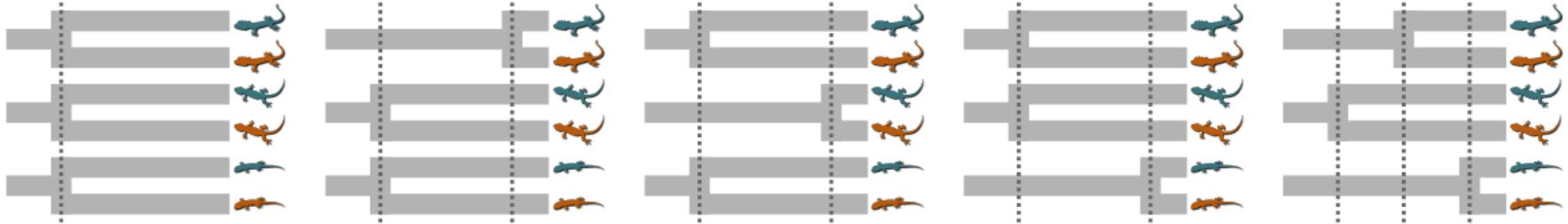
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Challenges:

1. Likelihood is tractable, but gene trees are difficult
2. Sampling over all possible models

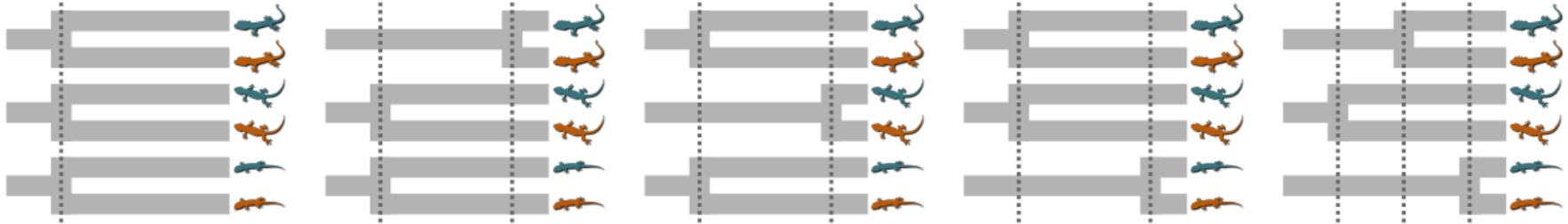
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Challenges:

1. Likelihood is tractable, but gene trees are difficult
2. Sampling over all possible models
 - 3 taxa = 5 models

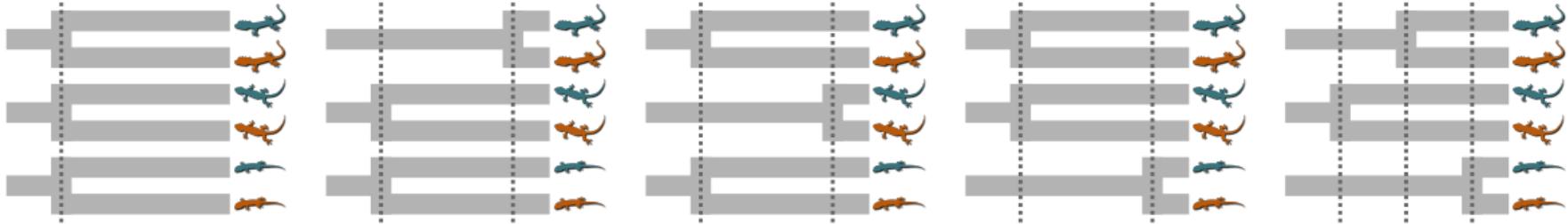
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We want to infer the model and divergence times given genetic data

Challenges:

1. Likelihood is tractable, but gene trees are difficult
2. Sampling over all possible models
 - ▶ 3 taxa = 5 models
 - ▶ 10 taxa = 115,975 models

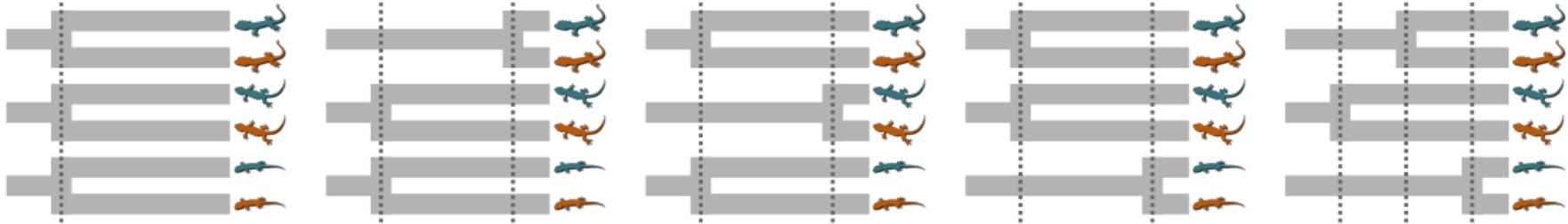
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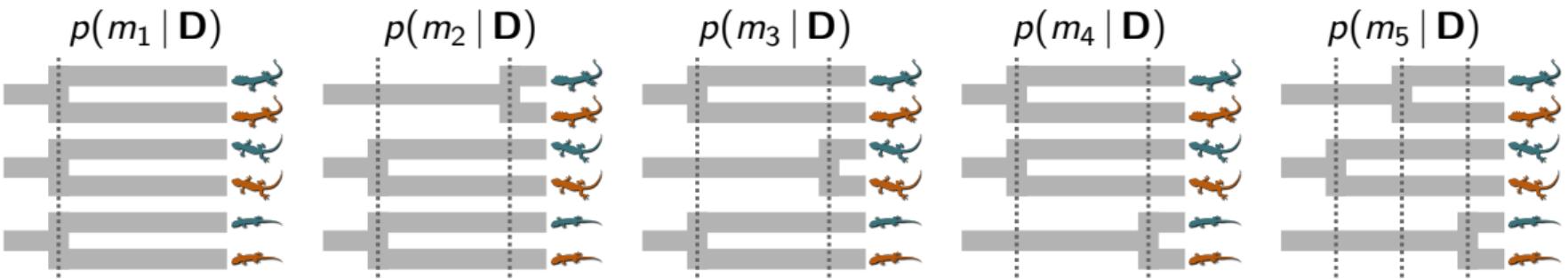
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We want to infer the model and divergence times given genetic data

Challenges:

1. Likelihood is tractable, but gene trees are difficult
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 - ▶ 3 taxa = 5 models
 - ▶ 10 taxa = 115,975 models
 - ▶ 20 taxa = 51,724,158,235,372 models!!

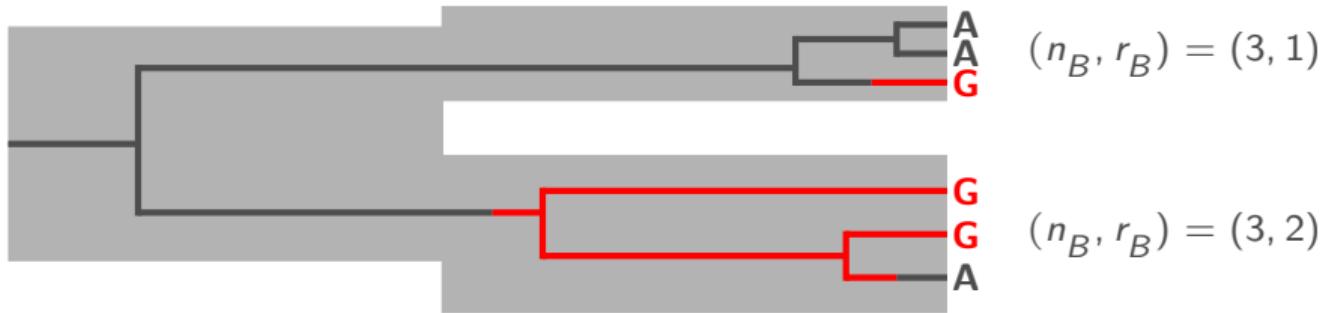


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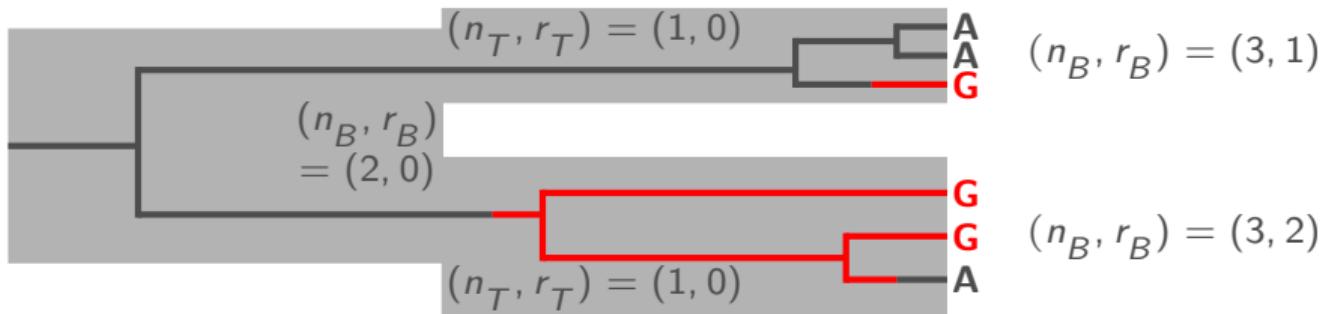
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Approximate Bayesian computation (ABC) methods do not perform well for this model-choice problem



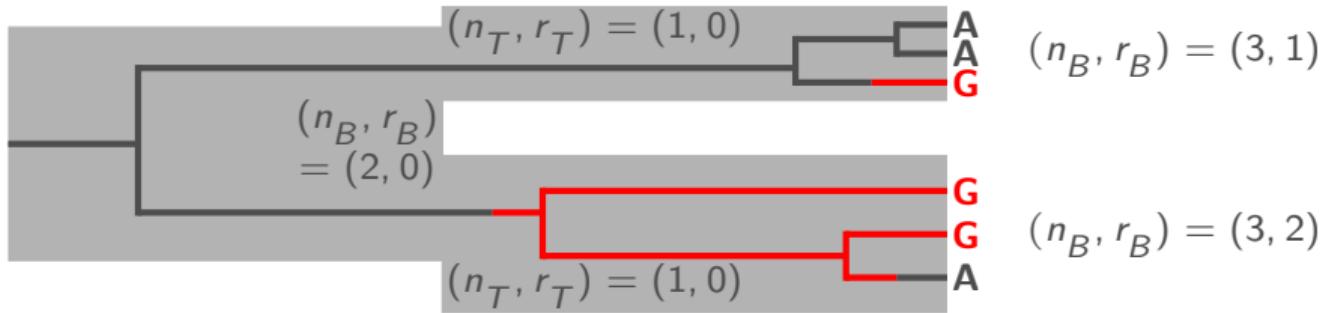
¹ T. Schmelzer and L. N. Trefethen (2007). *Electronic Transactions on Numerical Analysis* 29: 1–18

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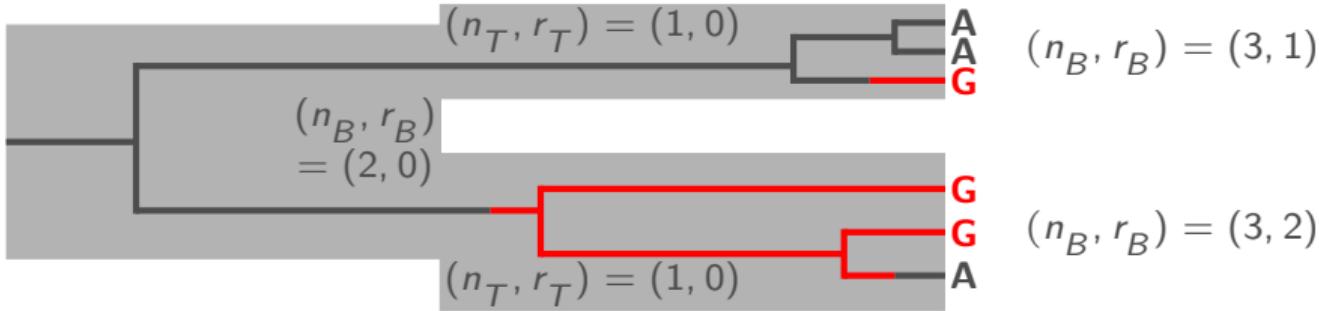
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	$(1, 0)$	$(1, 1)$	$(2, 0)$	$(2, 1)$	\cdots	(\mathbf{n}, \mathbf{n})
$(1, 0)$
$(1, 1)$
$(2, 0)$
$(2, 1)$
\vdots						
(\mathbf{n}, \mathbf{n})

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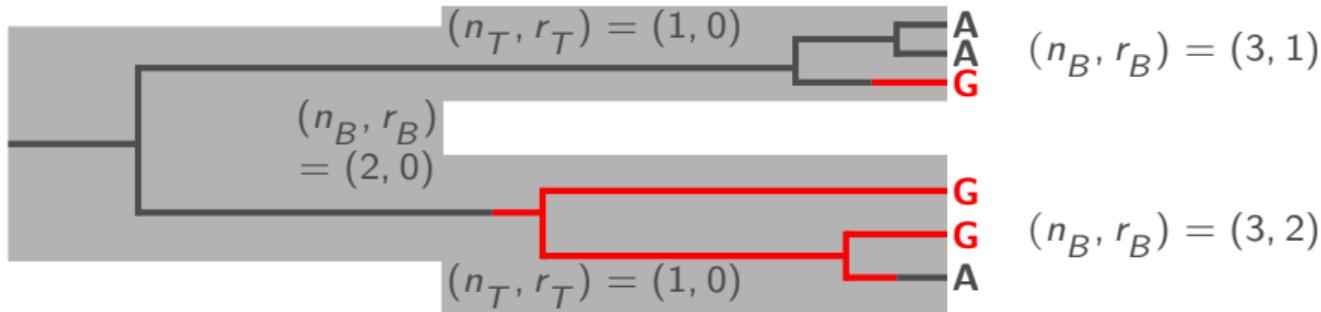
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	$(1, 0)$	$(1, 1)$	$(2, 0)$	$(2, 1)$	\cdots	(\mathbf{n}, \mathbf{n})	
$(1, 0)$	$Q_{(n,r);(n,r-1)} = (n - r + 1)v, \text{ mutation,}$
$(1, 1)$	$Q_{(n,r);(n,r+1)} = (r + 1)u, \text{ mutation,}$
$(2, 0)$	$Q_{(n,r);(n-1,r)} = \frac{(n-1-r)n}{2N_e(u+v)}, \text{ coalescence,}$
$(2, 1)$	$Q_{(n,r);(n-1,r-1)} = \frac{(r-1)n}{2N_e(u+v)}, \text{ coalescence,}$
\vdots							
(\mathbf{n}, \mathbf{n})	$Q_{(n,r);(n,r)} = -\frac{(n-1)n}{2N_e(u+v)} - (n - r)v - ru.$

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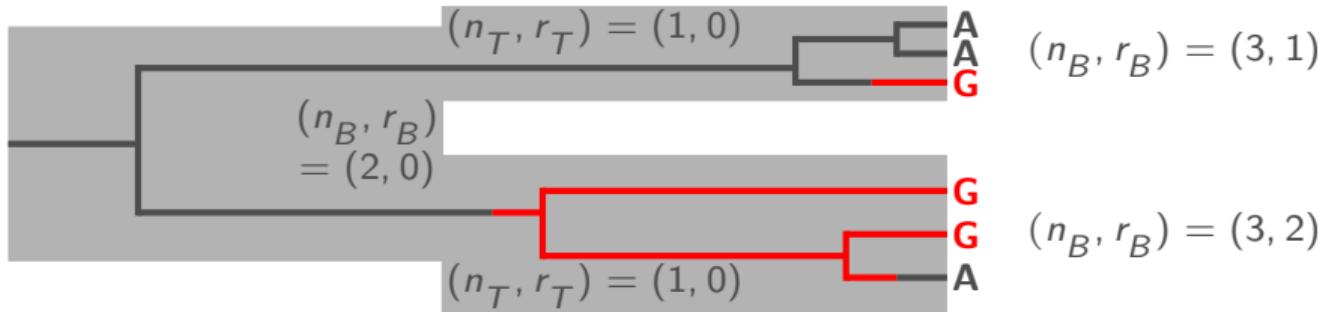


$$Q = \begin{matrix} & (1, 0) & (1, 1) & (2, 0) & (2, 1) & \cdots & (\mathbf{n}, \mathbf{n}) \\ (1, 0) & \cdot & \cdot & \cdot & \cdot & \cdots & \cdot \\ (1, 1) & \cdot & \cdot & \cdot & \cdot & \cdots & \cdot \\ (2, 0) & \cdot & \cdot & \cdot & \cdot & \cdots & \cdot \\ (2, 1) & \cdot & \cdot & \cdot & \cdot & \cdots & \cdot \\ \vdots & & & & & & \\ (\mathbf{n}, \mathbf{n}) & \cdot & \cdot & \cdot & \cdot & \cdots & \cdot \end{matrix} \quad \begin{aligned} Q_{(n,r);(n,r-1)} &= (n-r+1)v, \text{ mutation,} \\ Q_{(n,r);(n,r+1)} &= (r+1)u, \text{ mutation,} \\ Q_{(n,r);(n-1,r)} &= \frac{(n-1-r)n}{2N_e(u+v)}, \text{ coalescence,} \\ Q_{(n,r);(n-1,r-1)} &= \frac{(r-1)n}{2N_e(u+v)}, \text{ coalescence,} \\ Q_{(n,r);(n,r)} &= -\frac{(n-1)n}{2N_e(u+v)} - (n-r)v - ru. \end{aligned}$$

- ▶ e^{Qt} to keep track of all conditional probabilities along each branch (Carathéodory-Fejér method¹)

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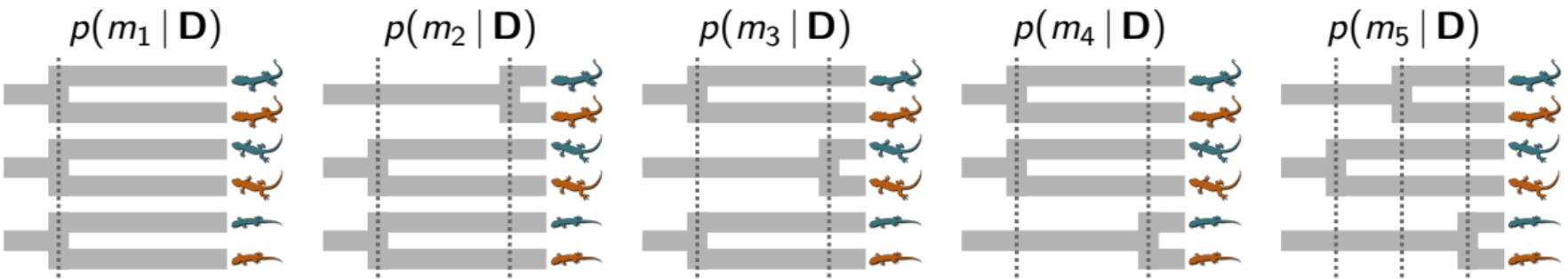


$$Q = \begin{matrix} & (1, 0) & (1, 1) & (2, 0) & (2, 1) & \cdots & (\mathbf{n}, \mathbf{n}) \\ (1, 0) & \cdot & \cdot & \cdot & \cdot & \cdots & \cdot \\ (1, 1) & \cdot & \cdot & \cdot & \cdot & \cdots & \cdot \\ (2, 0) & \cdot & \cdot & \cdot & \cdot & \cdots & \cdot \\ (2, 1) & \cdot & \cdot & \cdot & \cdot & \cdots & \cdot \\ \vdots & & & & & & \\ (\mathbf{n}, \mathbf{n}) & \cdot & \cdot & \cdot & \cdot & \cdots & \cdot \end{matrix} \quad \begin{aligned} Q_{(n,r);(n,r-1)} &= (n-r+1)v, \text{ mutation,} \\ Q_{(n,r);(n,r+1)} &= (r+1)u, \text{ mutation,} \\ Q_{(n,r);(n-1,r)} &= \frac{(n-1-r)n}{2N_e(u+v)}, \text{ coalescence,} \\ Q_{(n,r);(n-1,r-1)} &= \frac{(r-1)n}{2N_e(u+v)}, \text{ coalescence,} \\ Q_{(n,r);(n,r)} &= -\frac{(n-1)n}{2N_e(u+v)} - (n-r)v - ru. \end{aligned}$$

- ▶ e^{Qt} to keep track of all conditional probabilities along each branch (Carathéodory-Fejér method¹)
- ▶ At root, get likelihood of population tree integrated over all possible gene trees and mutational histories²

¹ T. Schmelzer and L. N. Trefethen (2007). *Electronic Transactions on Numerical Analysis* 29: 1–18

² D. Bryant et al. (2012). *Molecular Biology and Evolution* 29: 1917–1932



We want to infer the model and divergence times given genetic data

Challenges:

1. Likelihood is tractable, but gene trees are difficult
2. Sampling over all possible models
 - ▶ 3 taxa = 5 models
 - ▶ 10 taxa = 115,975 models
 - ▶ 20 taxa = 51,724,158,235,372 models!!

Approximate Bayesian computation (ABC) methods do not perform well for this model-choice problem

- ▶ We need a distribution over all ways of partitioning the population pairs to divergence-time classes
- ▶ The Dirichlet process (DP) is a convenient and flexible solution



Peter Dirichlet

- ▶ We need a distribution over all ways of partitioning the population pairs to divergence-time classes
- ▶ The Dirichlet process (DP) is a convenient and flexible solution
 - ▶ Common Bayesian nonparametric approach to assigning variables to an unknown number of categories



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Peter Dirichlet

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- ▶ The Dirichlet process (DP) is a convenient and flexible solution
 - ▶ Common Bayesian nonparametric approach to assigning variables to an unknown number of categories
 - ▶ Controlled by “concentration” parameter
 - ▶ Variables are exchangeable under the DP, allowing Gibbs sampling



Peter Dirichlet

Ecoevolvity

Estimating evolutionary coevality

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

- ▶ Analytically integrate over gene trees and mutational histories¹
- ▶ Dirichlet-process prior across divergence models
- ▶ Gibbs sampling² to numerically sample models

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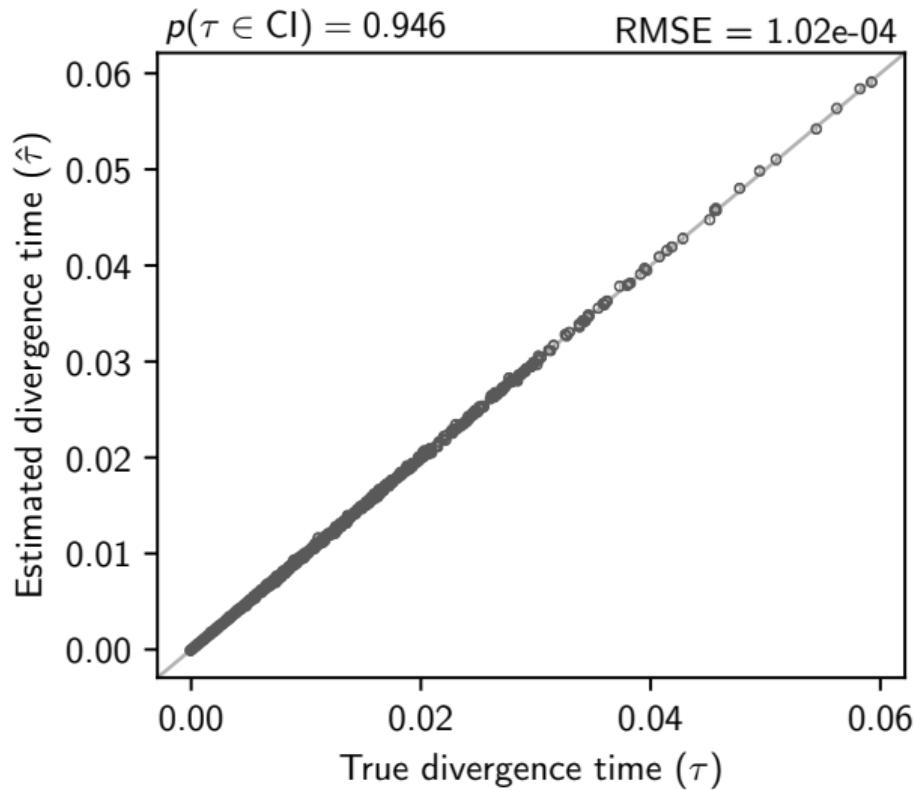
- ▶ *Goal: Fast, full-likelihood Bayesian method to infer patterns of co-diversification from genome-scale data*

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

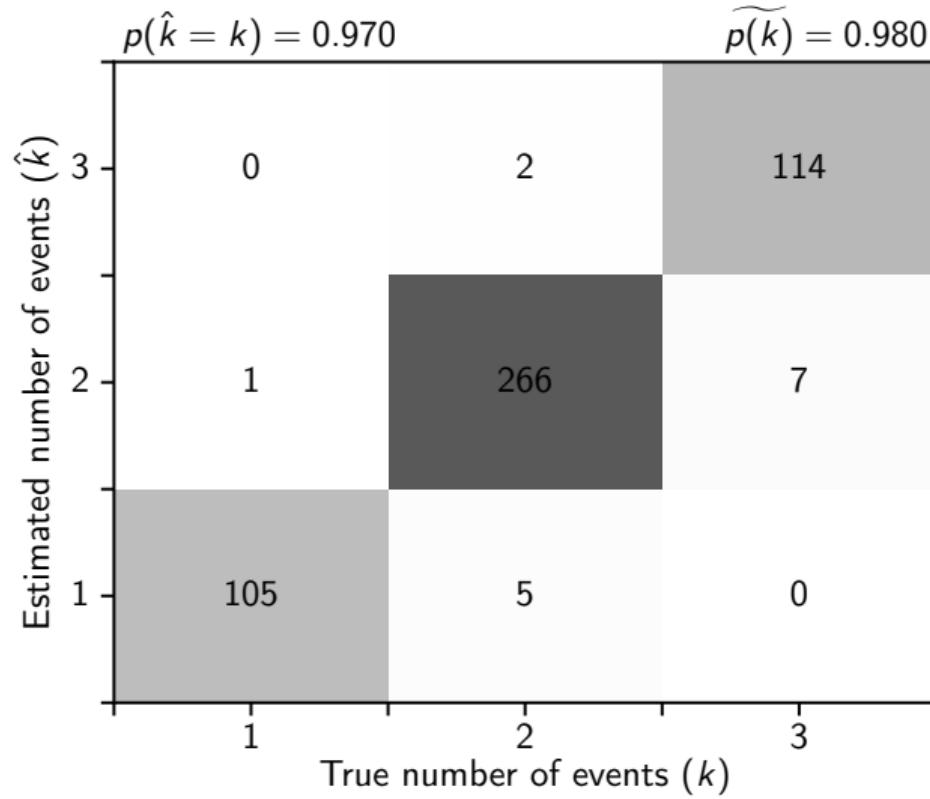
² R. M. Neal (2000). *Journal of Computational and Graphical Statistics* 9: 249–265

Does it work?

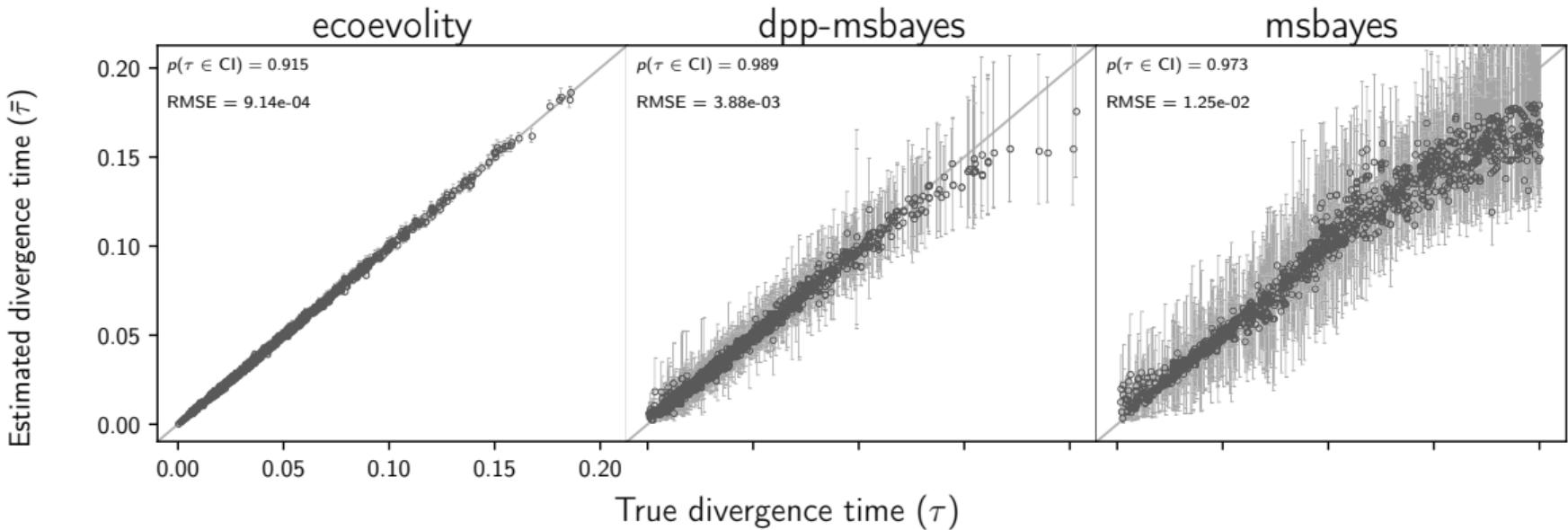
Simulation results



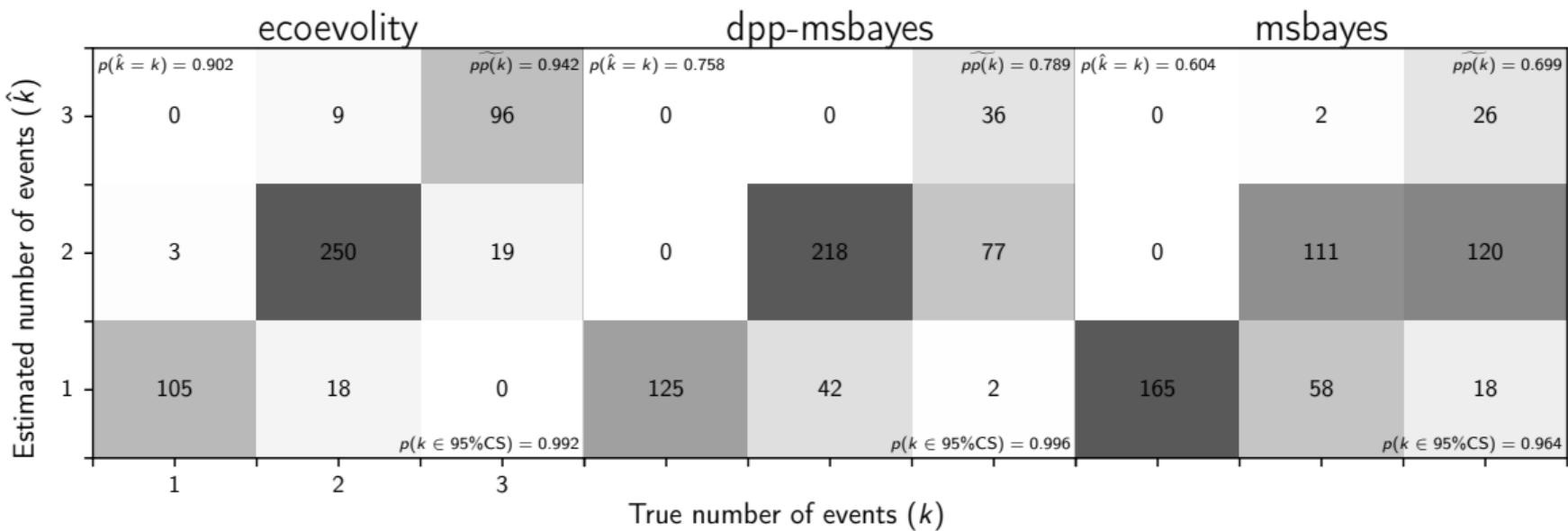
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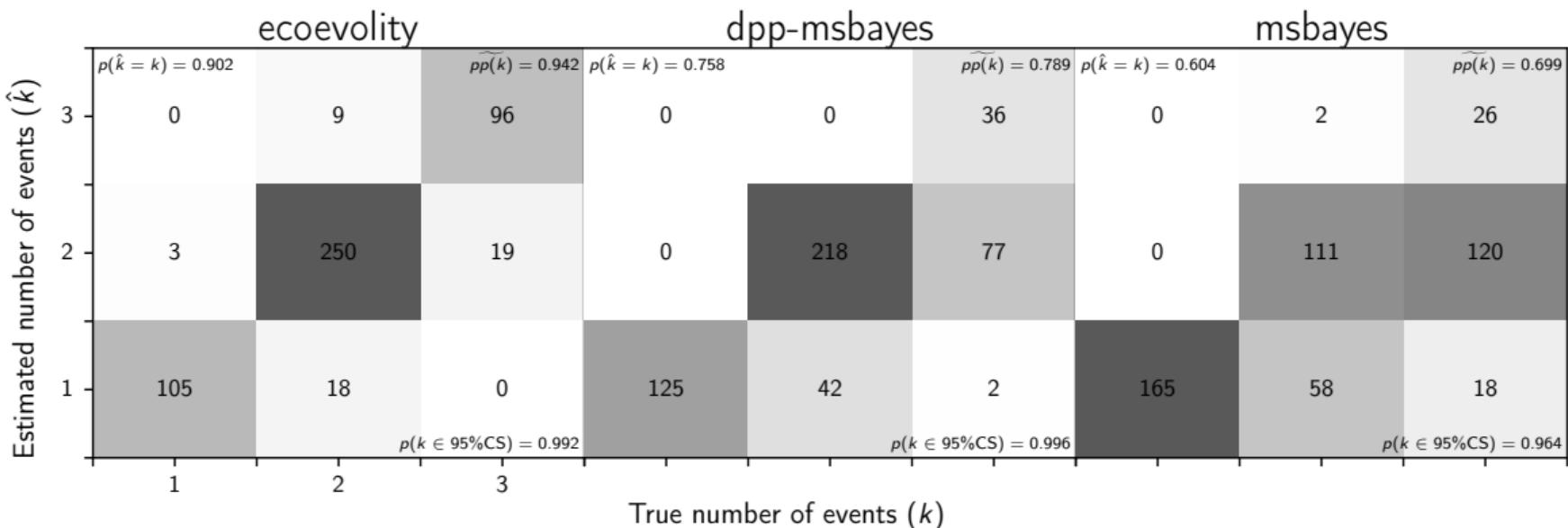
“Bake-off” results



“Bake-off” results



“Bake-off” results



Average run time:

33.4 minutes

4.4 days



Scan for sea-level animation

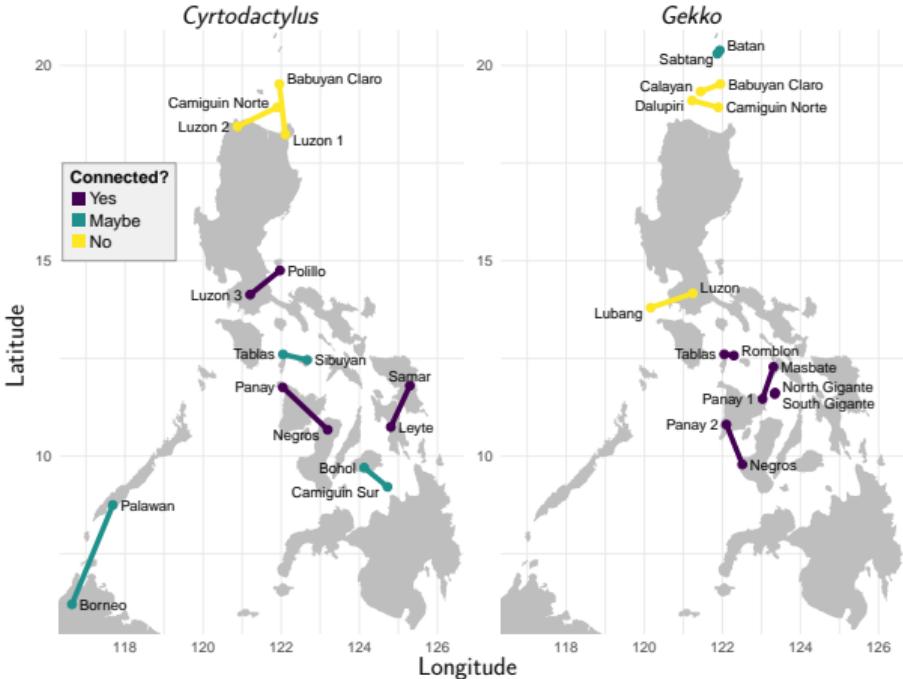


Scan for sea-level animation



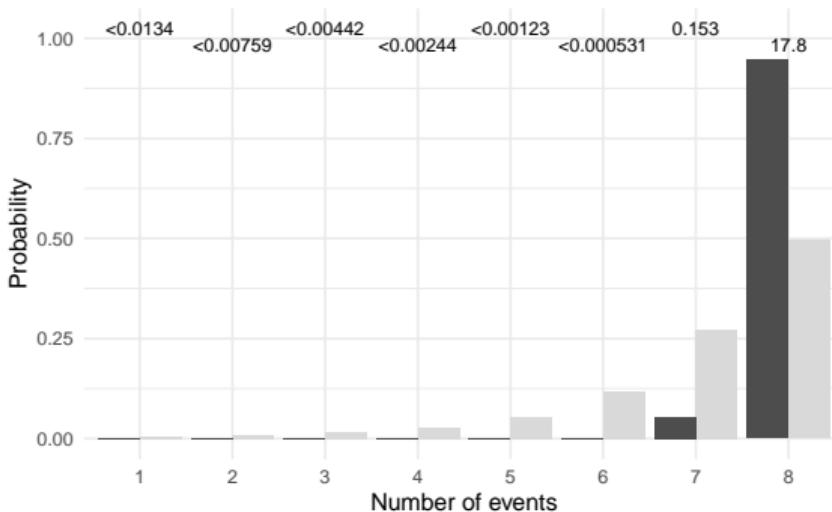
Scan for sea-level animation

**Did fragmentation of islands
promote diversification?**

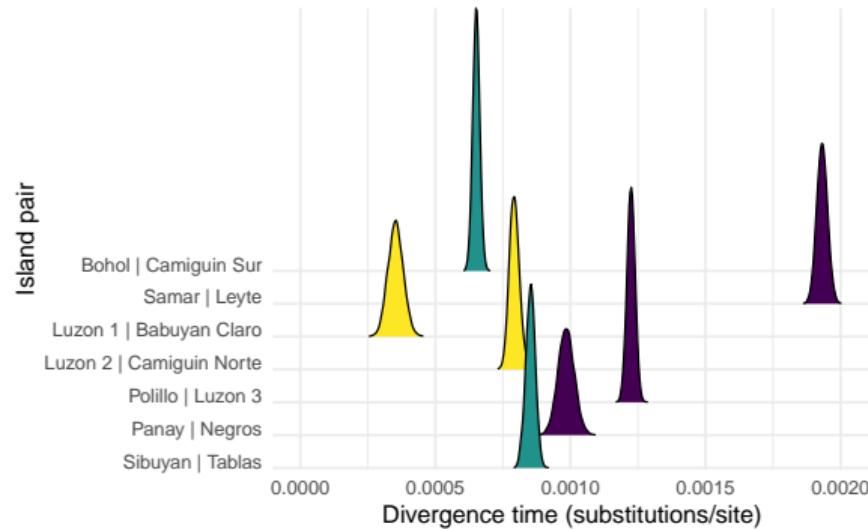
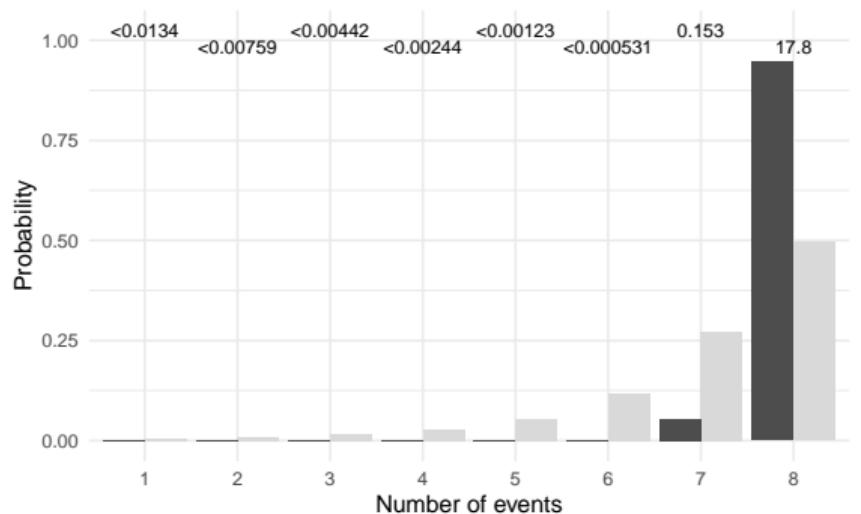


- ▶ Sampled 2–5 individuals from 8 pairs of populations for both *Cyrtodactylus* and *Gekko*
- ▶ Collected short DNA sequences (RADseq) from across genome of each individual

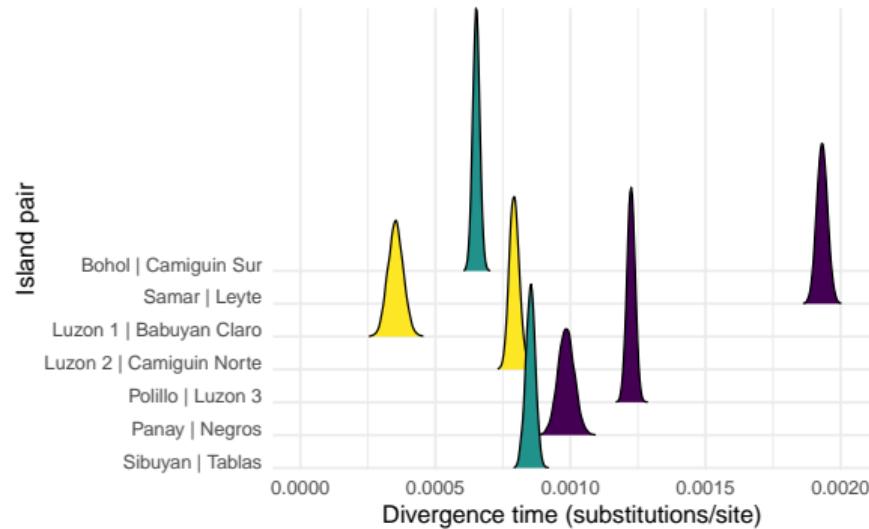
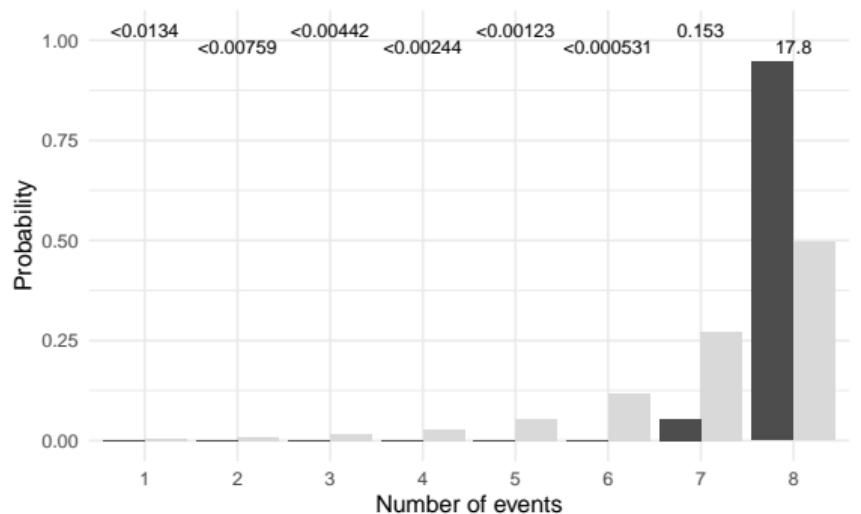
Results: *Cyrtodactylus*



Results: *Cyrtodactylus*



Results: *Cyrtodactylus*



Strong support for independent divergences

Take-home points

- ▶ Support against the climate-driven “species-pump” hypothesis

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- ▶ Habitat heterogeneity and rare over-water dispersal via rafting on vegetation perhaps more important

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- ▶ Support against the climate-driven “species-pump” hypothesis
- ▶ Habitat heterogeneity and rare over-water dispersal via rafting on vegetation perhaps more important
- ▶ Full-likelihood, Bayesian approach is faster and more accurate than ABC

Open science: everything is available...

Software:

- ▶ Ecoevolity:
phyletica.org/ecoevolity

Open-Science Notebooks:

- ▶ Gecko RADseq:
github.com/phyletica/gekgo
- ▶ Simulation analyses:
github.com/phyletica/ecoevolity-experiments
github.com/phyletica/ecoevolity-model-prior
github.com/phyletica/codiv-sanger-bake-off

Approaches to the problem

A pairwise approach (keep it “simple”)

A fully phylogenetic approach



Biogeography

- ▶ Environmental changes that affect whole communities of species

Genome evolution

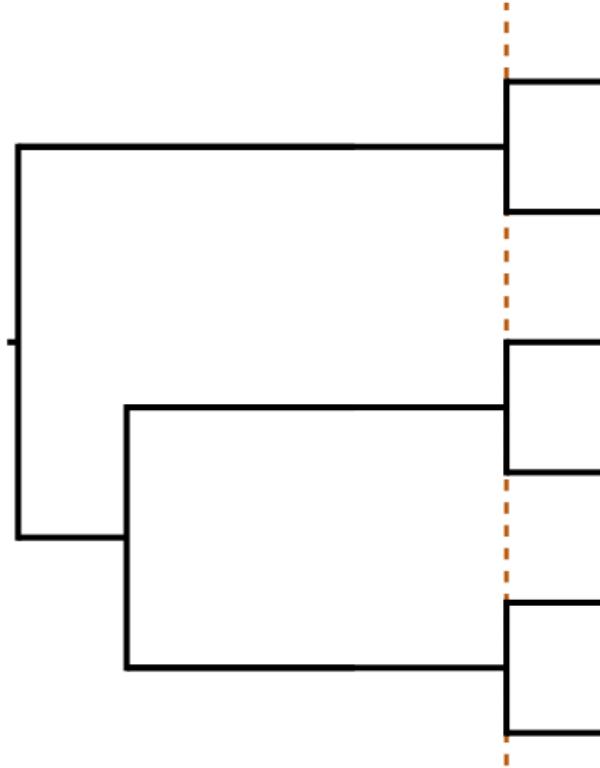
- ▶ Duplication of a chromosome segment harboring gene families

Epidemiology

- #### ► Transmission at social gatherings

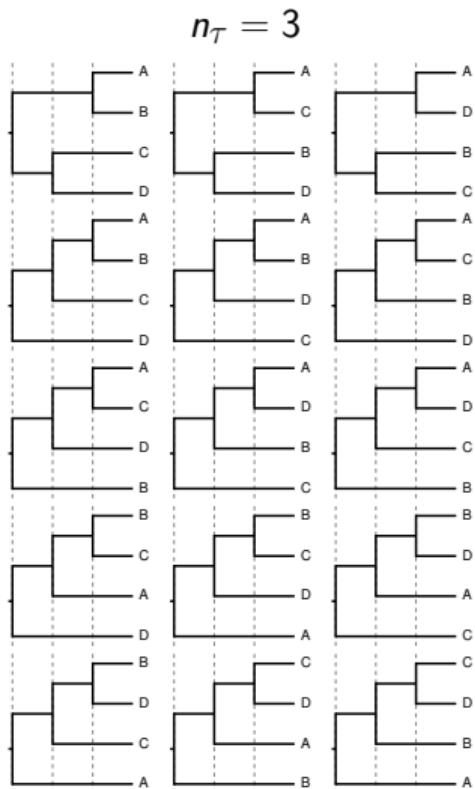
Endosymbiont evolution (e.g., parasites, microbiome)

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



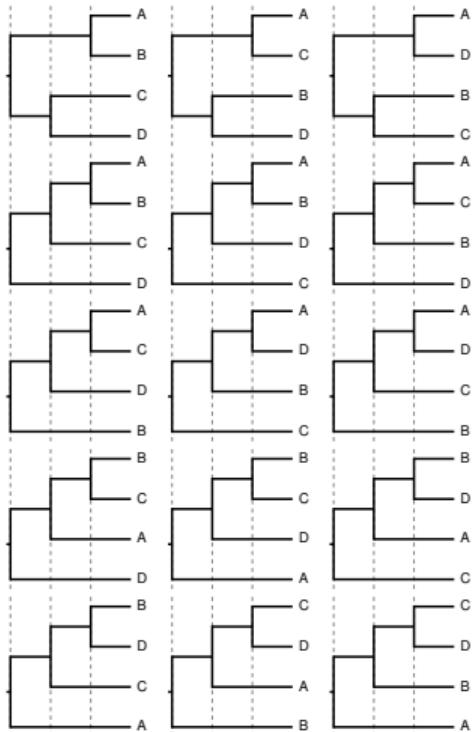
Generalizing tree space

Generalizing tree space

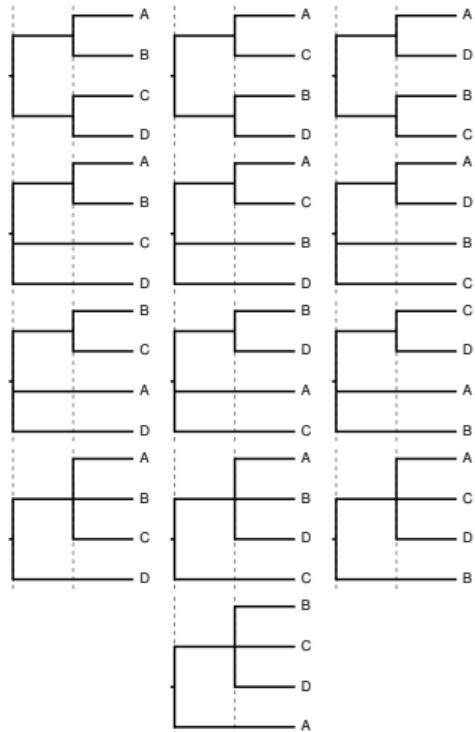


Generalizing tree space

$$n_T = 3$$



$$n_T = 2$$

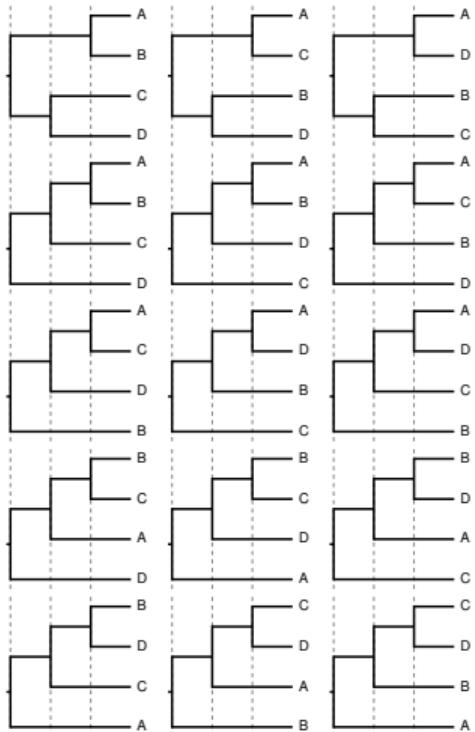


$$n_T = 1$$

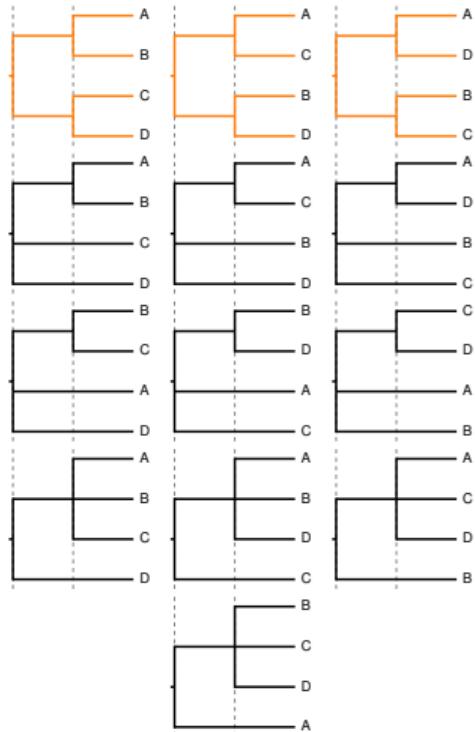


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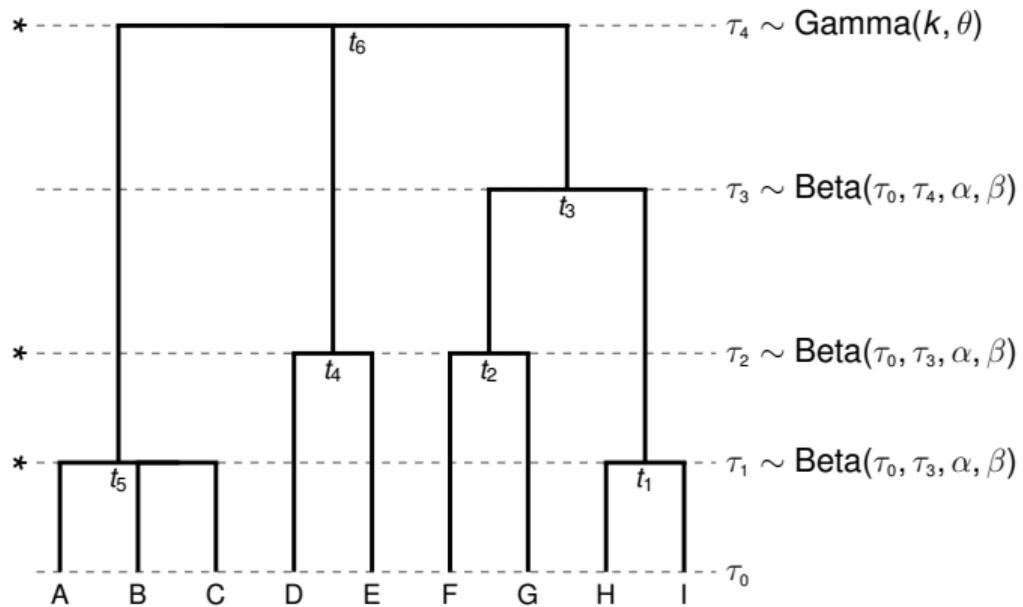


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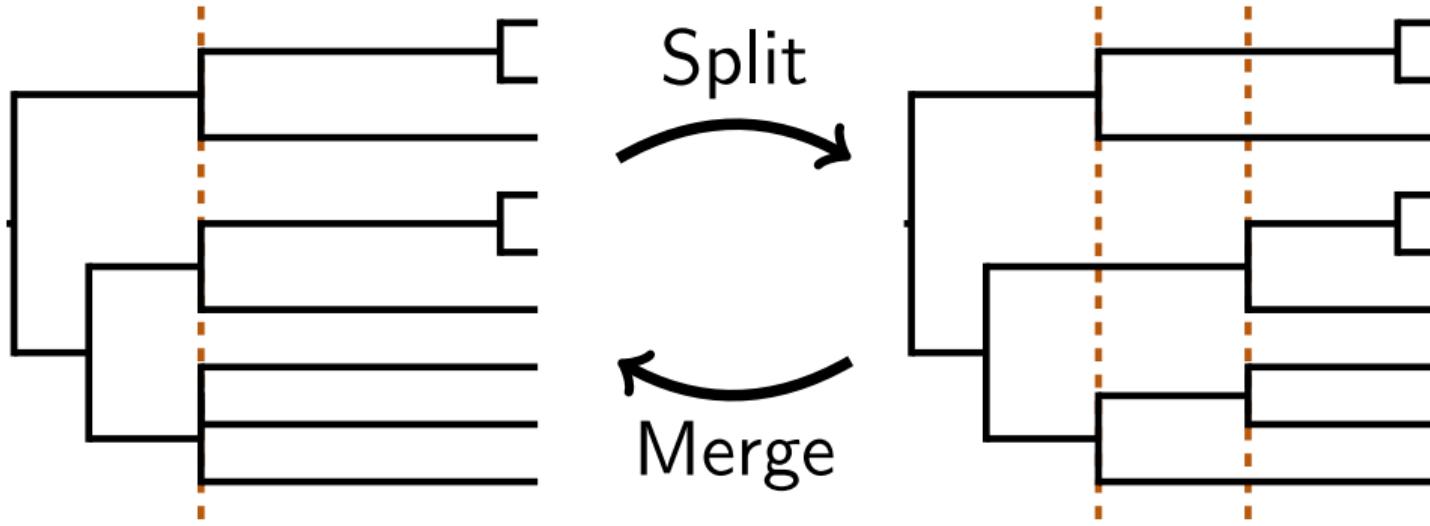


Generalized tree distribution

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

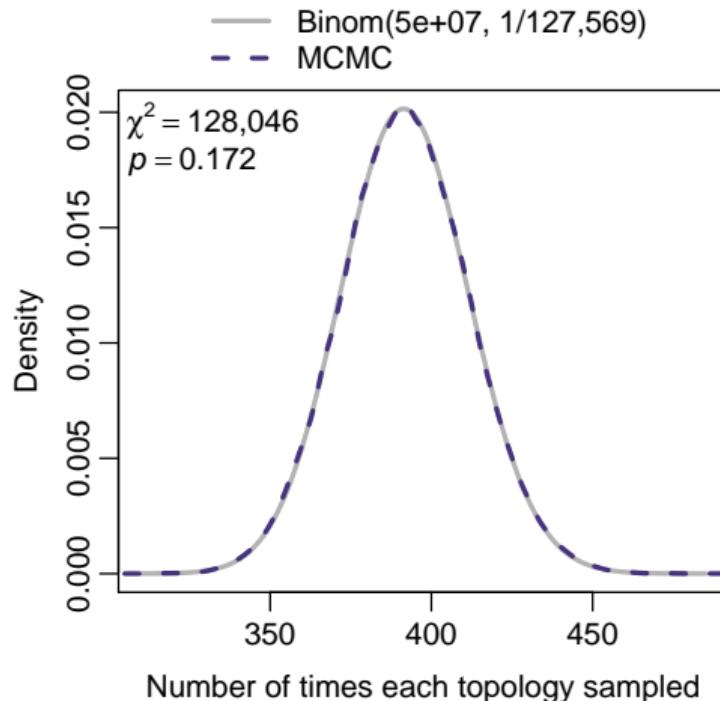


Inferring trees with shared divergences



Reversible-jump MCMC

Validating rjMCMC with 7-leaf tree



The rjMCMC algorithms sample the expected generalized tree distribution

*Phyco*Eval

Phylogenetic coevality

J. R. Oaks et al. (2021). *bioRxiv*

Ecoevolity

Estimating evolutionary coevality

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- ▶ Tree model

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

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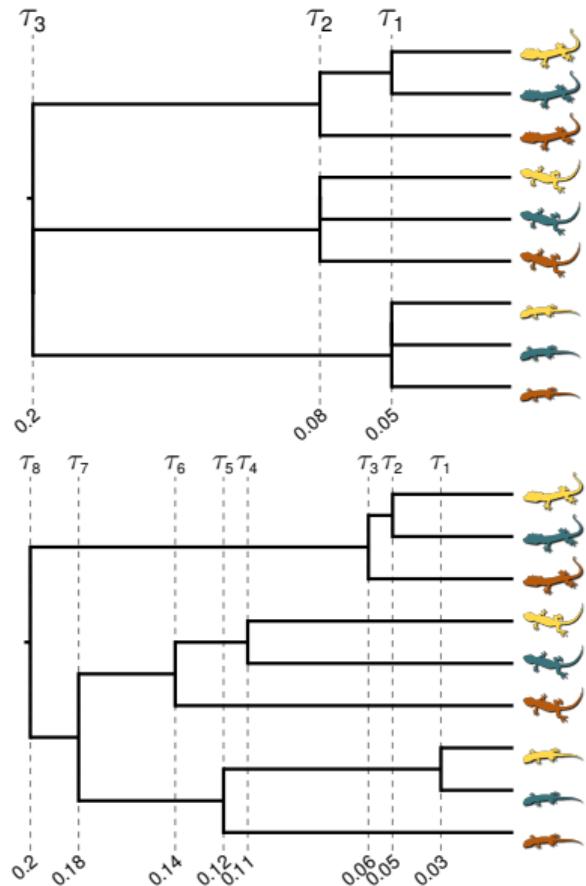
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- ▶ *Goal: Co-estimation of phylogeny and shared divergences from genomic data*

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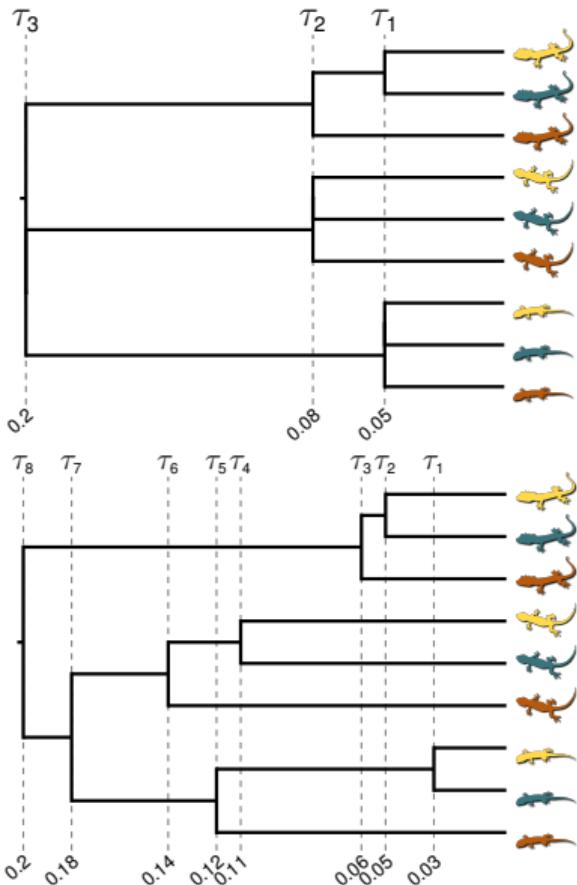
Methods: Simulations

- ▶ Simulated 100 data sets with 50,000 base pairs



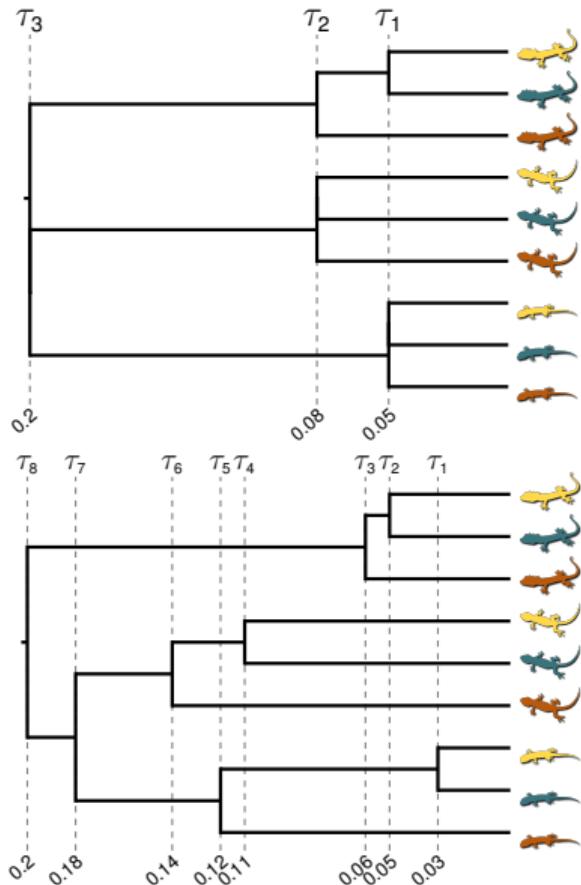
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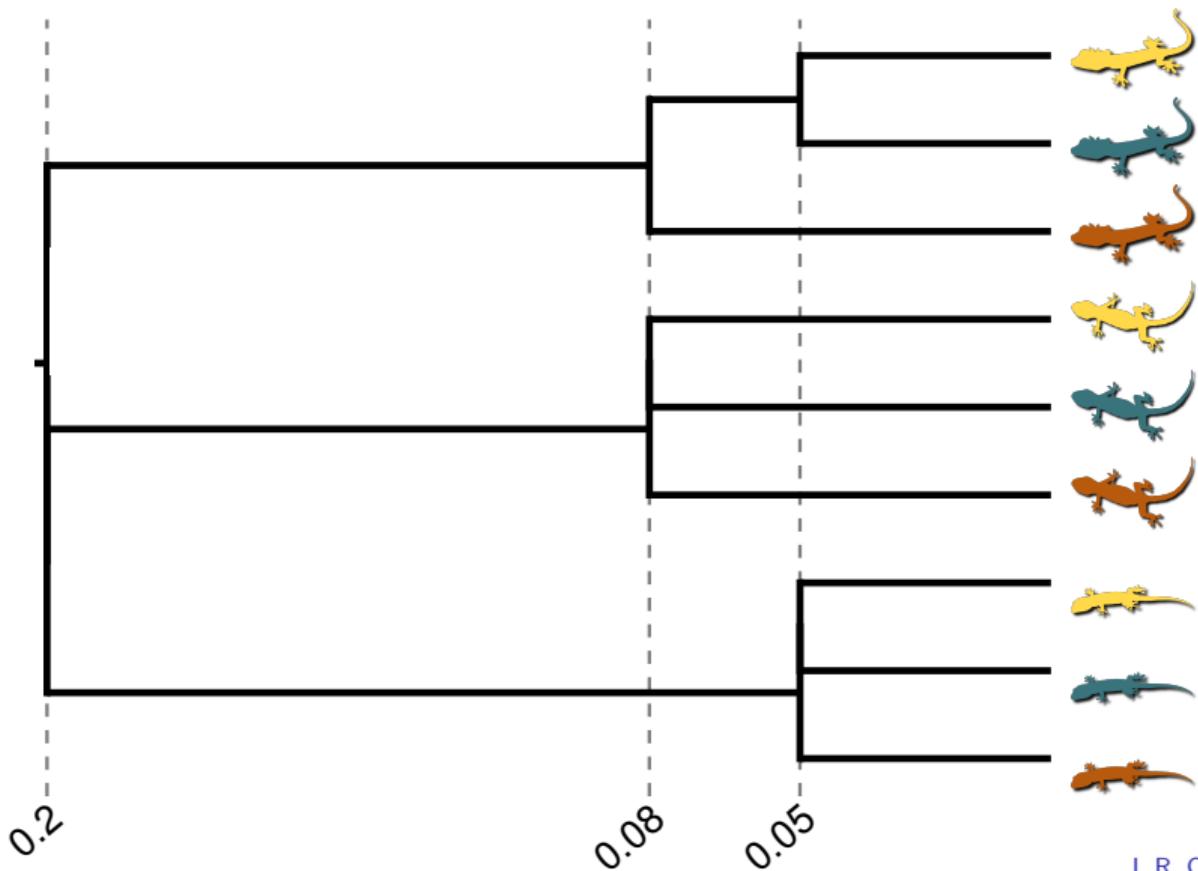
- ▶ Simulated 100 data sets with 50,000 base pairs
- ▶ Analyzed each data set with:
 - ▶ M_G = Generalized tree model
 - ▶ M_{IB} = Independent-bifurcating tree model

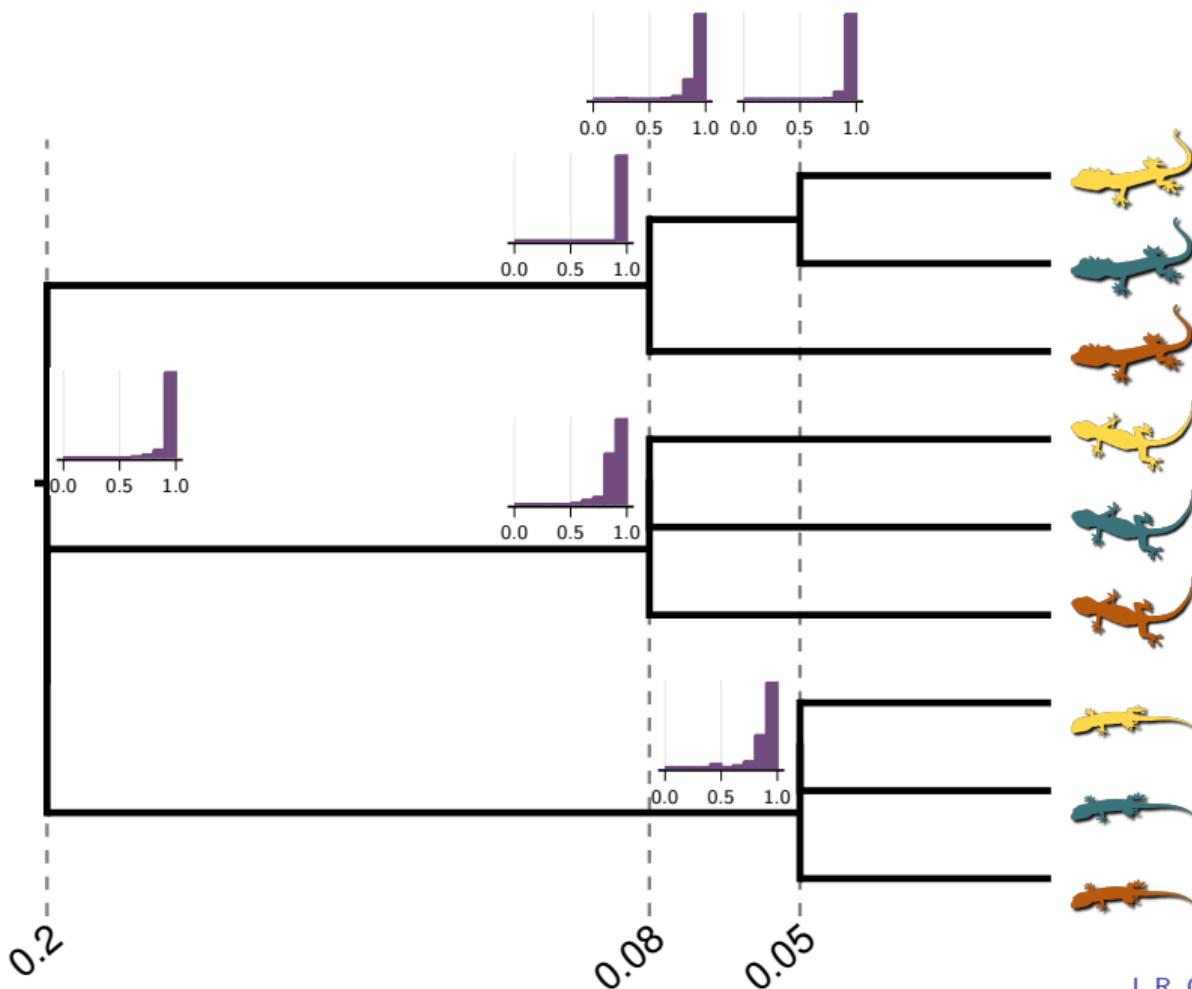


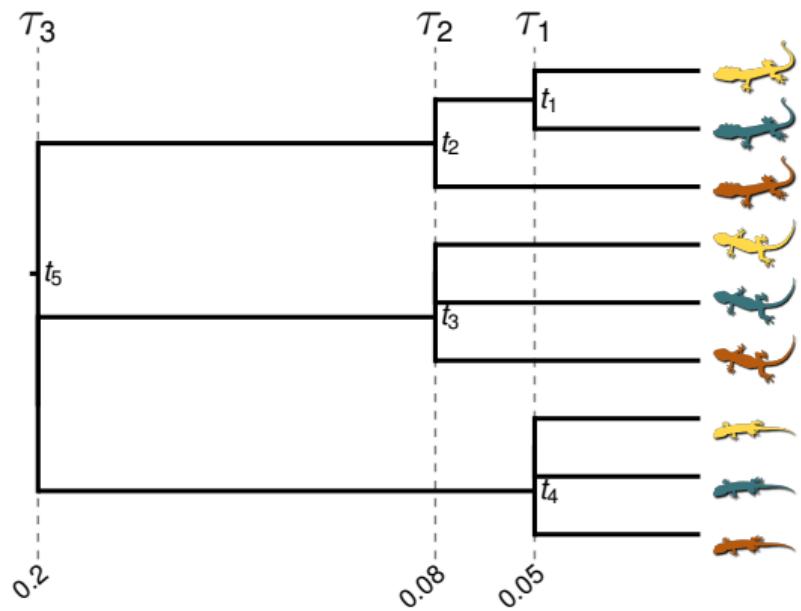
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- ▶ Simulated 100 data sets where topology and div times randomly drawn from M_G and M_{IB}



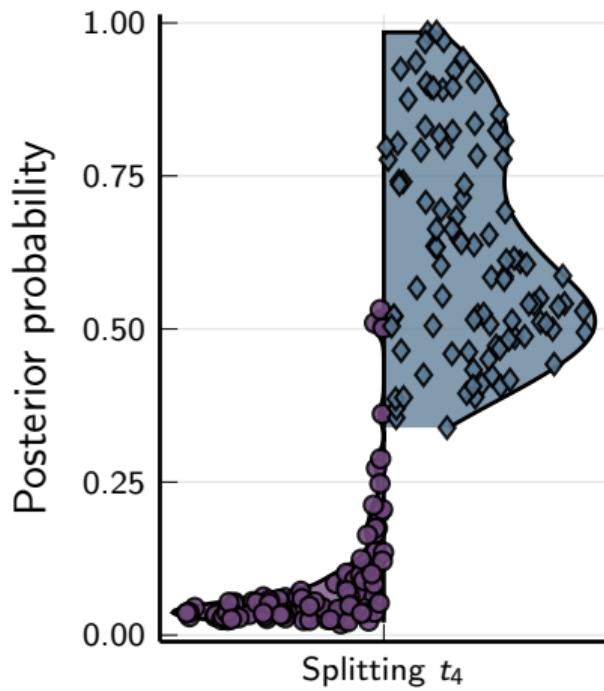
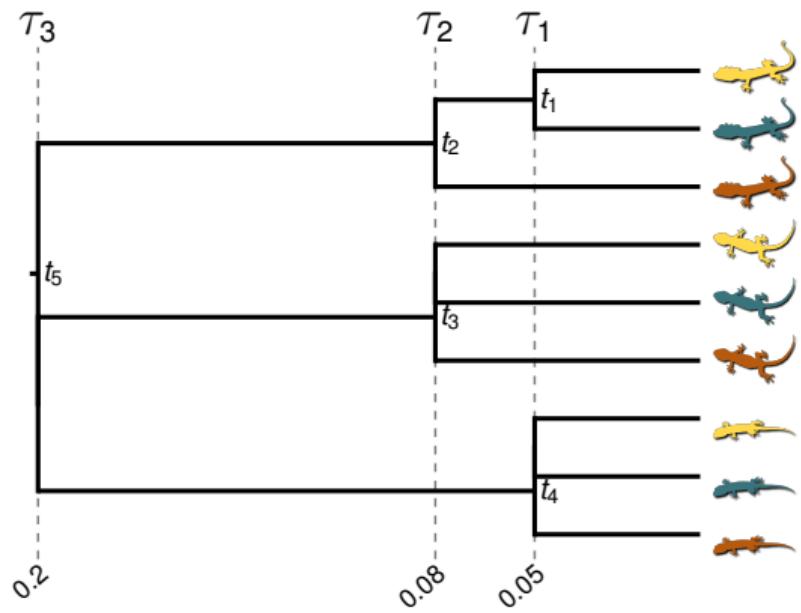






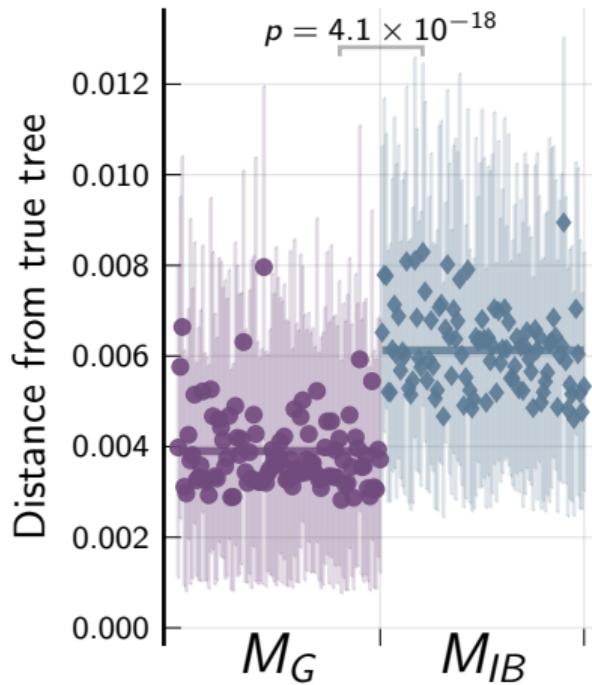
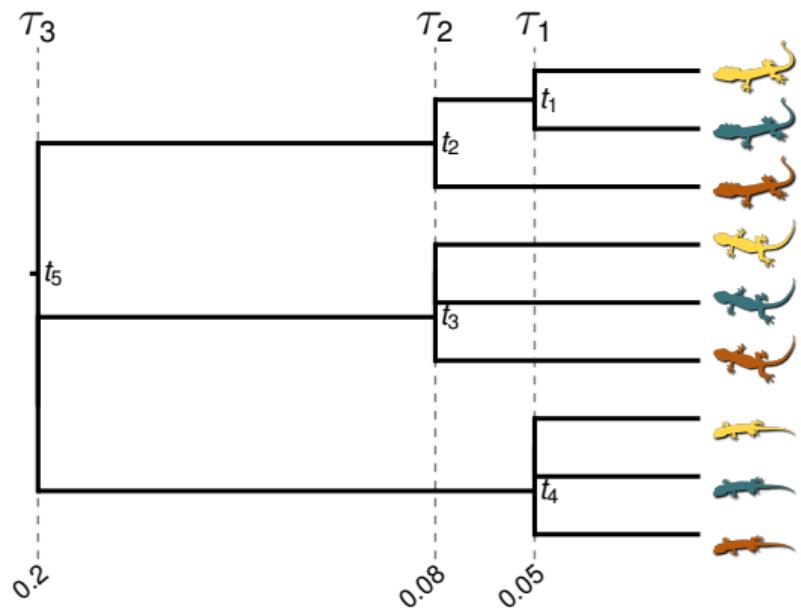
● M_G = Generalized model

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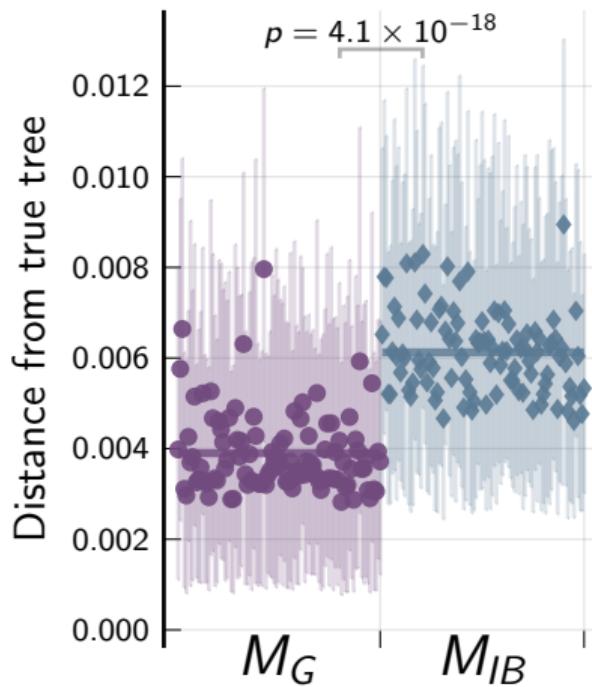
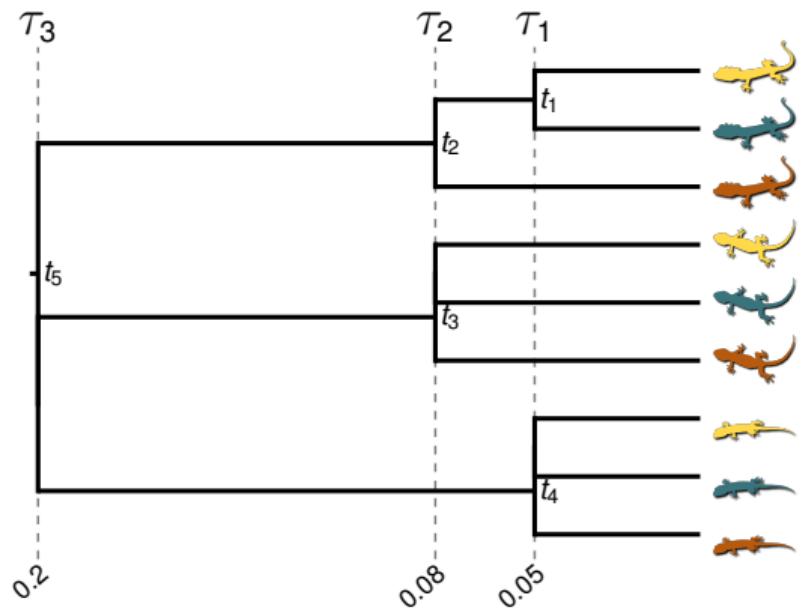
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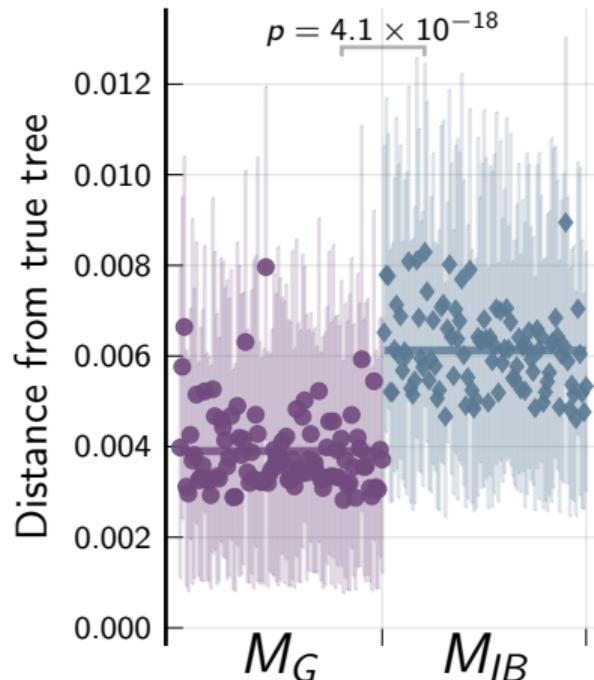
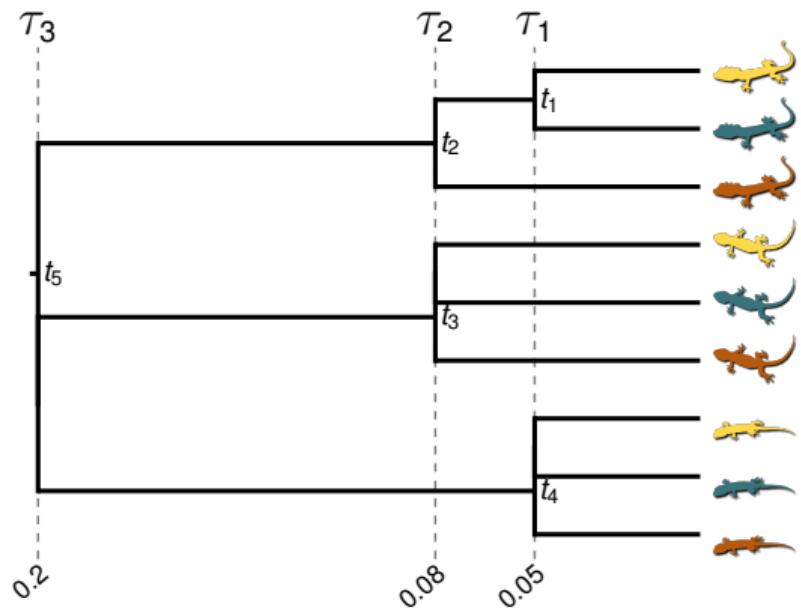
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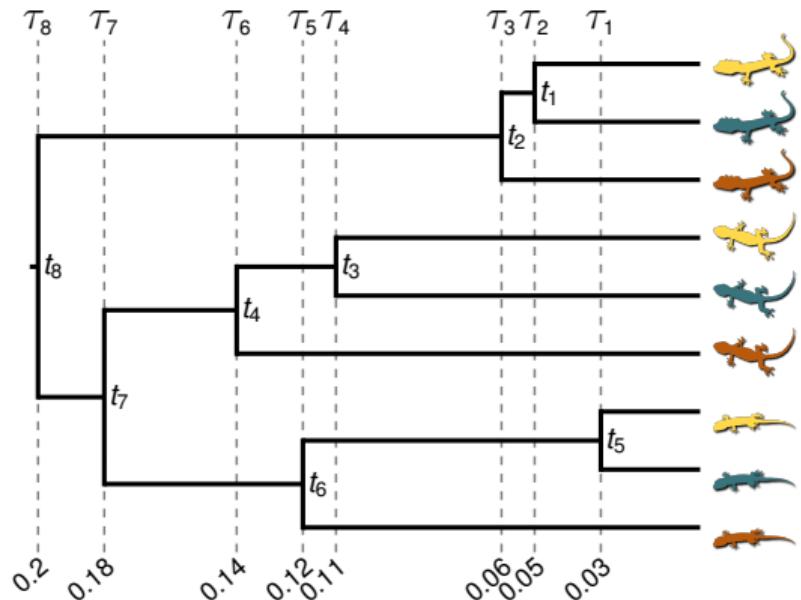
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M_G significantly better at inferring trees with shared divergences

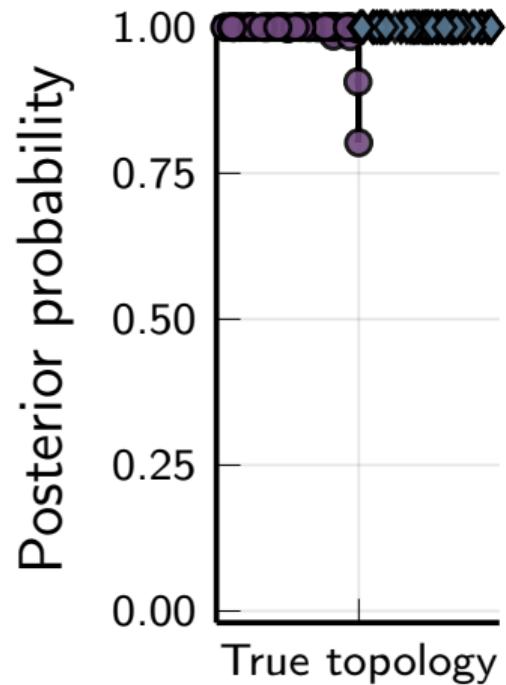
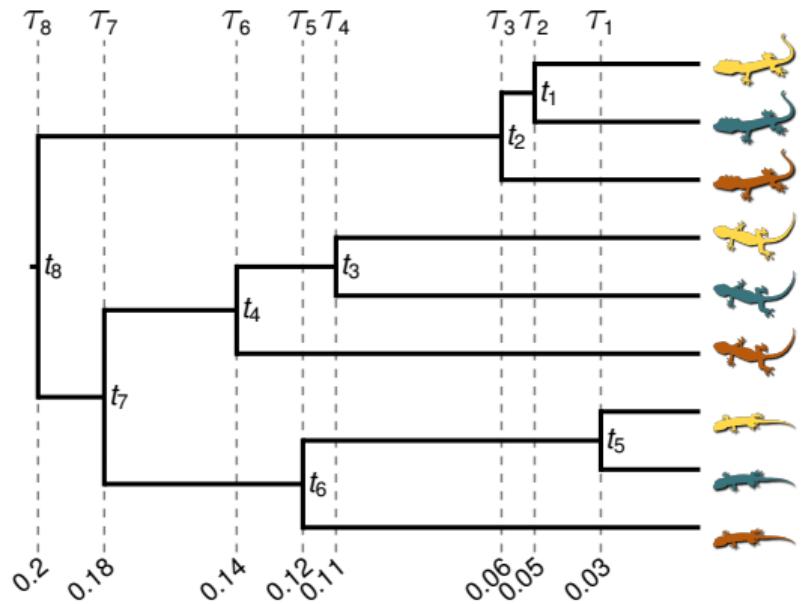
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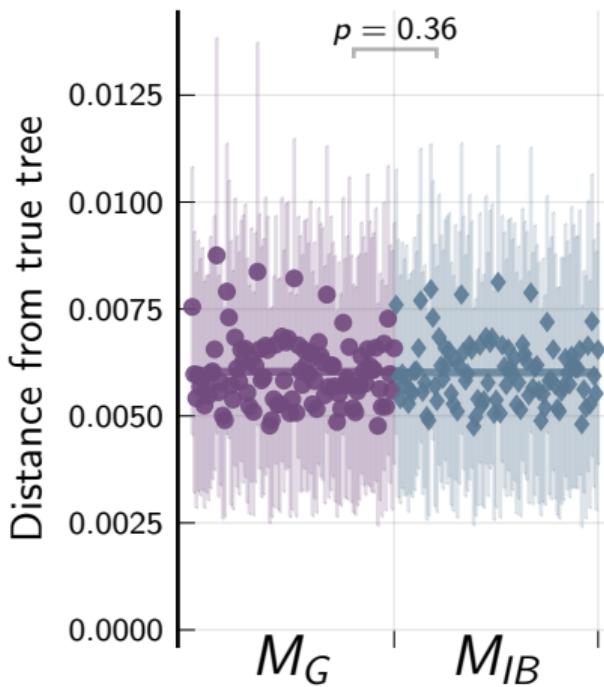
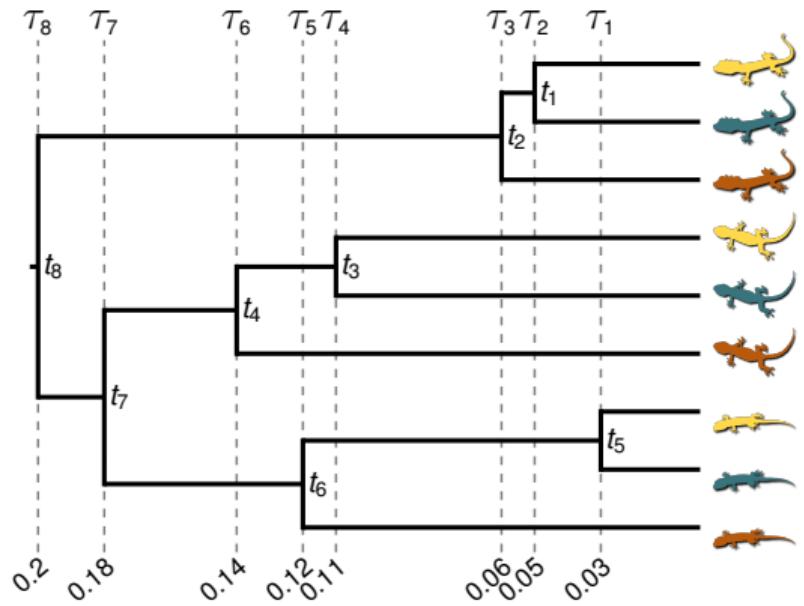
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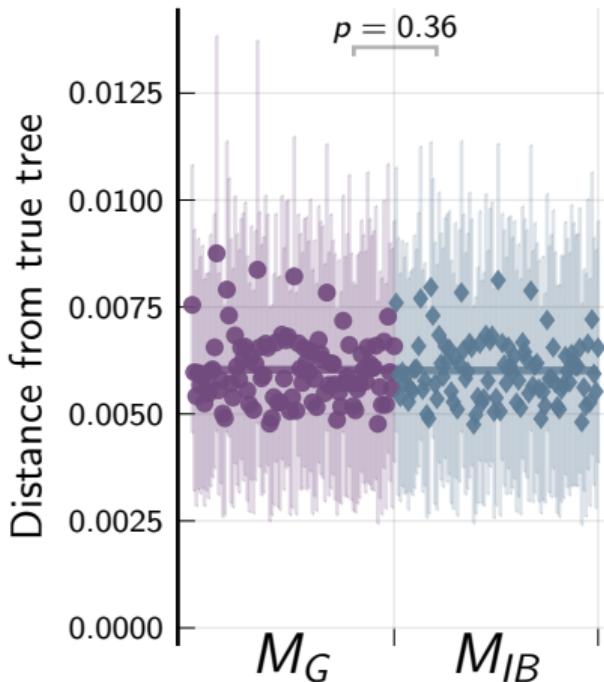
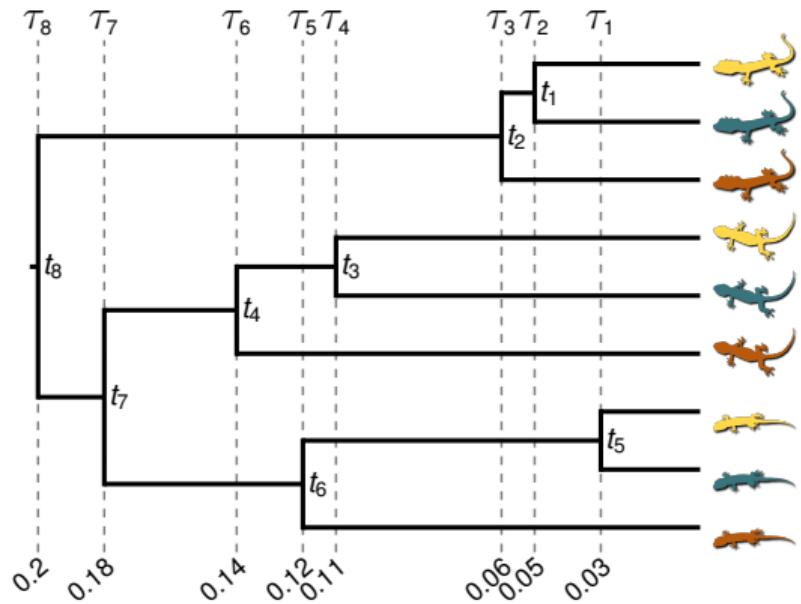
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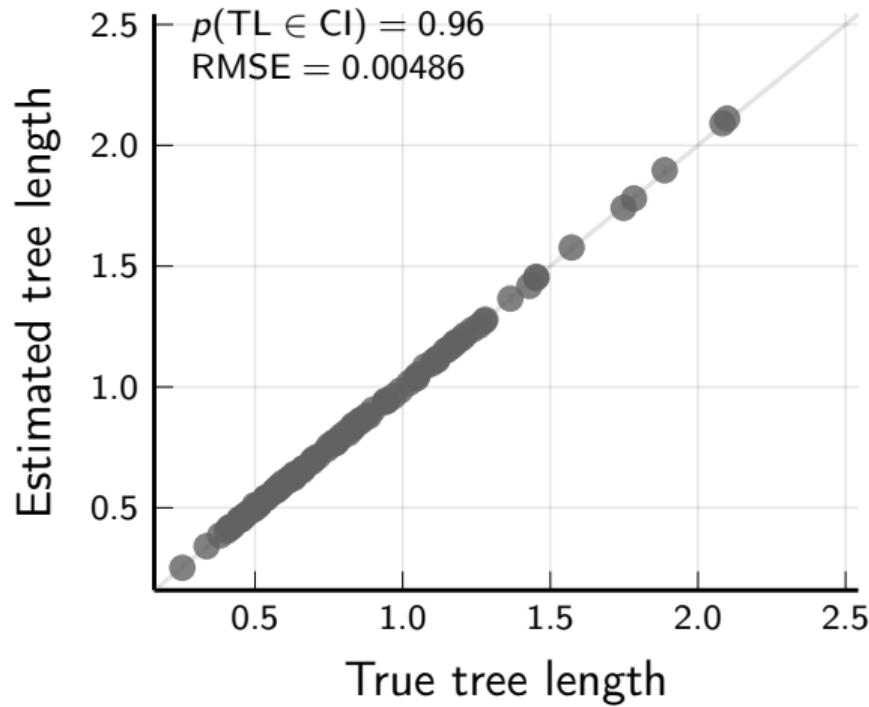
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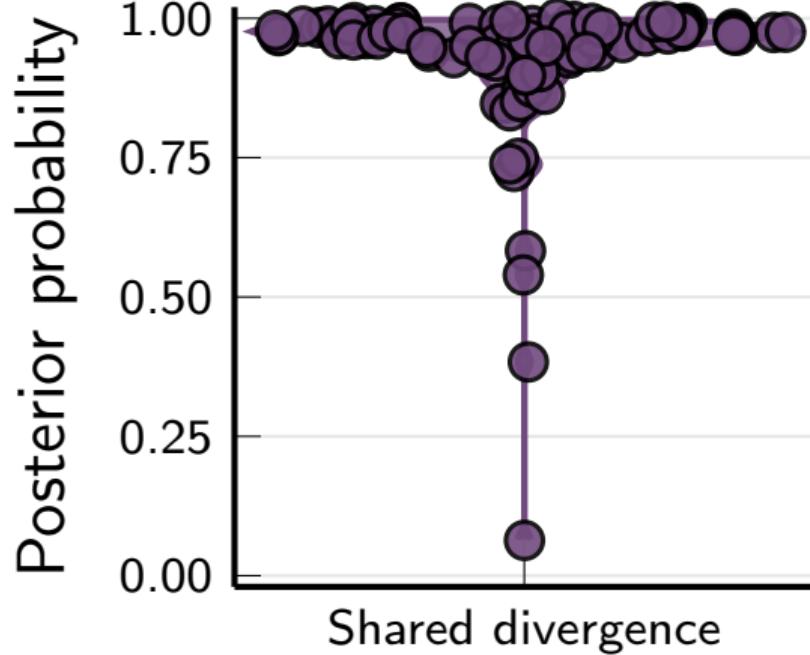
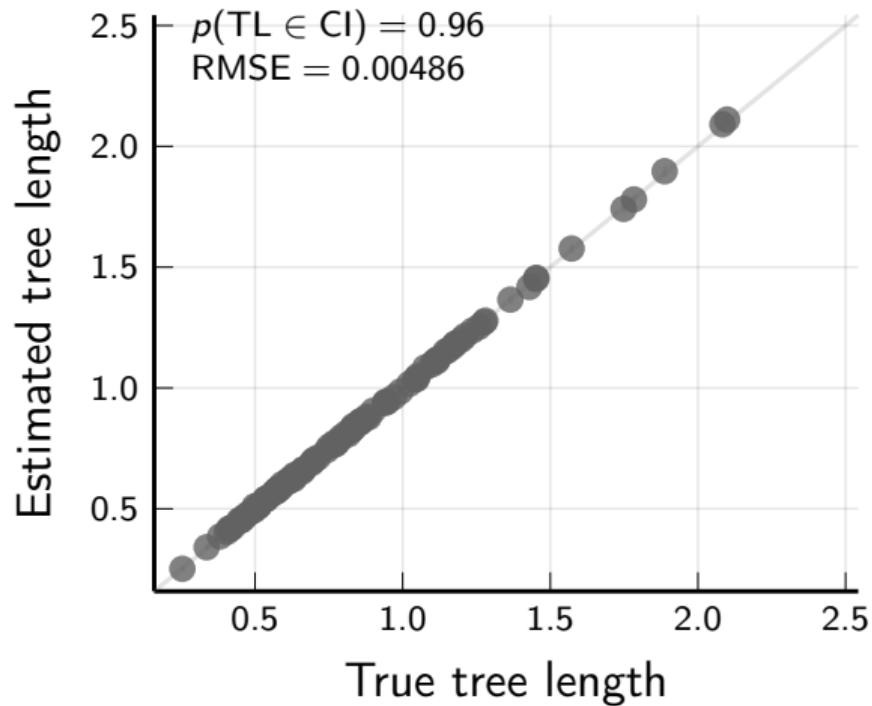


M_G performs as well as true model when divergences are independent

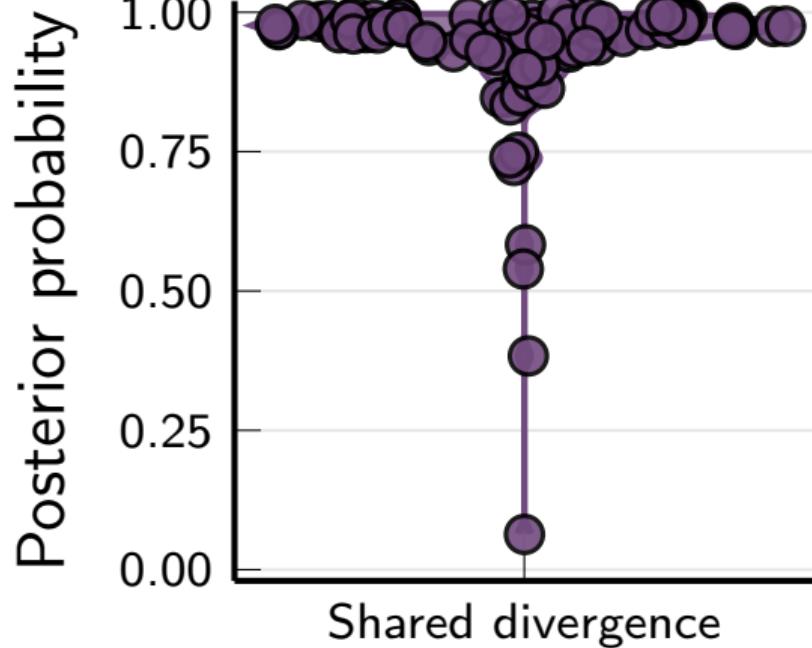
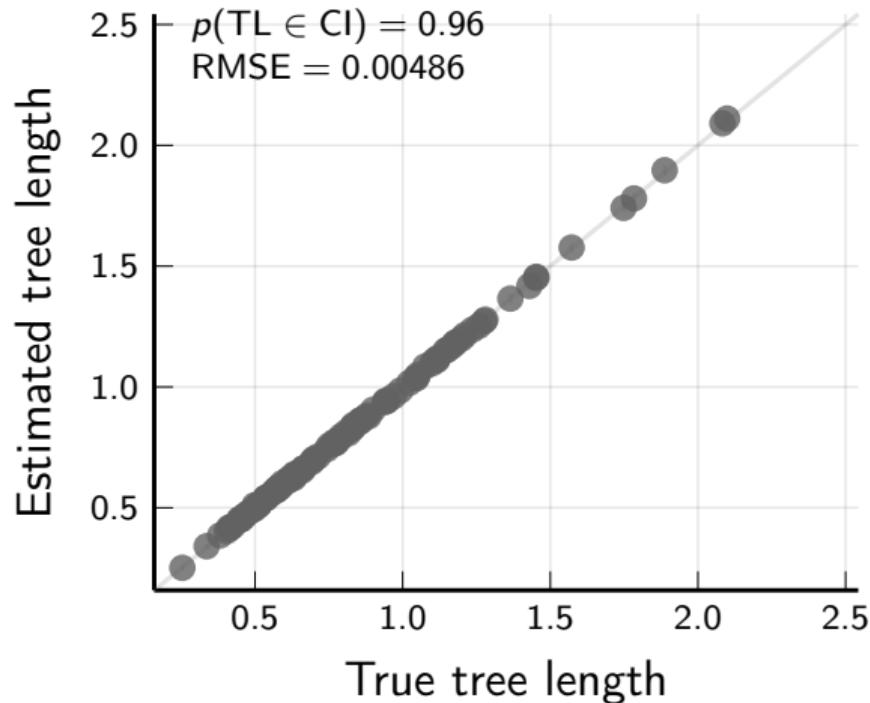
Results: random M_G trees



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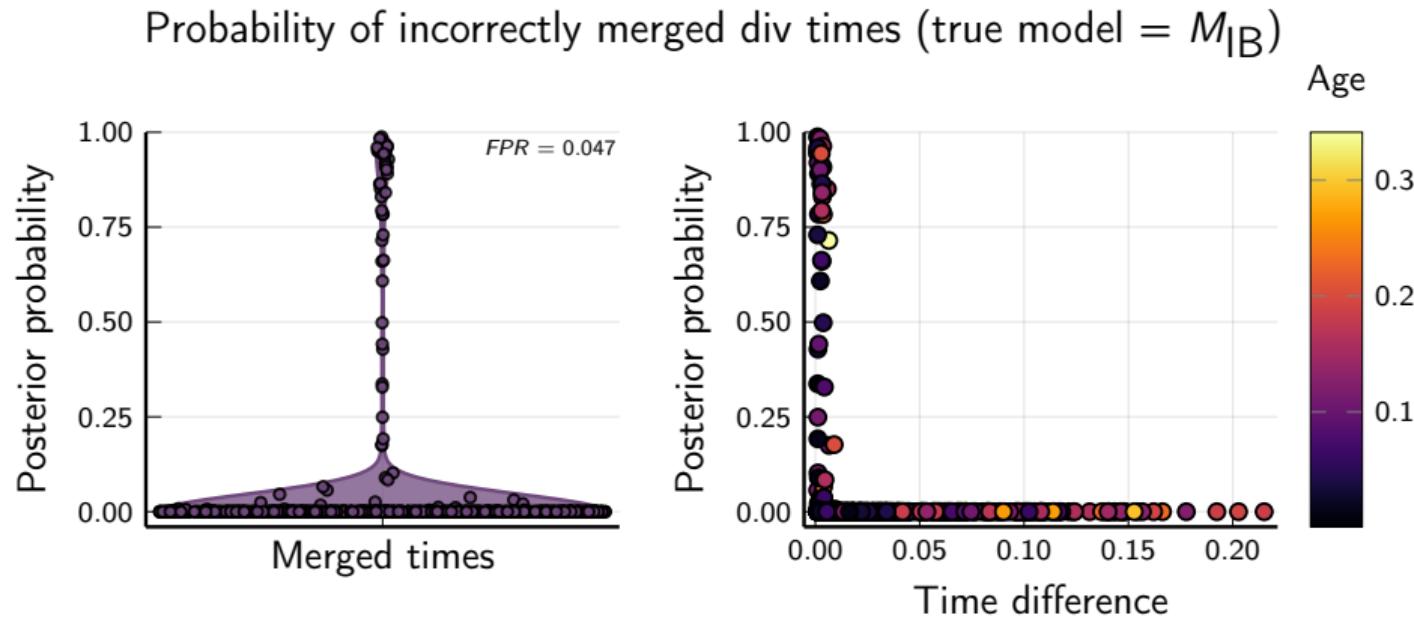


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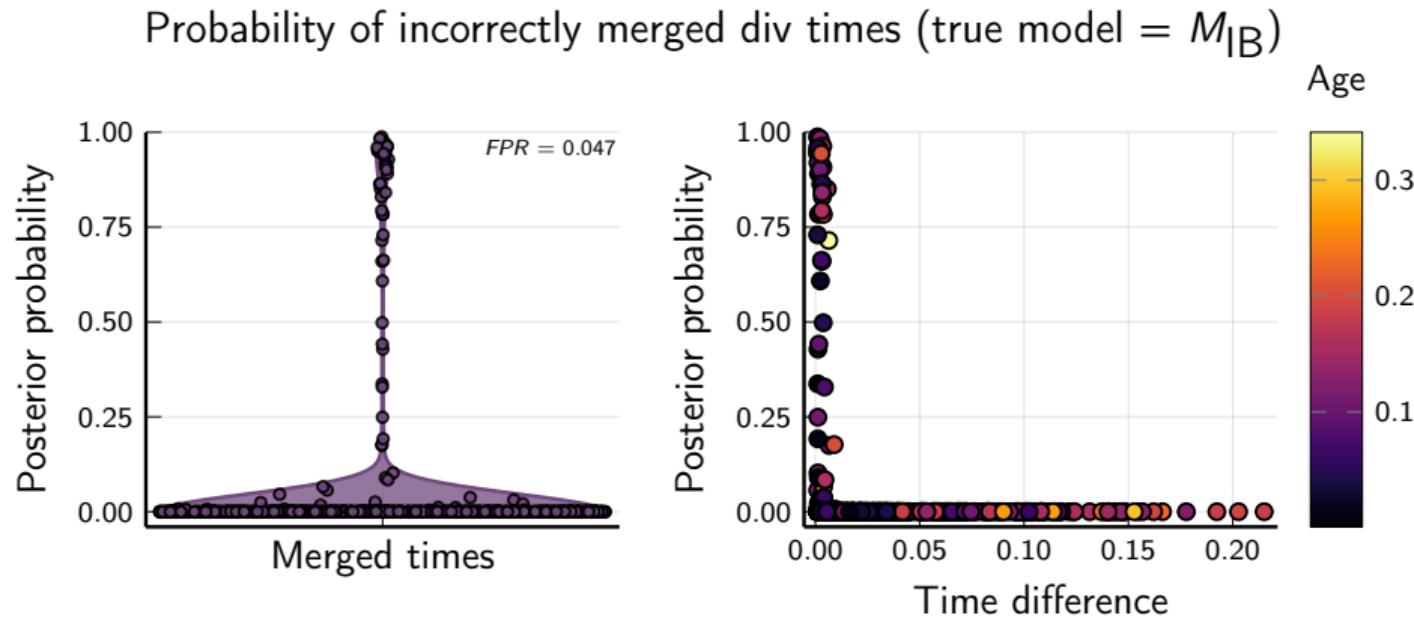


M_G performs well with data simulated on random trees with shared divergences

Results: random M_{IB} trees



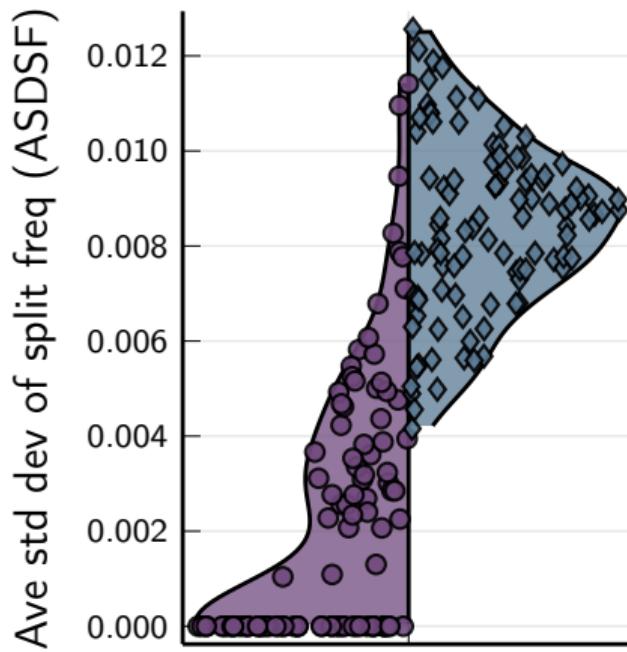
Results: random M_{IB} trees



M_G has low false positive rate

● M_G = Generalized model

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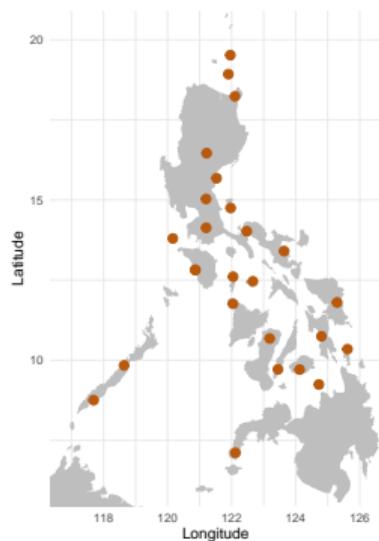
Generalizing tree space improves MCMC convergence and mixing



Scan for sea-level animation

**Did fragmentation of islands
promote diversification?**

Cyrtodactylus



©Rafe M. Brown

Gekko



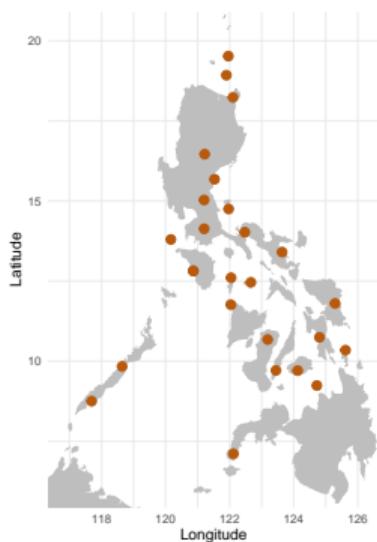
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Cyrtodactylus



©Rafe M. Brown

1702 loci
155,887 sites



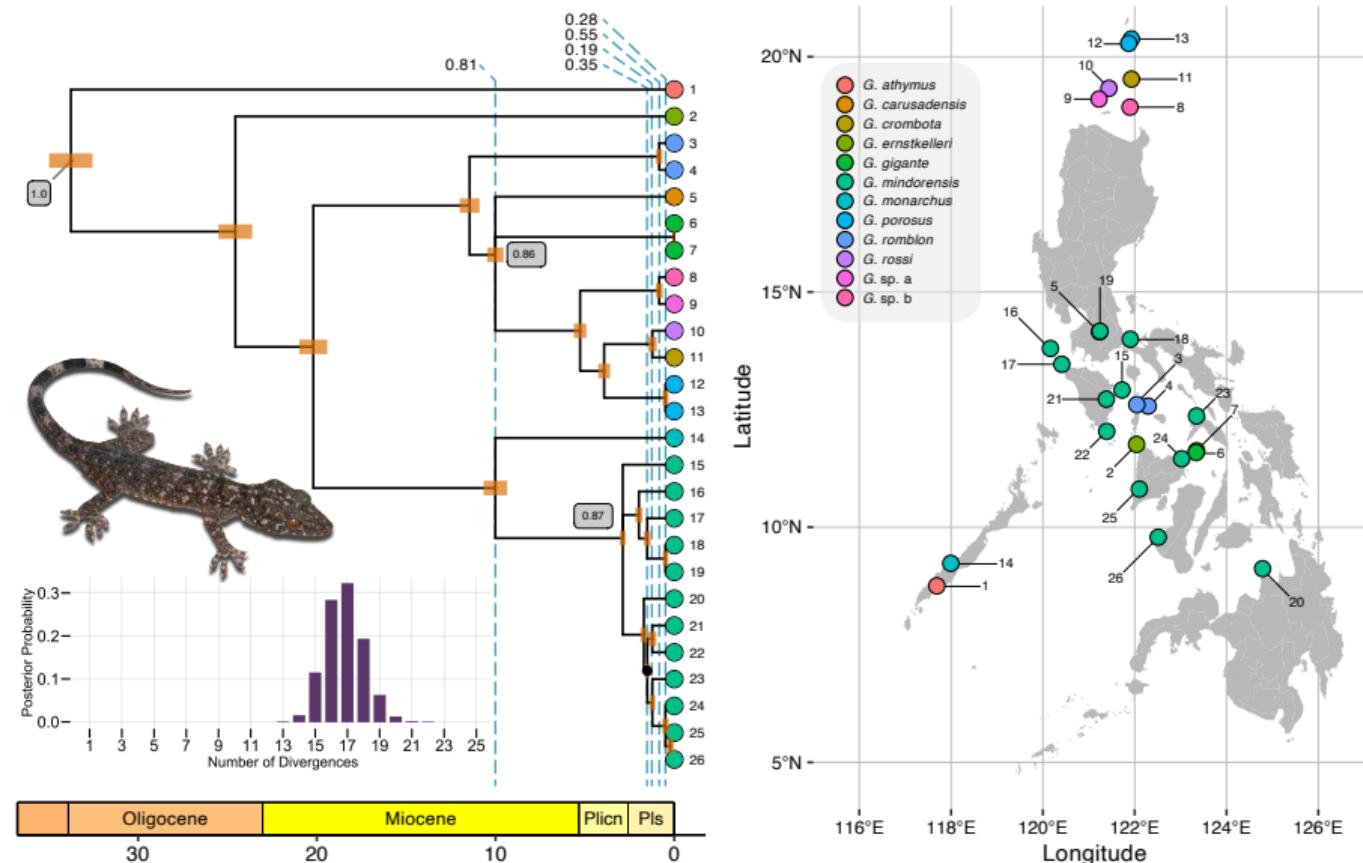
Gekko



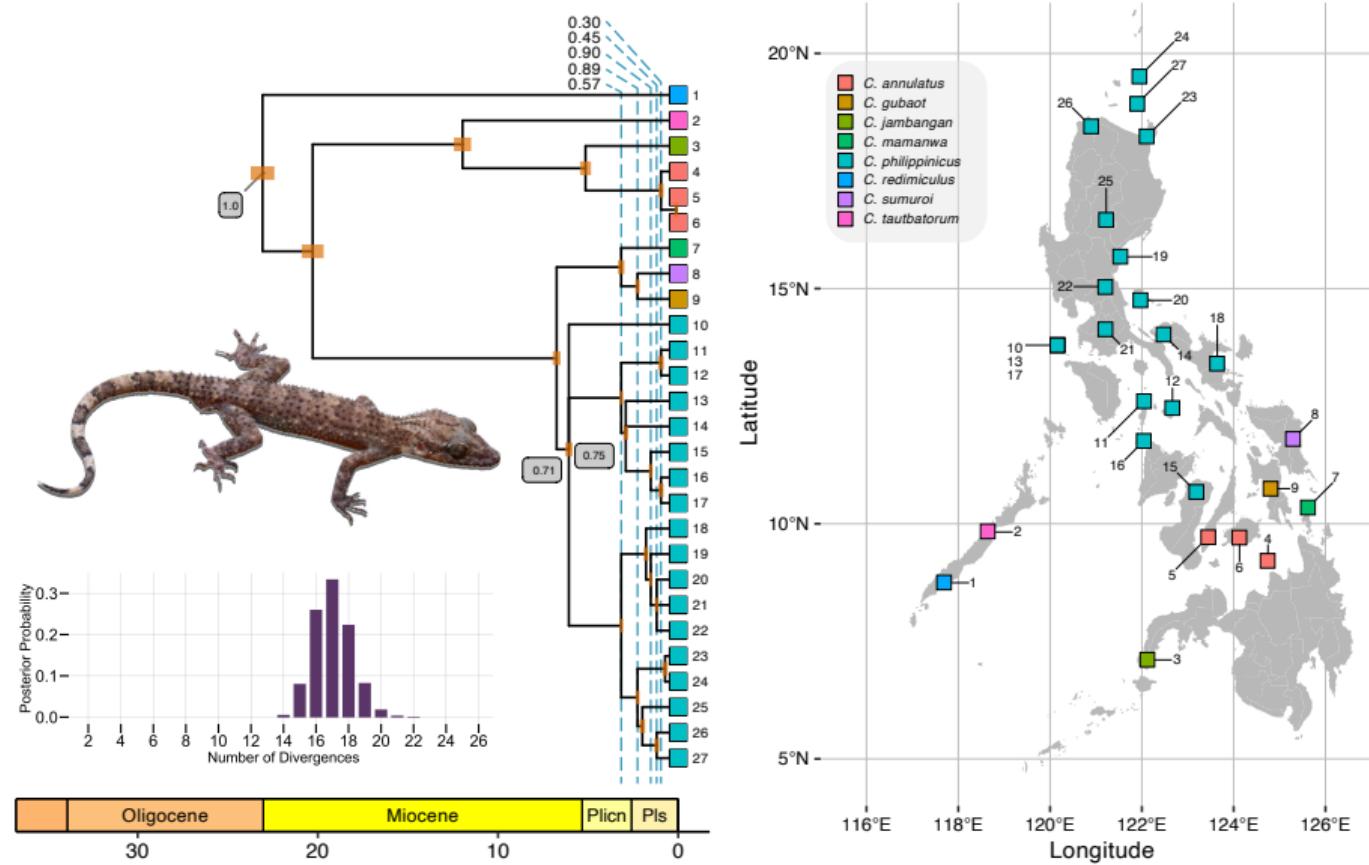
©Rafe M. Brown

1033 loci
94,813 sites

Gekko



Cyrtodactylus



Take-home points

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

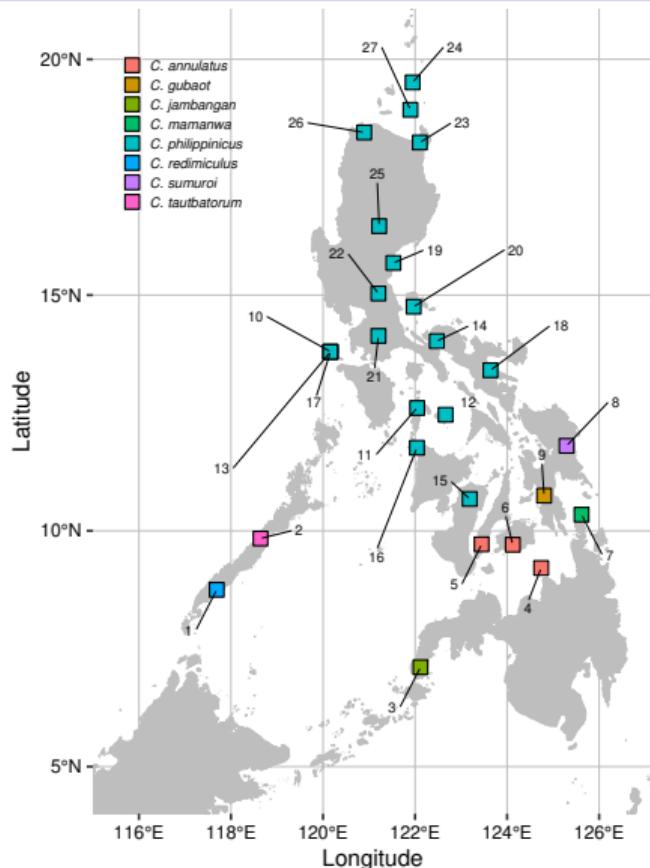
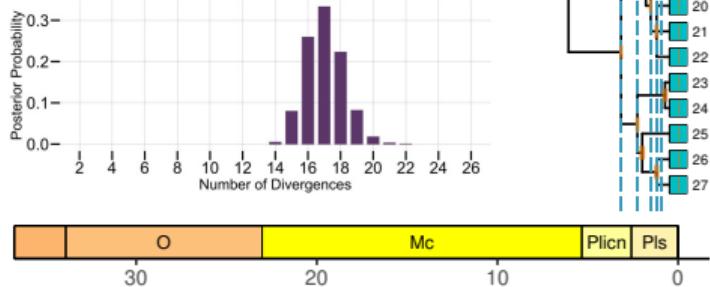
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- ▶ We can accurately infer phylogenies with shared divergences with moderately sized data sets
- ▶ Generalizing tree space avoids spurious support and improves MCMC mixing
- ▶ Among Philippine gekkonids, we found support for shared divergences predicted by sea-level changes

Cyrtodactylus



Open science: everything is available...

Software:

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

Open-Science Notebooks:

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

Ongoing work

Theory/methods

- ▶ Develop process-based and trait-dependent distributions over the space of generalized trees
 - ▶ “Birth-death-burst” model

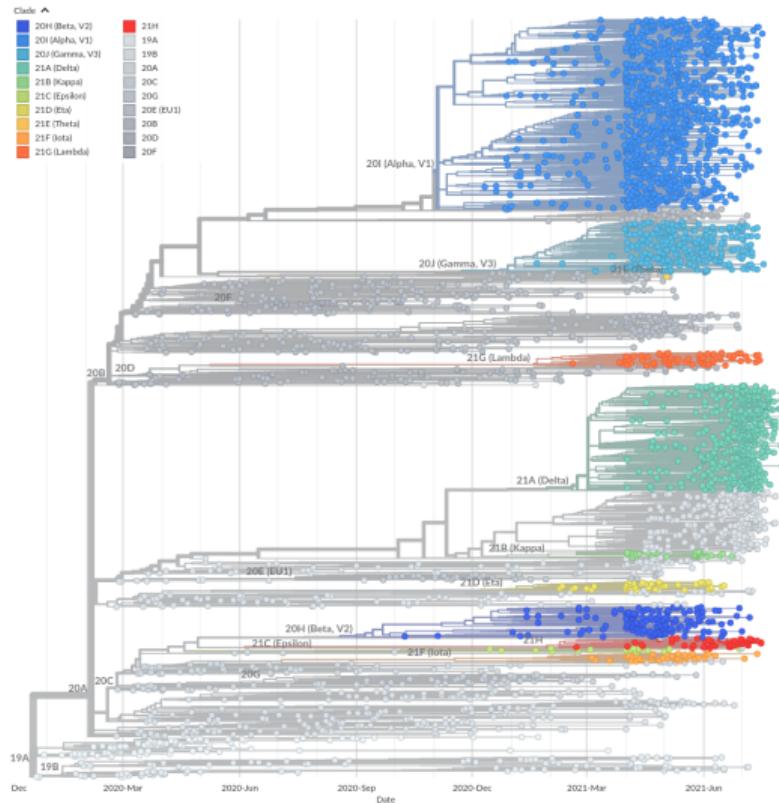
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Applications

- ▶ Epidemiological dynamics of “super-spreading” events during the COVID-19 pandemic



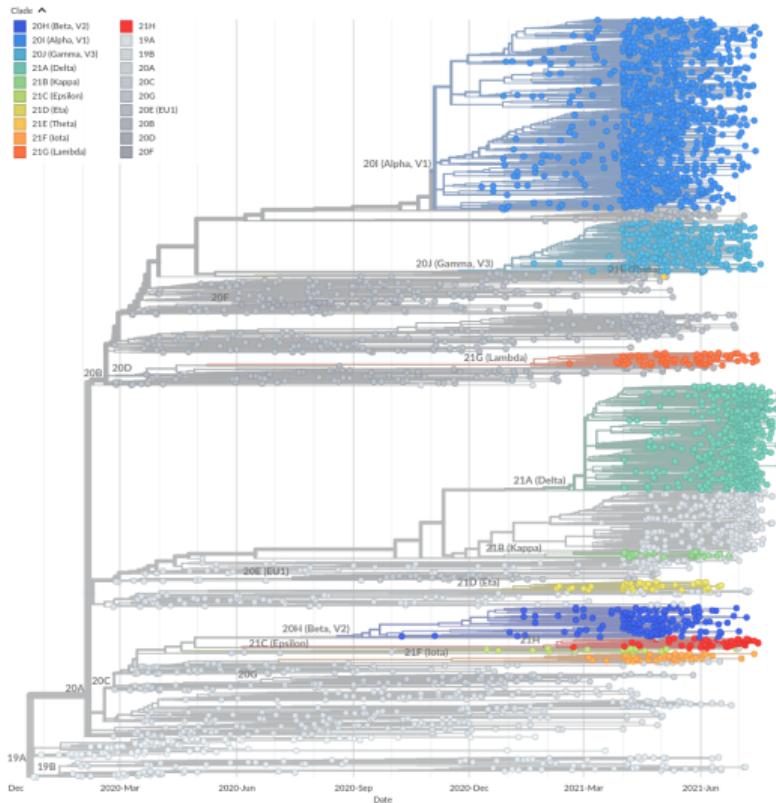
Ongoing work

Theory/methods

- ▶ Develop process-based and trait-dependent distributions over the space of generalized trees
 - ▶ “Birth-death-burst” model

Applications

- ▶ Epidemiological dynamics of “super-spreading” events during the COVID-19 pandemic
 - ▶ Estimate rate of spread via social gatherings



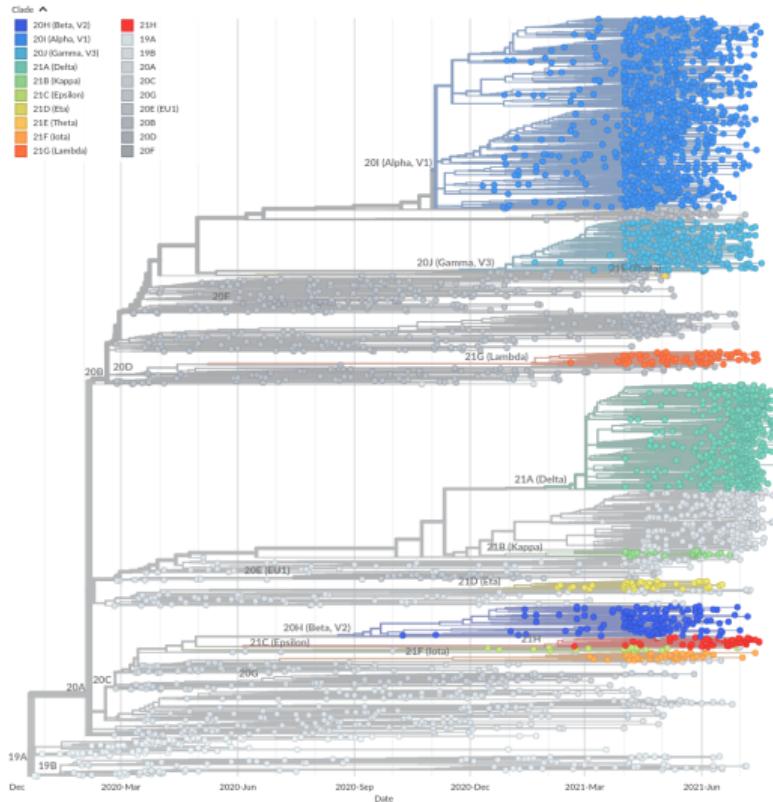
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 - ▶ Estimate rate of spread via social gatherings
 - ▶ Test if this differs among variants



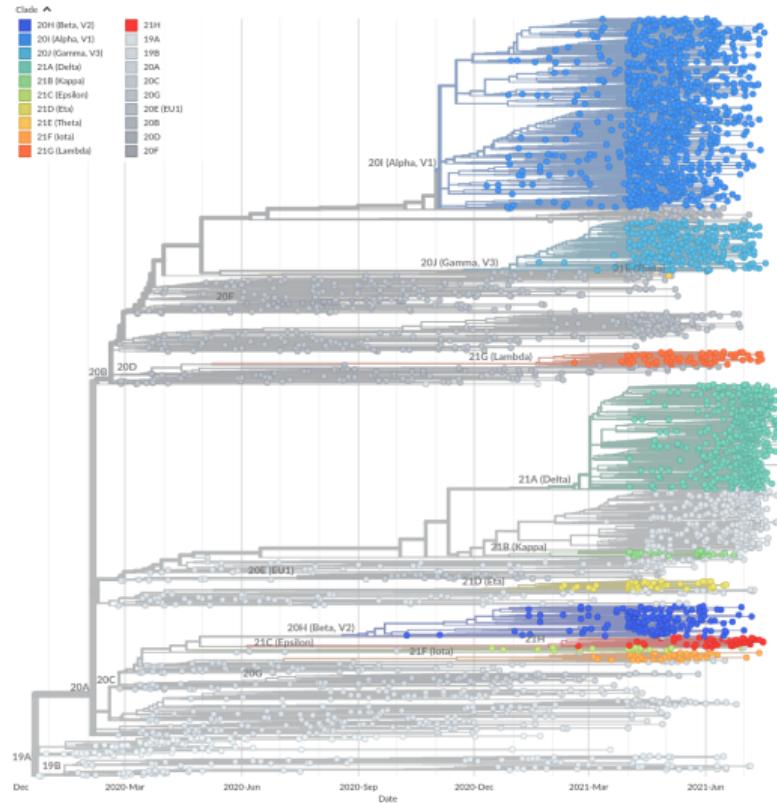
Ongoing work

Theory/methods

- ▶ Develop process-based and trait-dependent distributions over the space of generalized trees
 - ▶ “Birth-death-burst” model

Applications

- ▶ Epidemiological dynamics of “super-spreading” events during the COVID-19 pandemic
 - ▶ Estimate rate of spread via social gatherings
 - ▶ Test if this differs among variants
 - ▶ Quantify the effect of holidays



Acknowledgments

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

Computation:

- ▶ Alabama Supercomputer Authority
- ▶ Auburn University Hopper Cluster

Funding:



Photo credits:

- ▶ Rafe Brown
- ▶ Perry Wood, Jr.
- ▶ PhyloPic

Questions?

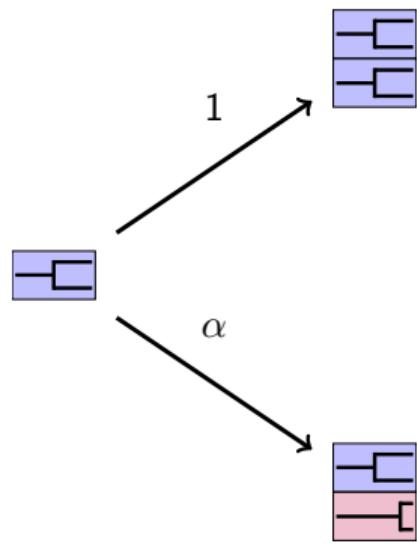
joaks@auburn.edu

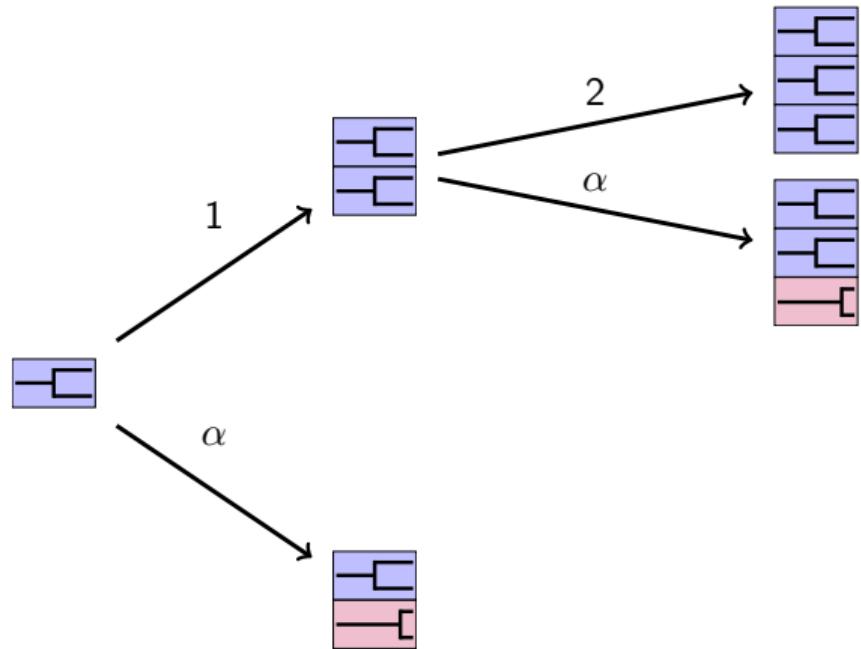
phyletica.org

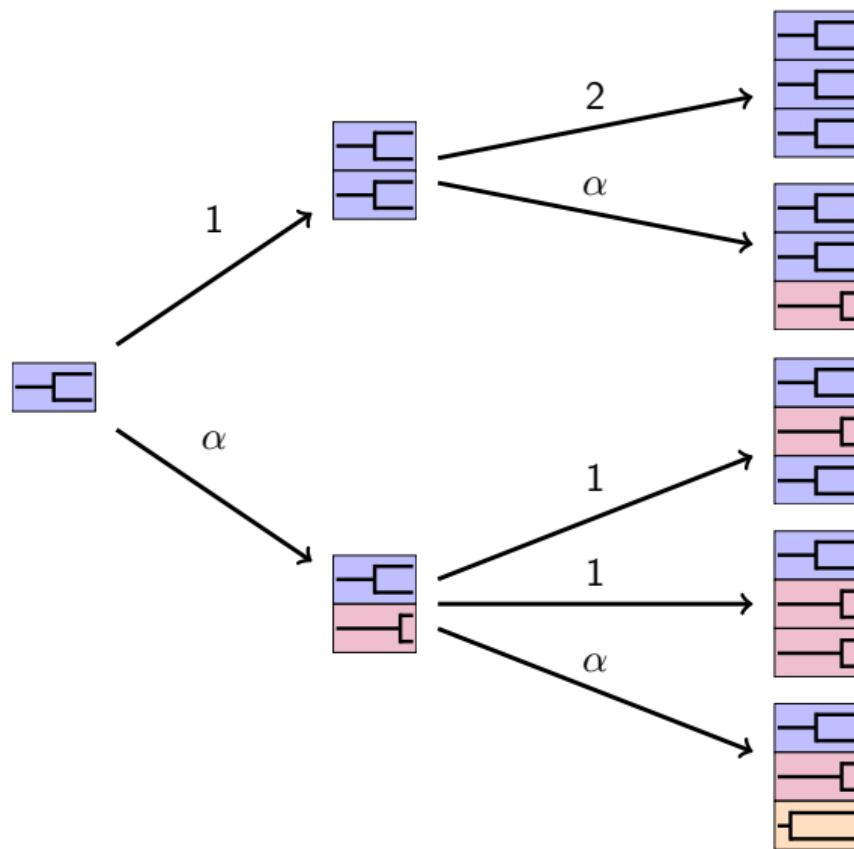


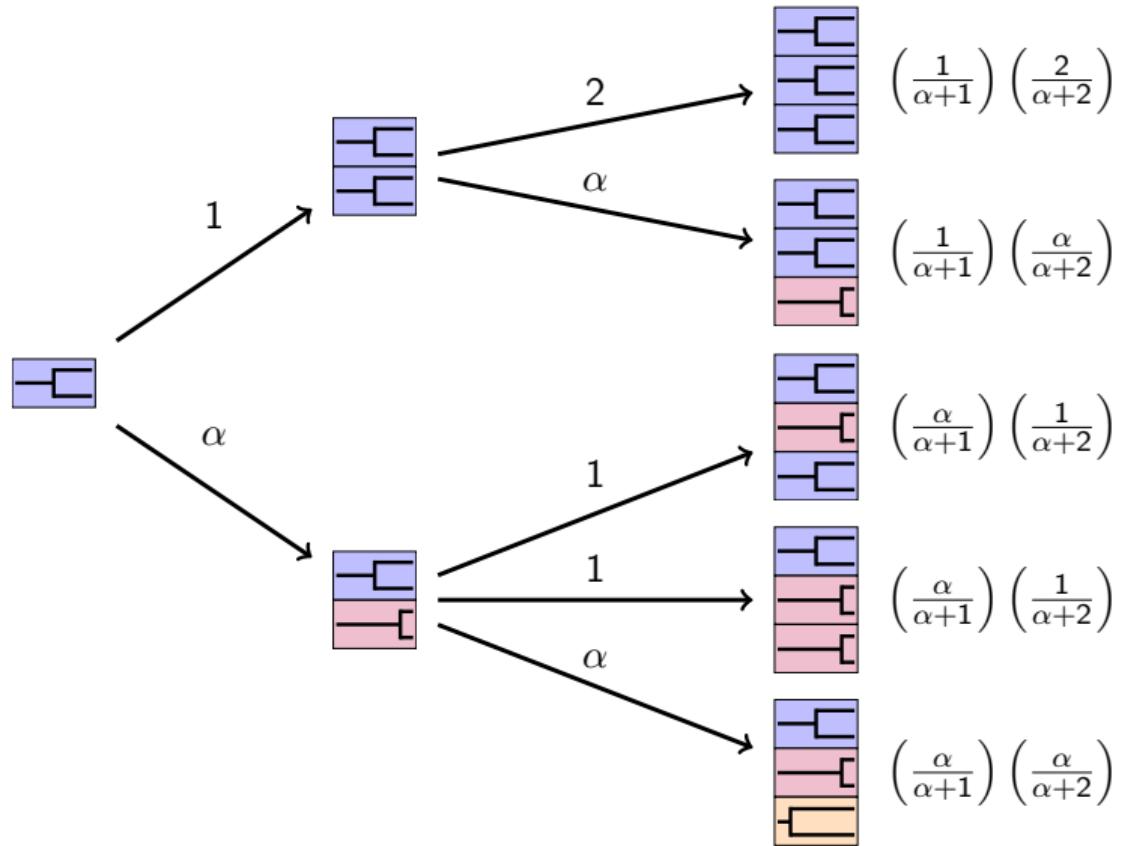
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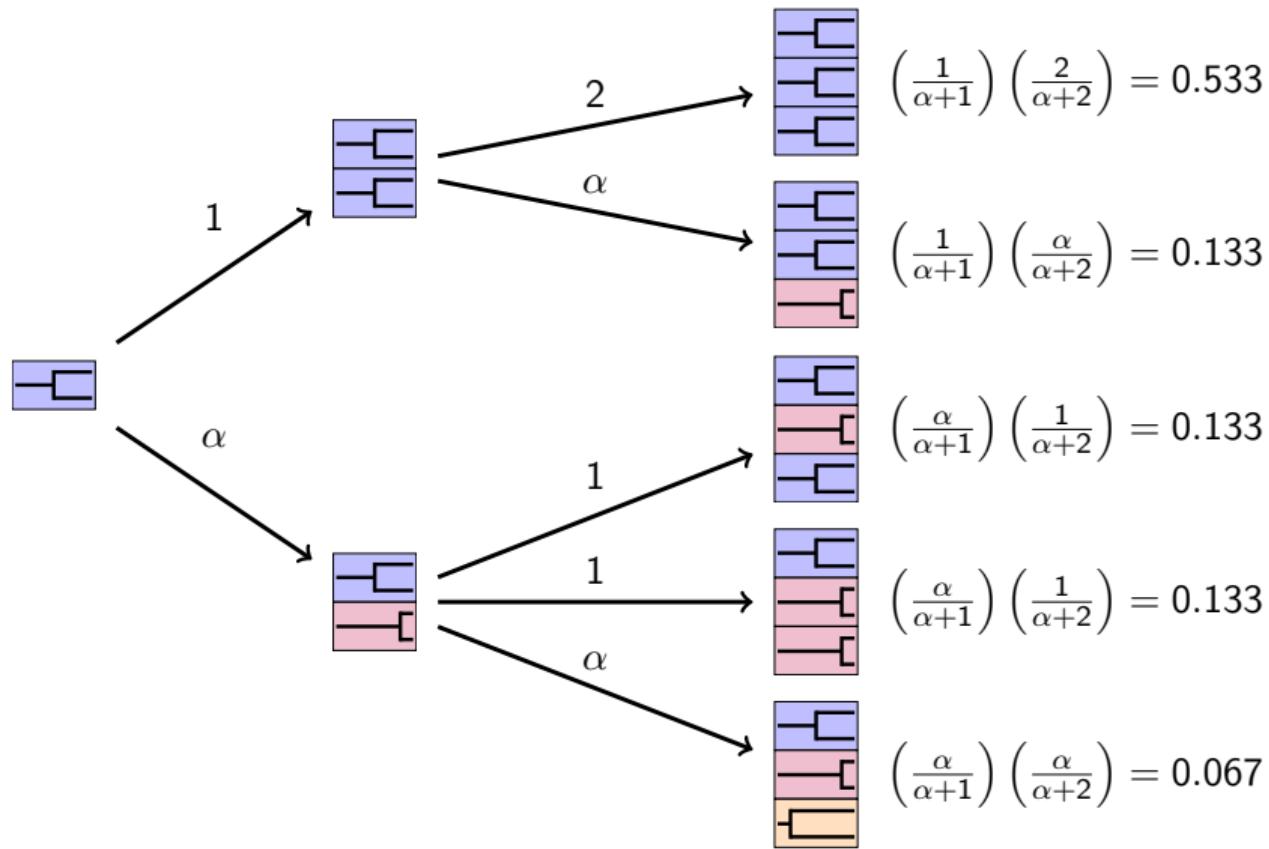




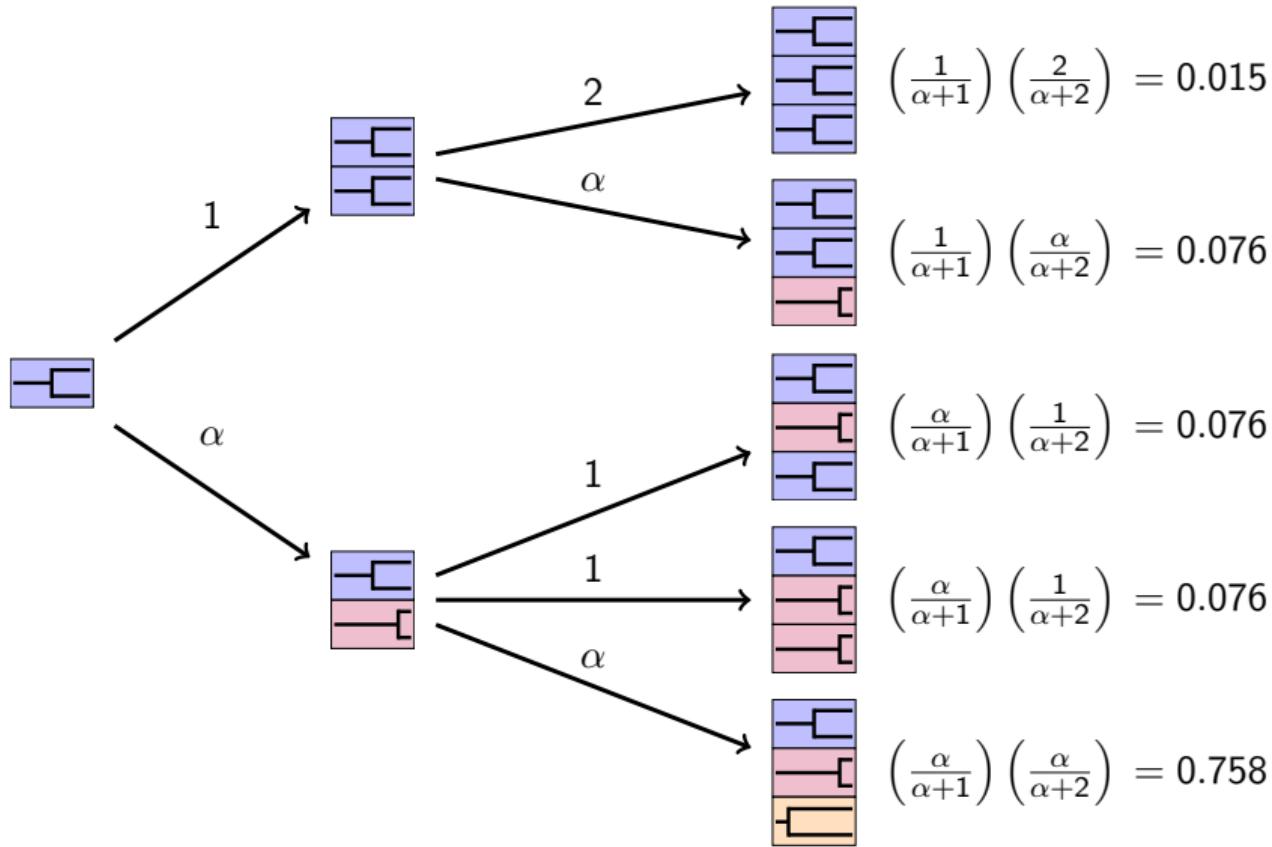




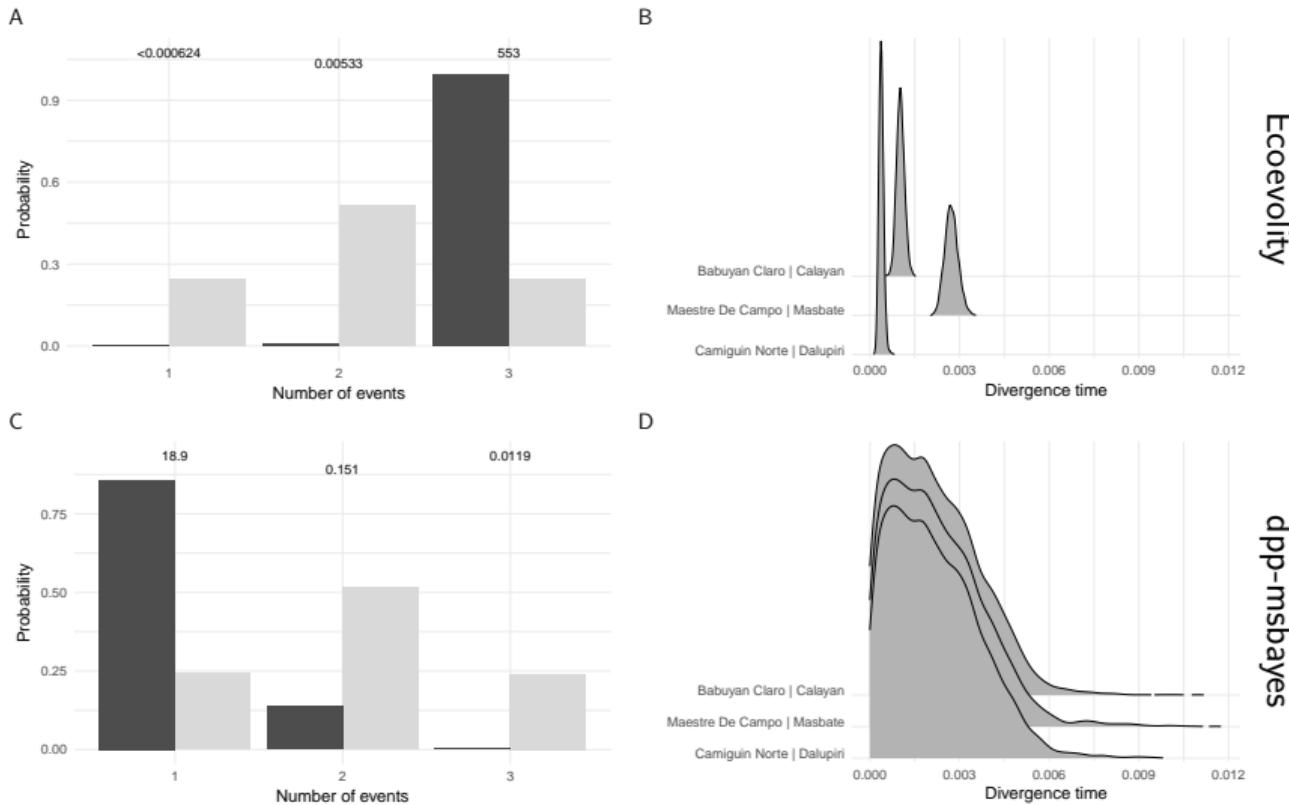
$$\alpha = 0.5$$



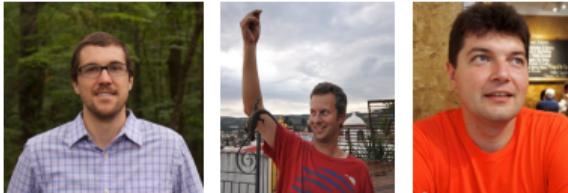
$$\alpha = 10.0$$



ABC vs ecoevolity results



Why so different?



J. R. Oaks et al. (2019). *Systematic Biology* 68: 681–697



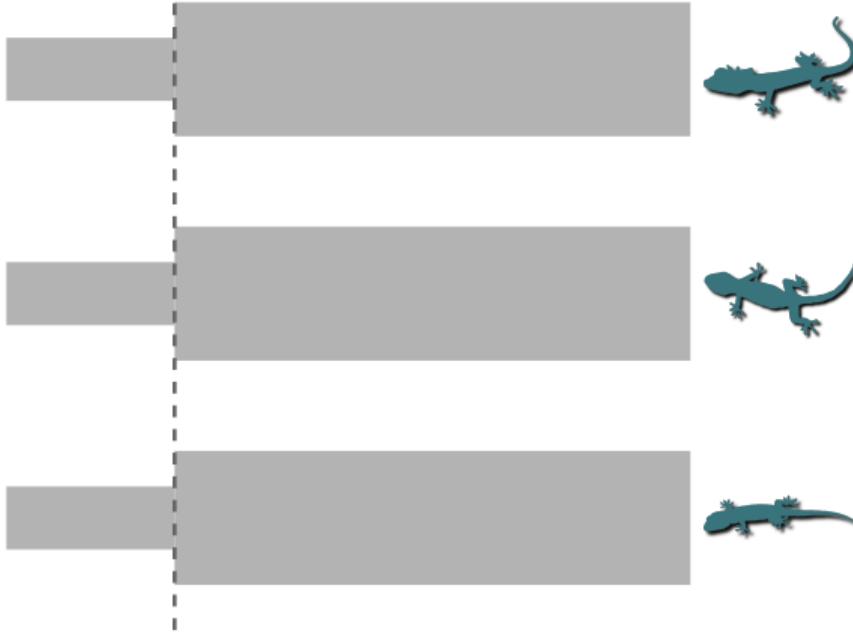
Interactive coin-flipping demo

tl;dr:

Averaging likelihood with respect to “diffuse” priors creates a strong penalty against divergence-time parameters

An aside for a related problem with population demography

τ_1



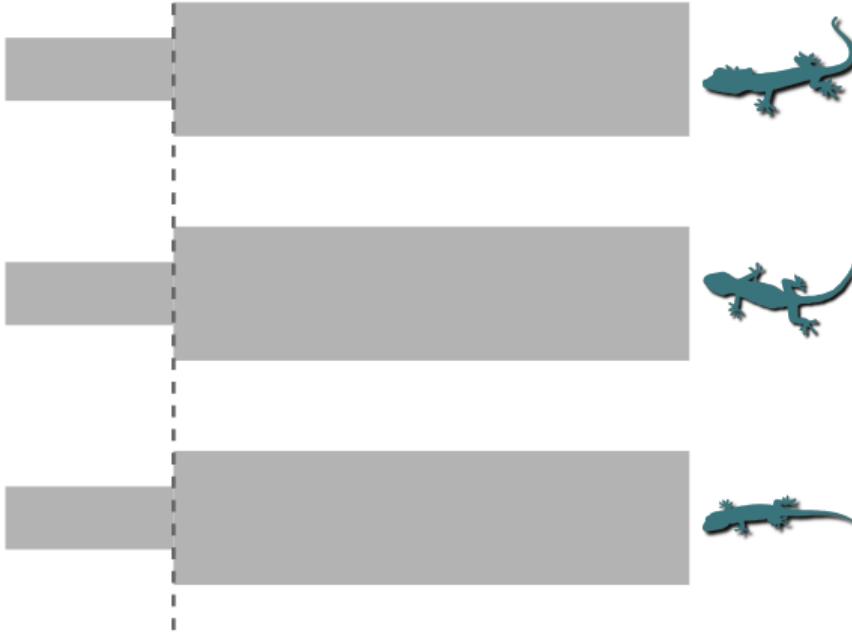
- ▶ Recent interest in testing shared demographic changes

¹ Y. L. Chan, D. Schanzenbach, and M. J. Hickerson (2014). *Molecular Biology and Evolution* 31: 2501–2515

² A. T. Xue and M. J. Hickerson (2015). *Molecular Ecology* 24: 6223–6240

³ A. T. Xue and M. J. Hickerson (2017). *Molecular Ecology Resources* 17: e212–e224

τ_1



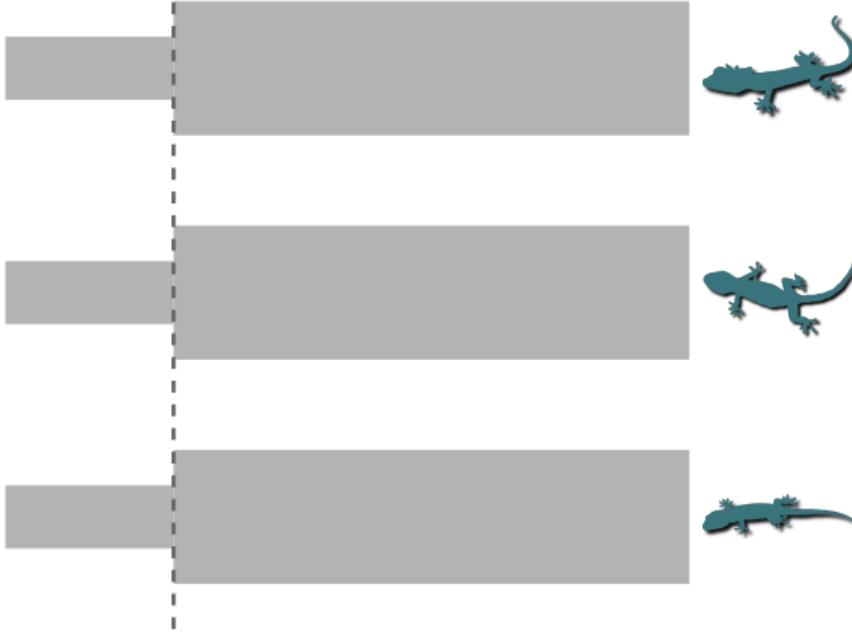
- ▶ Recent interest in testing shared demographic changes
- ▶ Several nice ABC approaches^{1,2,3}
 - ▶ Inferred simultaneous expansion of 5 Alaskan populations of sticklebacks (posterior probability = 0.99)²

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τ_1



- ▶ Recent interest in testing shared demographic changes
- ▶ Several nice ABC approaches^{1,2,3}
 - ▶ Inferred simultaneous expansion of 5 Alaskan populations of sticklebacks (posterior probability = 0.99)²
 - ▶ It's a tricky inference problem
 - ▶ Change in population size can become unidentifiable in 3 ways

¹ Y. L. Chan, D. Schanzenbach, and M. J. Hickerson (2014). *Molecular Biology and Evolution* 31: 2501–2515

² A. T. Xue and M. J. Hickerson (2015). *Molecular Ecology* 24: 6223–6240

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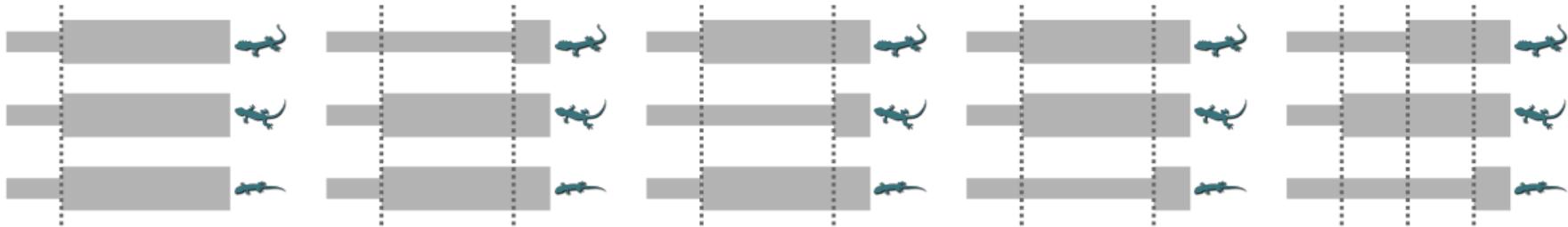
$$p(m_1 | \mathbf{D})$$

$$p(m_2 | \mathbf{D})$$

$$p(m_3 | \mathbf{D})$$

$$p(m_4 | \mathbf{D})$$

$$p(m_5 | \mathbf{D})$$



Given genomic data, can we infer the correct model and the timing of the demographic events?

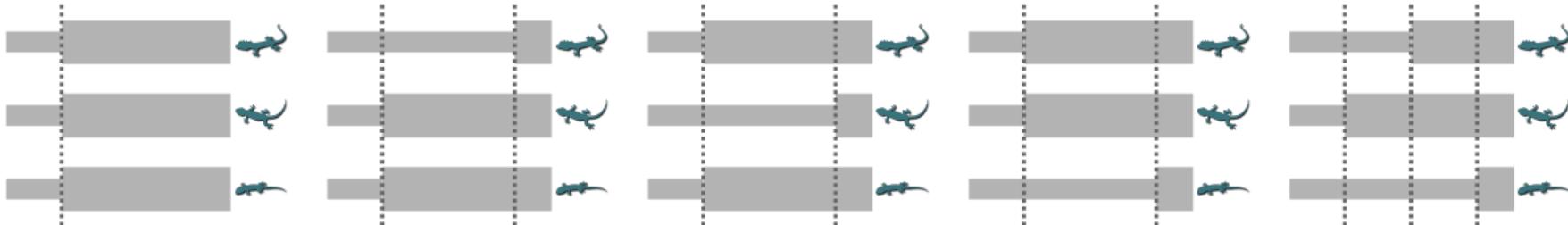
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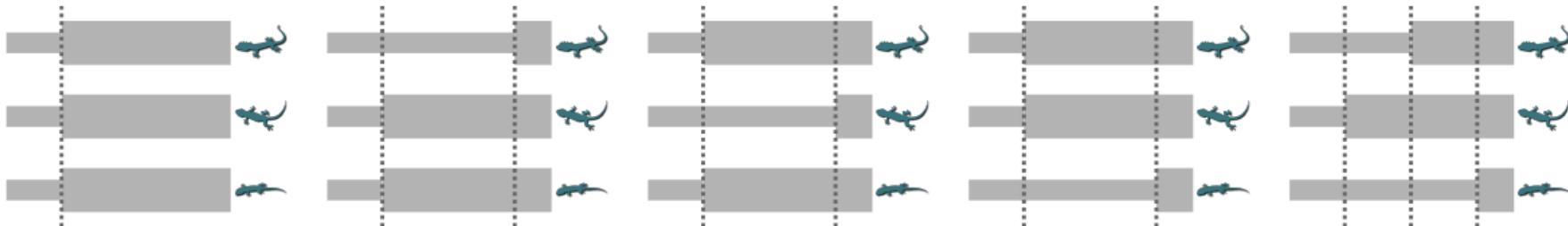
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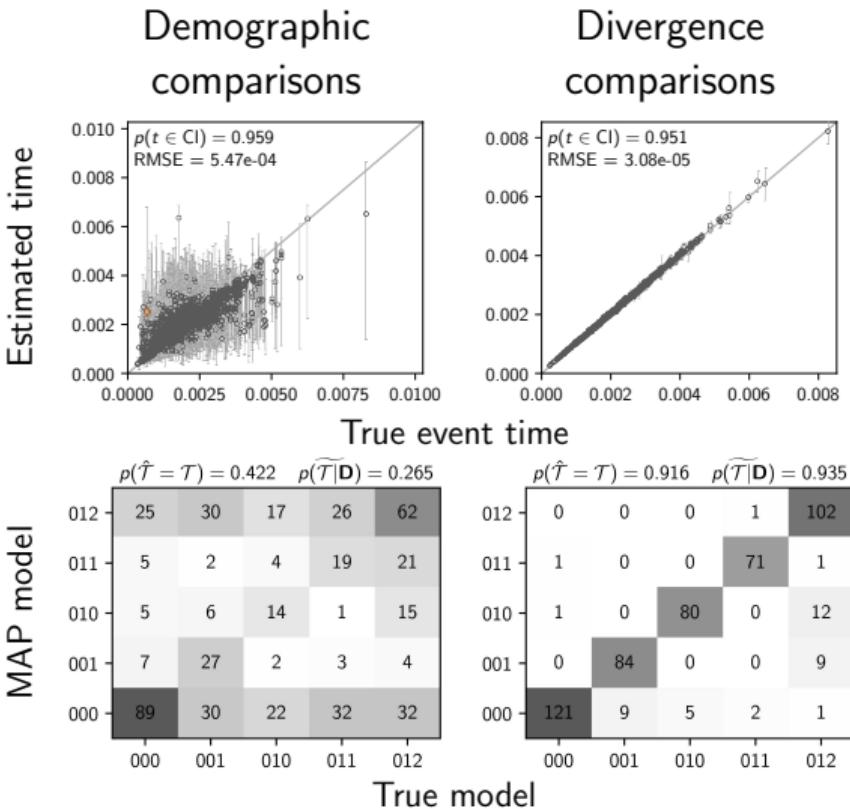


Given genomic data, can we infer the correct model and the timing of the demographic events?



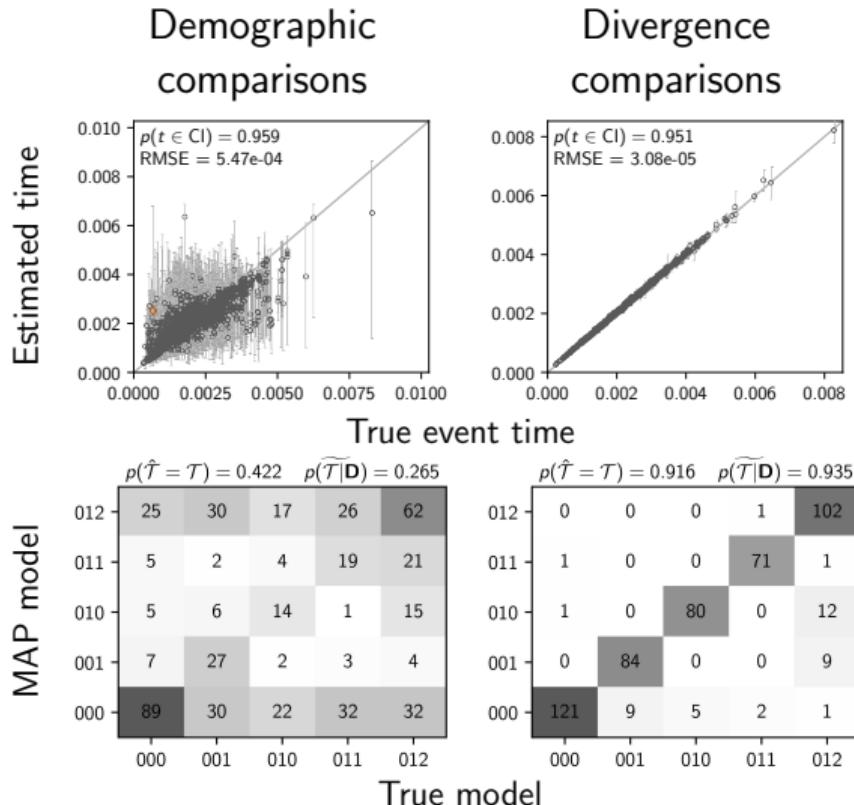
- ▶ Implemented full-likelihood Bayesian approach in ecoevolity
- ▶ Assessed performance with simulations
- ▶ Applied to stickleback genomic data

Simulation results



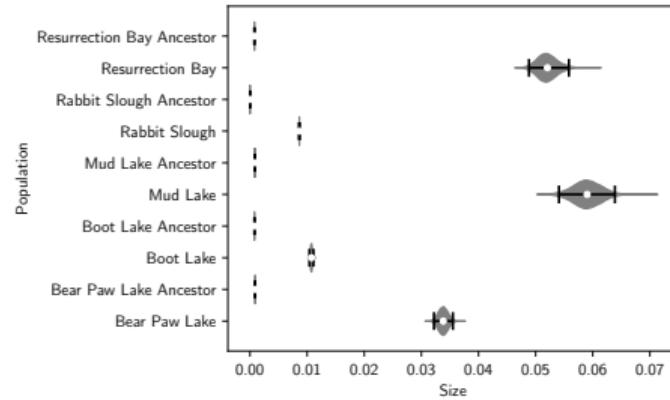
Simulation results

Simulations confirm theoretical expectations that changes in population size are difficult to estimate



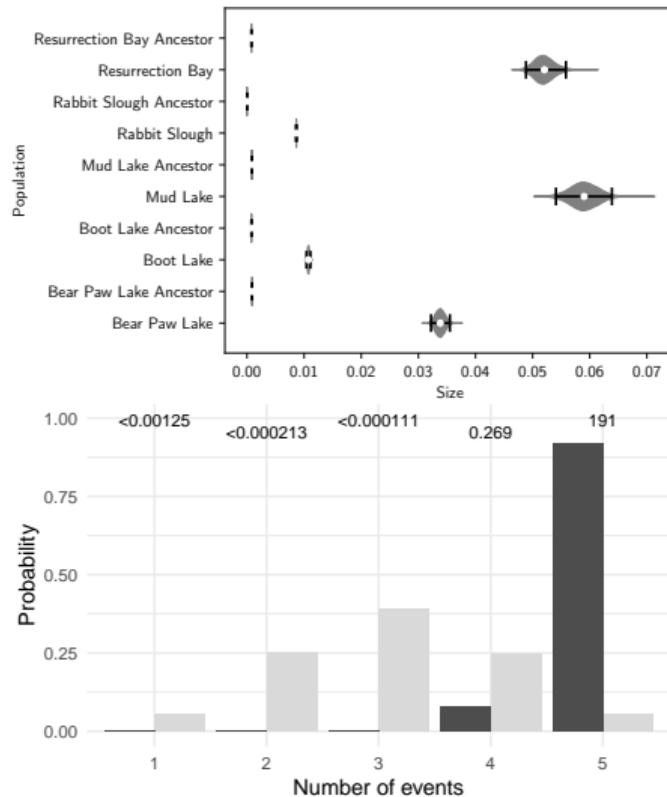
Stickleback results

- ▶ Strong support for expansions in all 5 populations; consistent with ABC results



Stickleback results

- ▶ Strong support for expansions in all 5 populations; consistent with ABC results
- ▶ Strong support all 5 expansions were independent; exact opposite of ABC results



Open science: everything is available...

Software:

- ▶ Ecoevolity: phyletica.org/ecoevolity

Open-Science Notebooks:

github.com/phyletica/ecoevolity-demog-experiments