

Full Bayesian comparative biogeography of Philippine geckos challenges predictions of climate-driven vicariant speciation

Evolution 2019

Jamie Oaks

Auburn University

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GitHub: [joaks1](https://github.com/joaks1) & [phyletica](https://github.com/phyletica)

Twitter: [@jamoaks](https://twitter.com/jamoaks)

Slides: phyletica.org/slides/evol2019.pdf

Cameron Siler

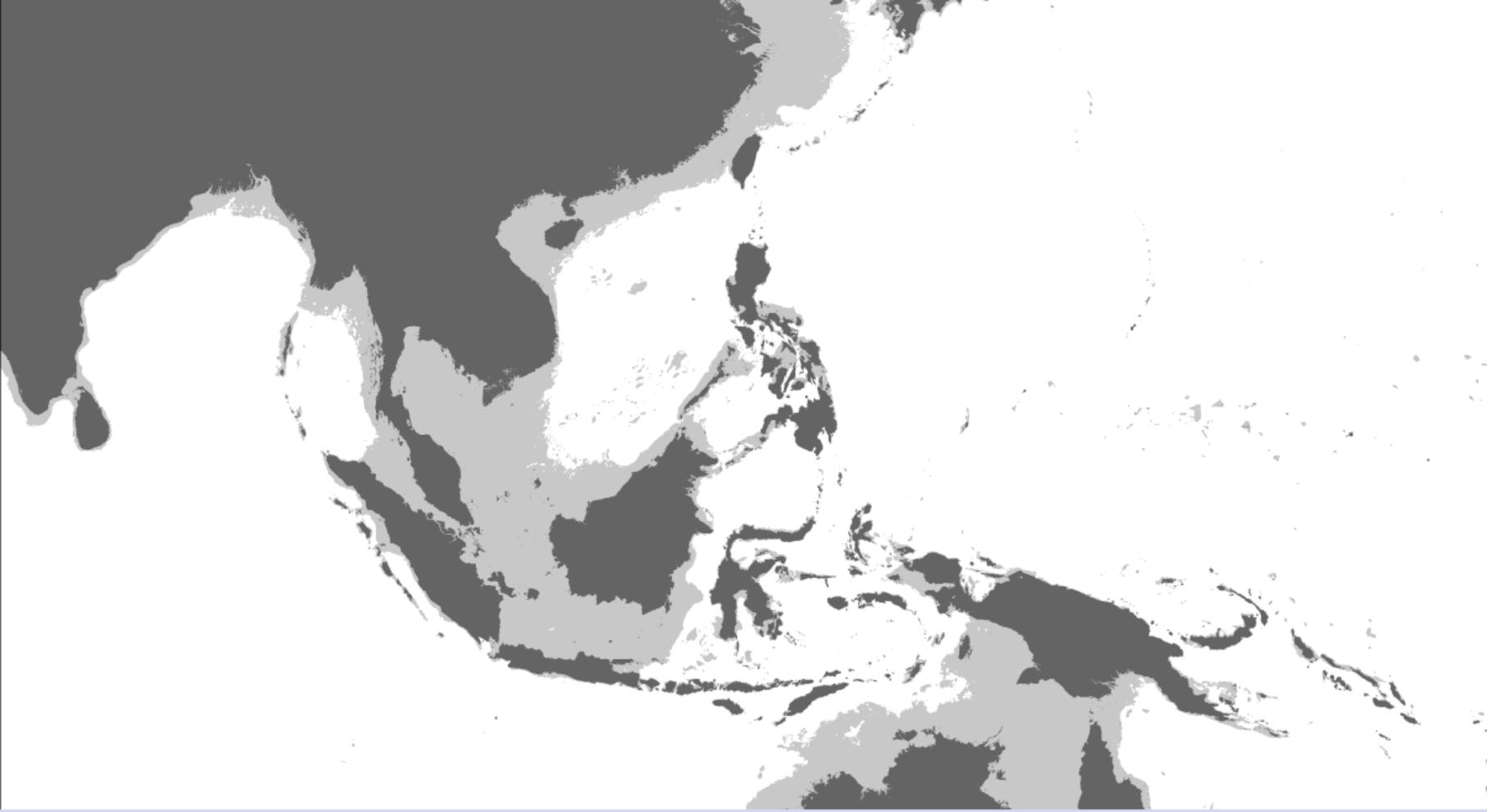
University of Oklahoma

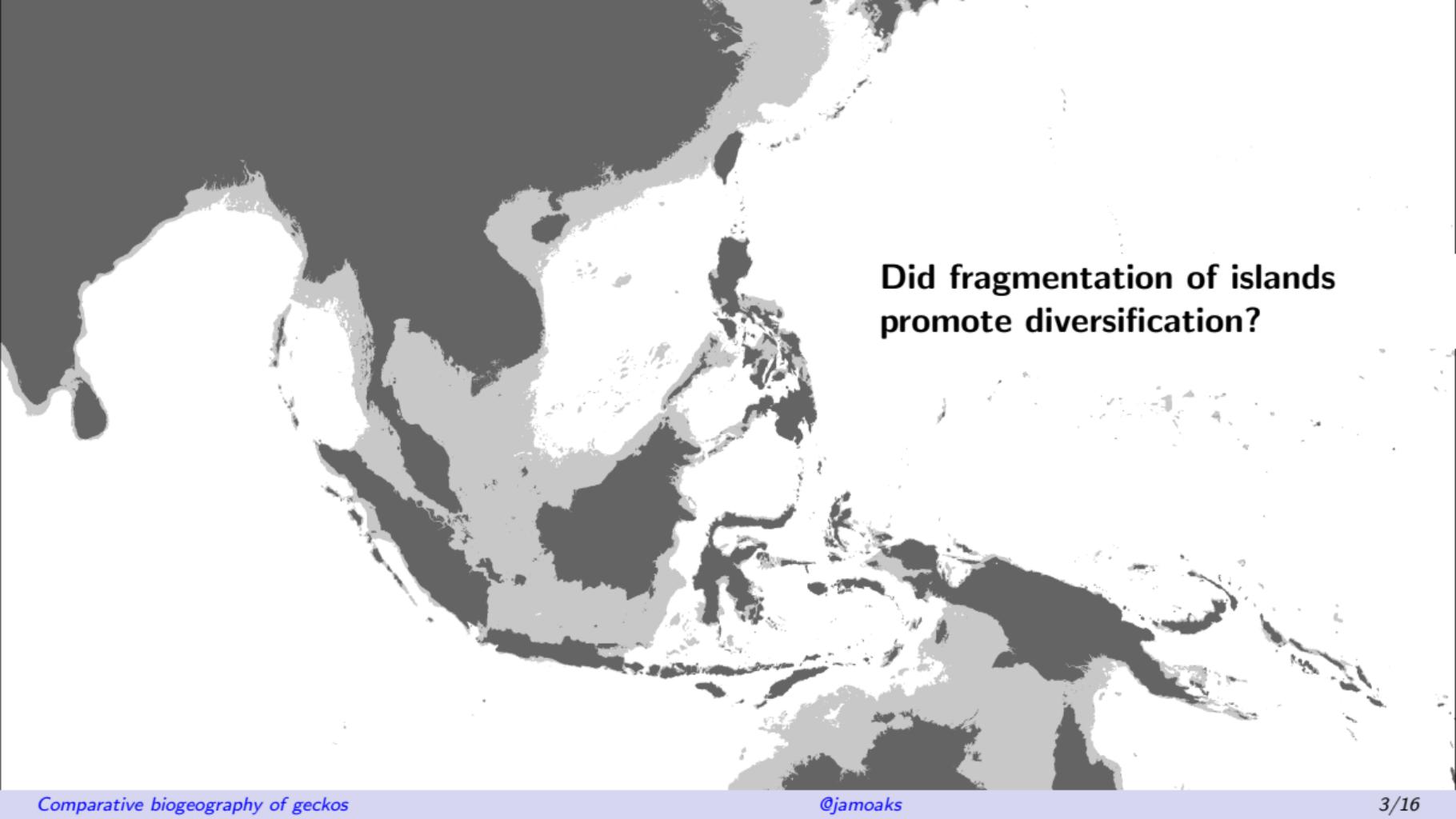
Rafe Brown

University of Kansas

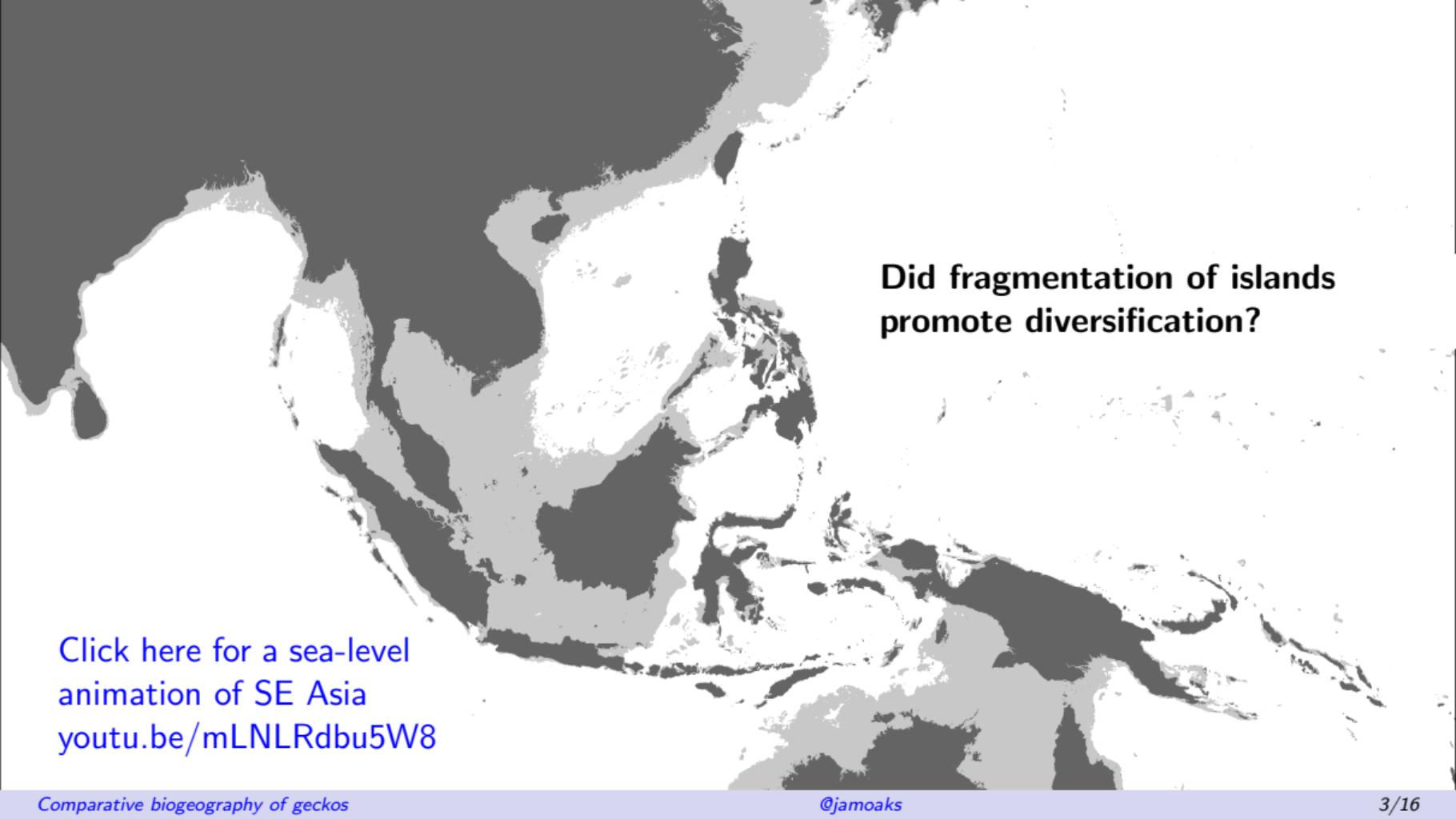
Thanks to ASN, SSE, SSB, and all organizers!





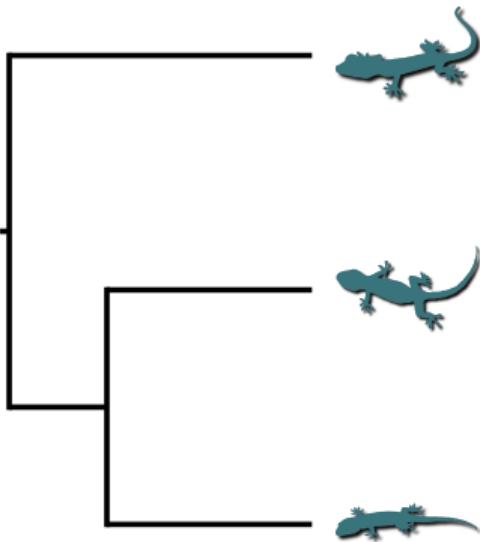


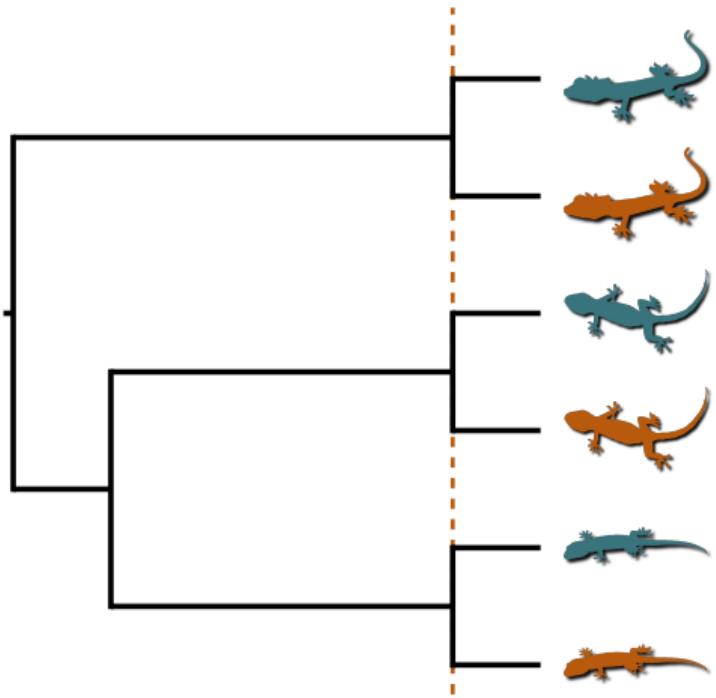
Did fragmentation of islands promote diversification?



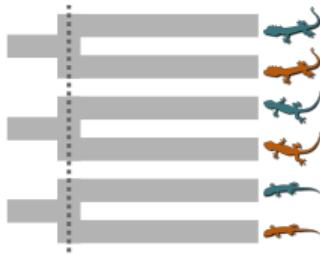
Did fragmentation of islands promote diversification?

Click here for a sea-level
animation of SE Asia
youtu.be/mLNLRdbu5W8

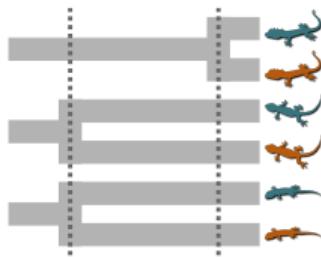




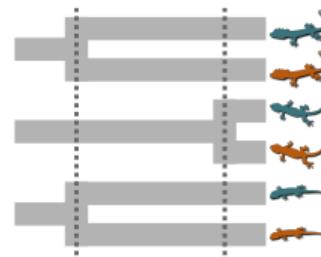
m_1



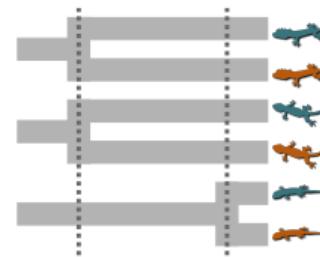
m_2



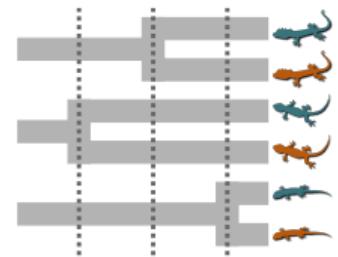
m_3

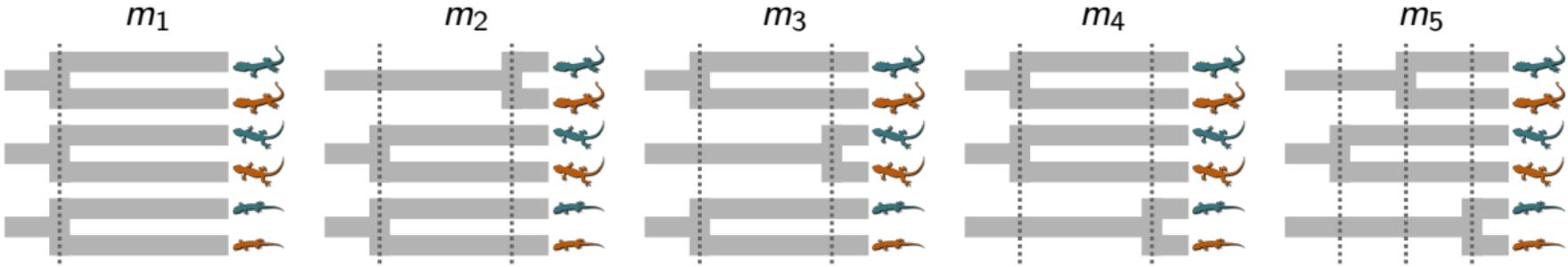


m_4



m_5

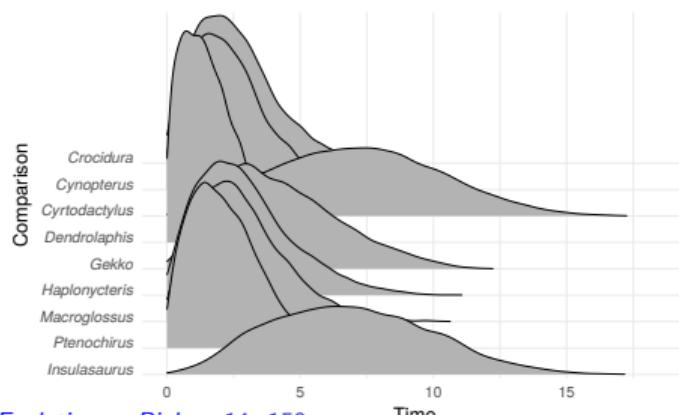
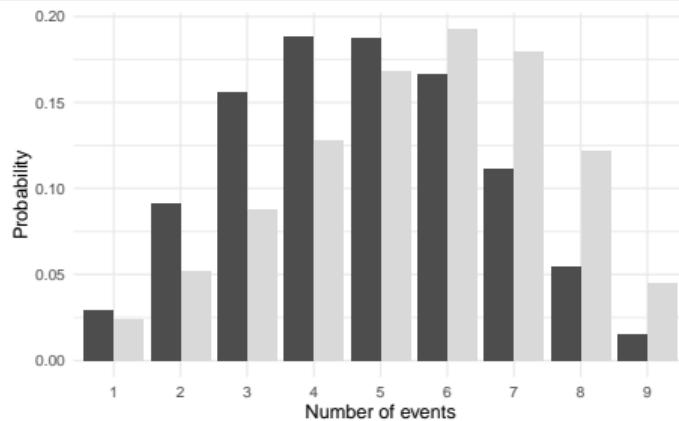




We want to infer the model and divergence times given genetic data

Previous tests of “species-pump”

- ▶ Our previous attempts using ABC left little information in summary statistics to inform divergence times^{1,2}

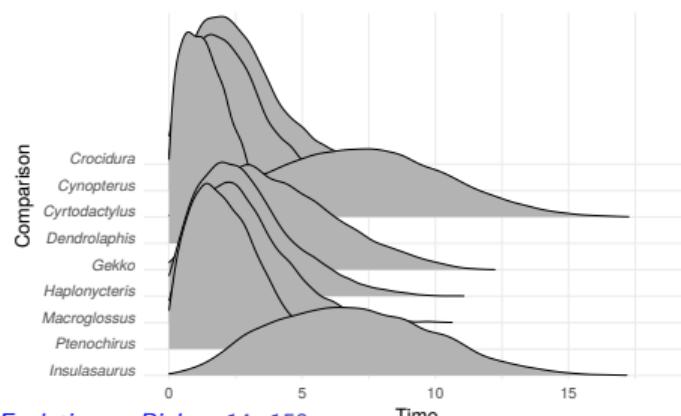
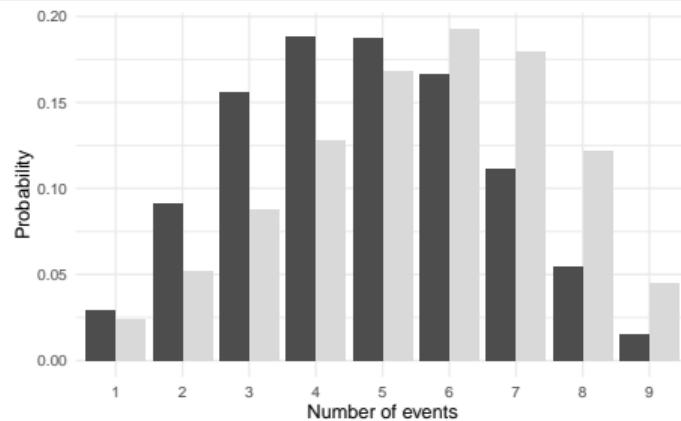


¹ J. R. Oaks et al. (2013). *Evolution* 67: 991–1010. ² J. R. Oaks (2014). *BMC Evolutionary Biology* 14: 150

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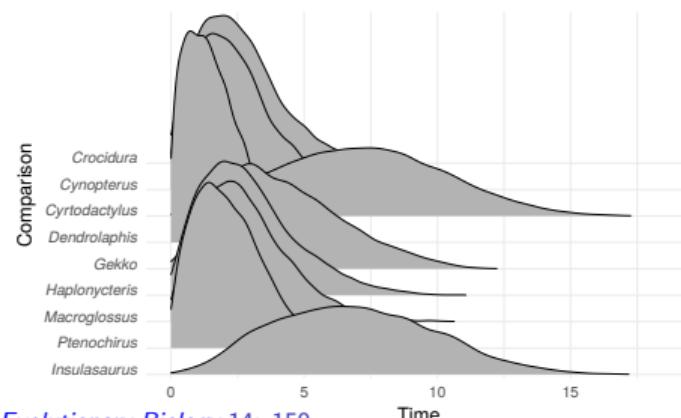
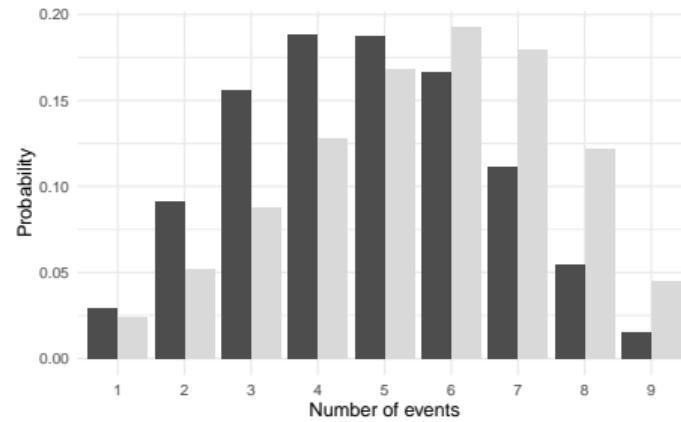
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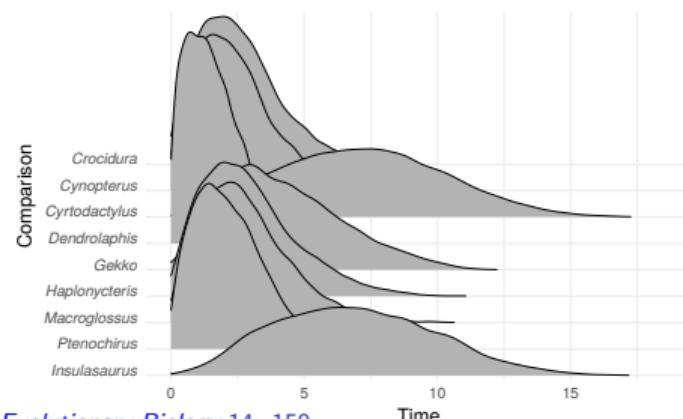
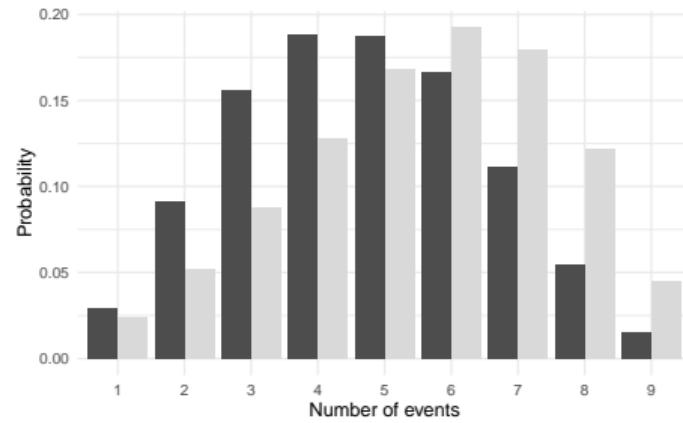
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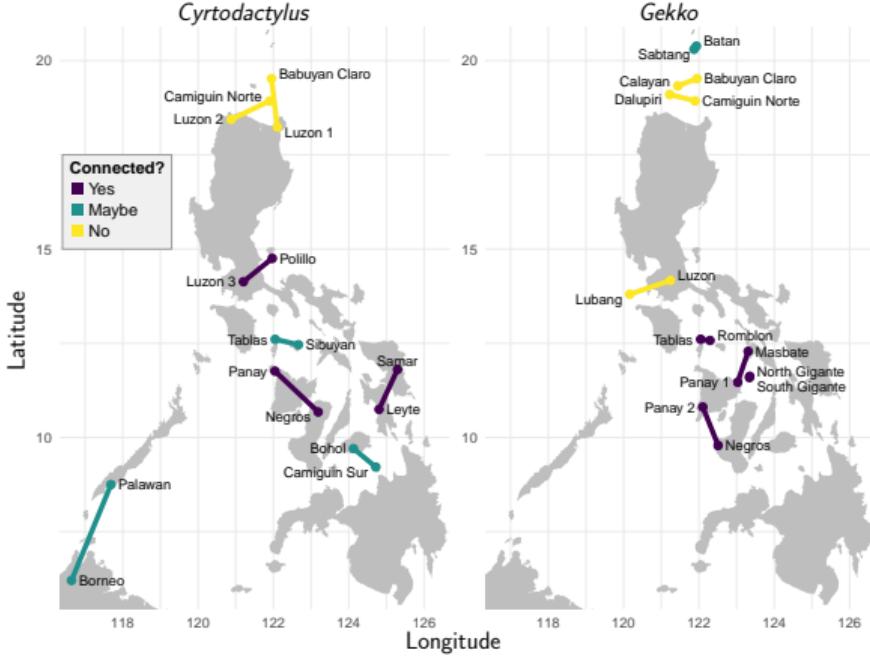
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Our goal is to do both



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- ▶ 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

Analyzed RADseq data with full-likelihood Bayesian comparative phylogeographic method¹:

Ecoevolity: Estimating evolutionary coevality

¹ J. R. Oaks (2019). *Systematic Biology* 68: 371–395

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

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- ▶ Analytically integrate over coalescent genealogies and mutational histories²
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- ▶ *Goal: Fast, full-likelihood Bayesian method to infer patterns of co-diversification from genome-scale data*
- ▶ Used simulations to assess how well ecoevolity works given the gekkonid RADseq data

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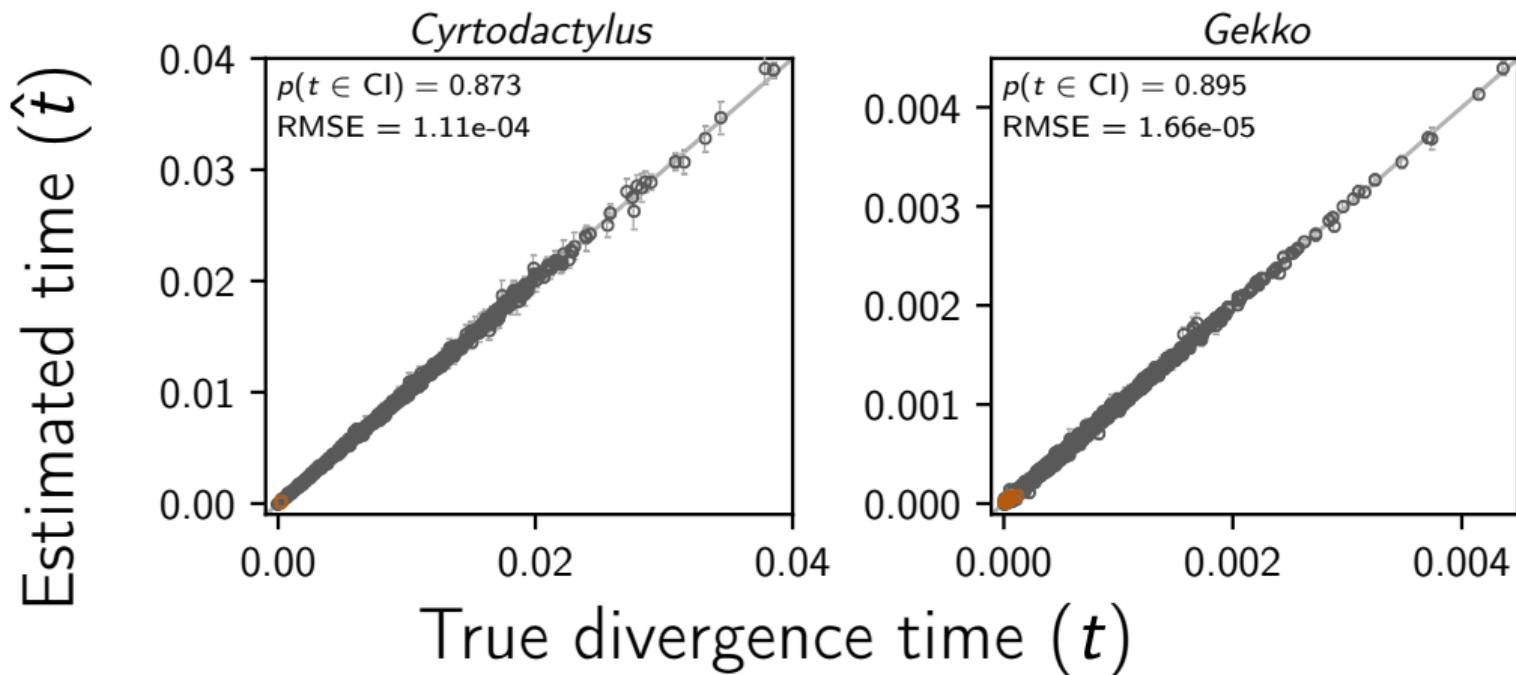
Want to learn more?

- ▶ Check out Kerry Cobb's poster (Saturday at 5:30pm ExHallBC_18)
- ▶ I'll be at the software bazaar (Sunday at 6:30pm)

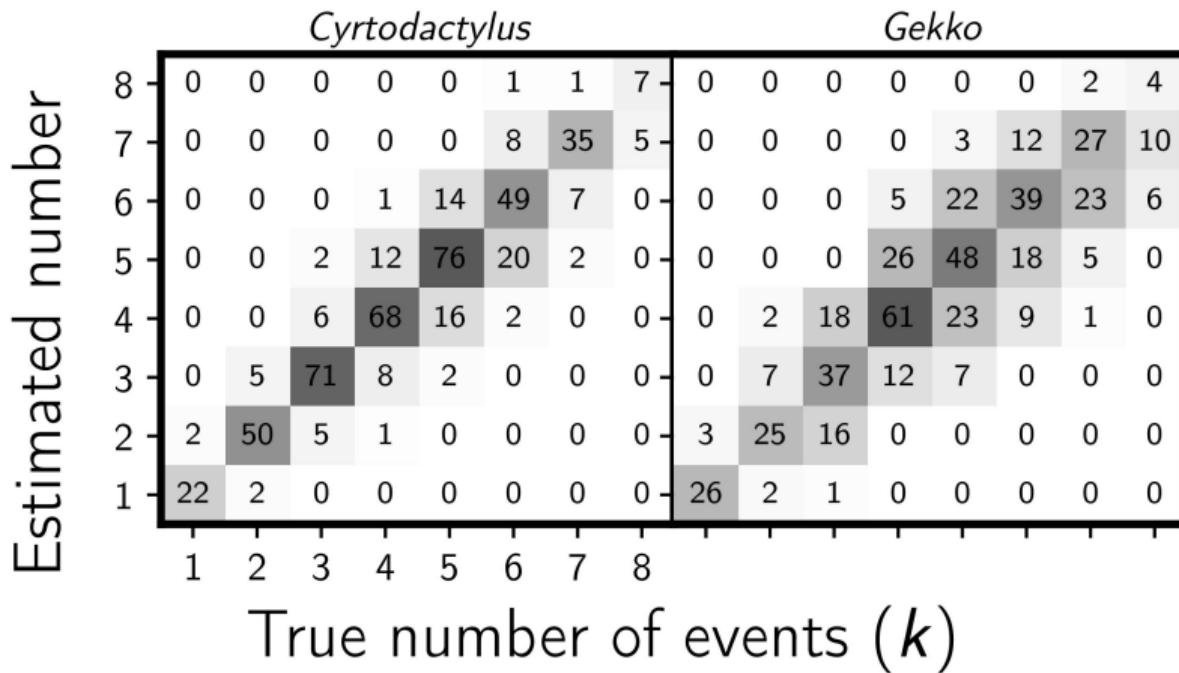
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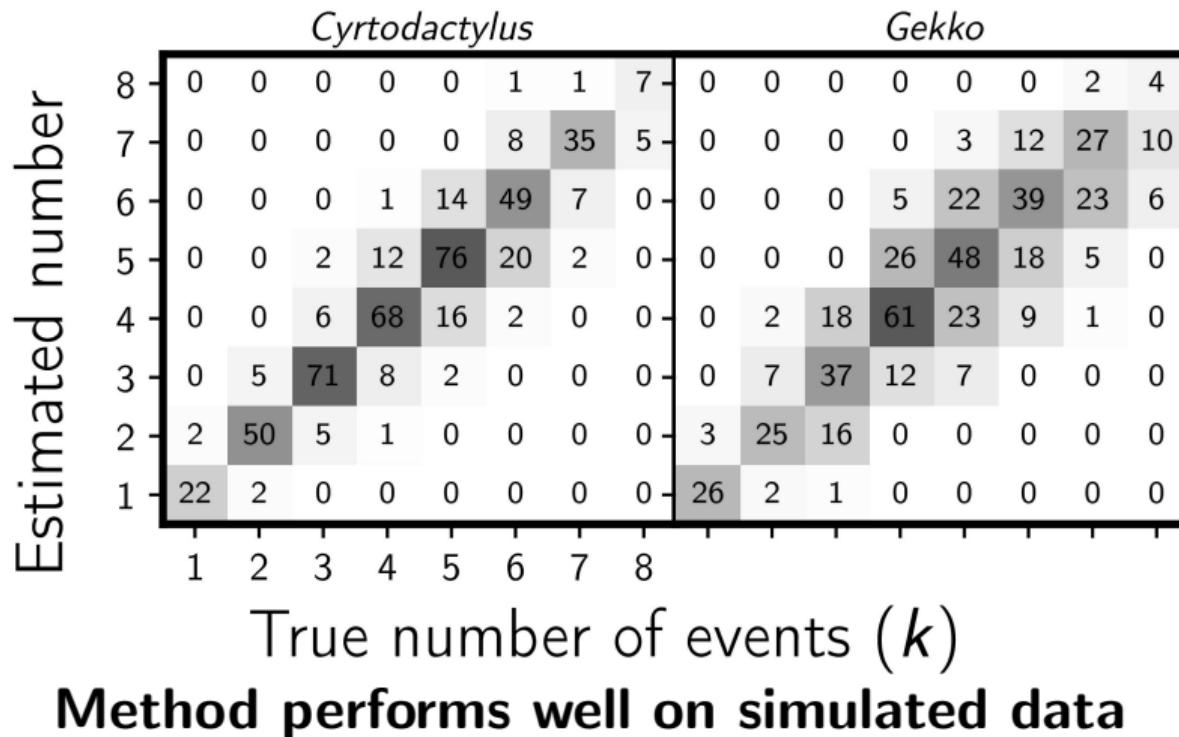
Results: Simulations



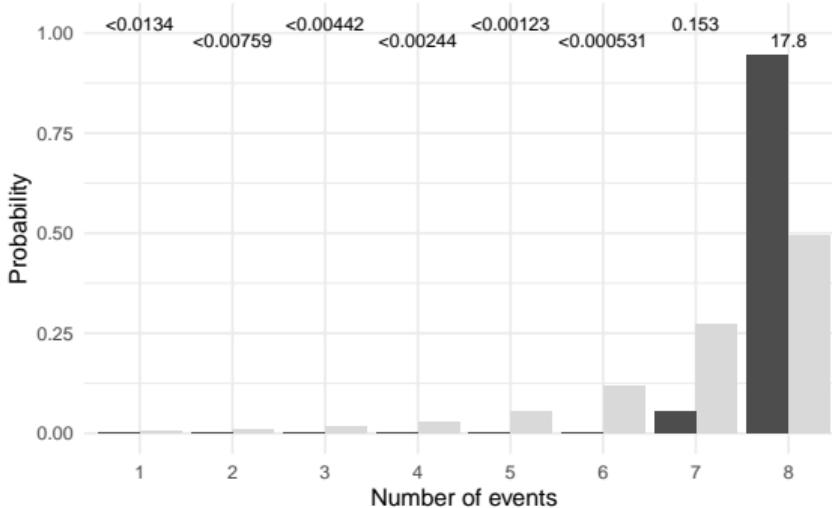
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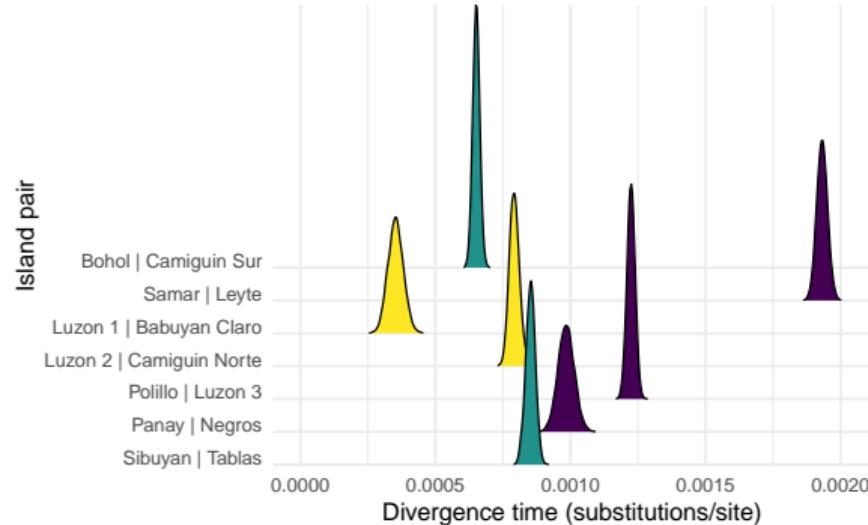
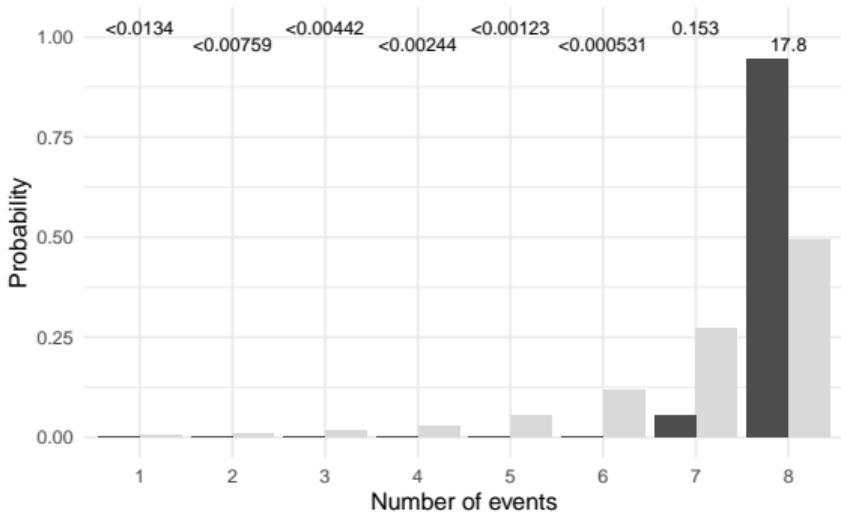


Results: *Cyrtodactylus*

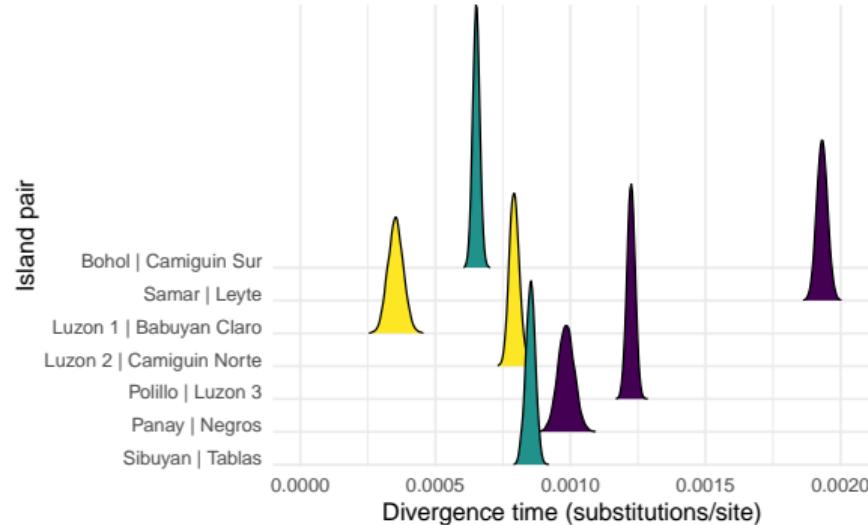
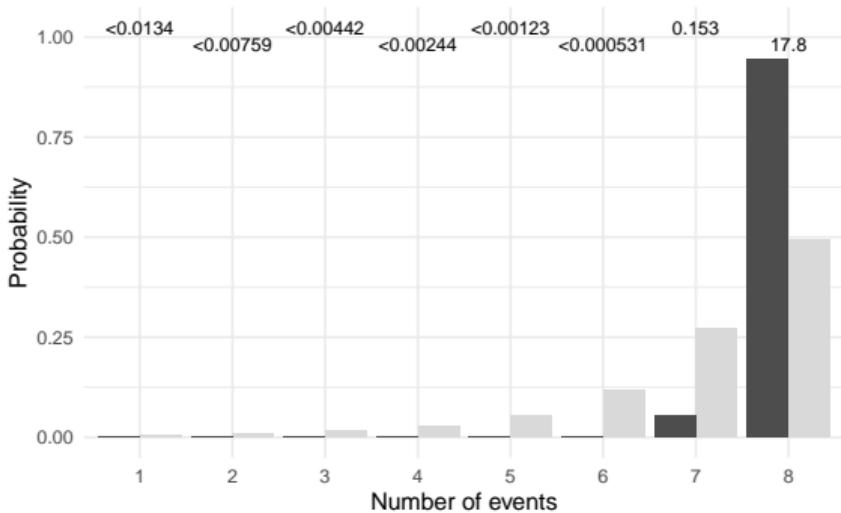


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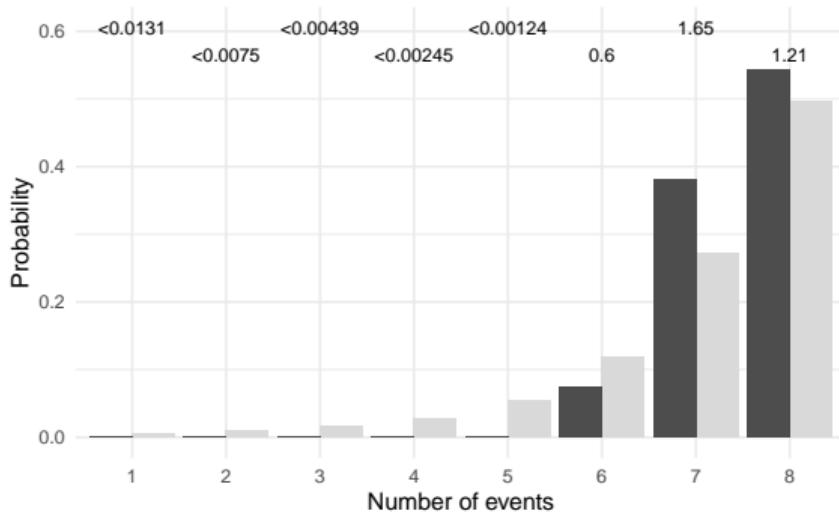


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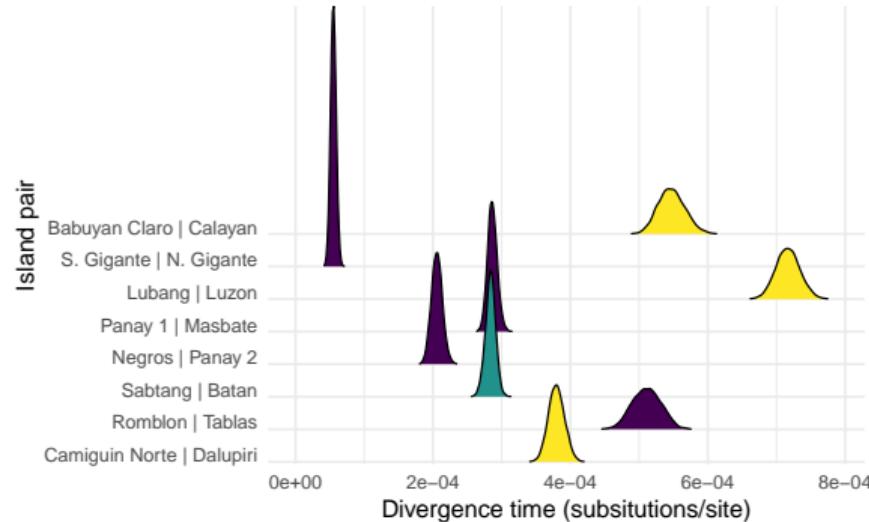
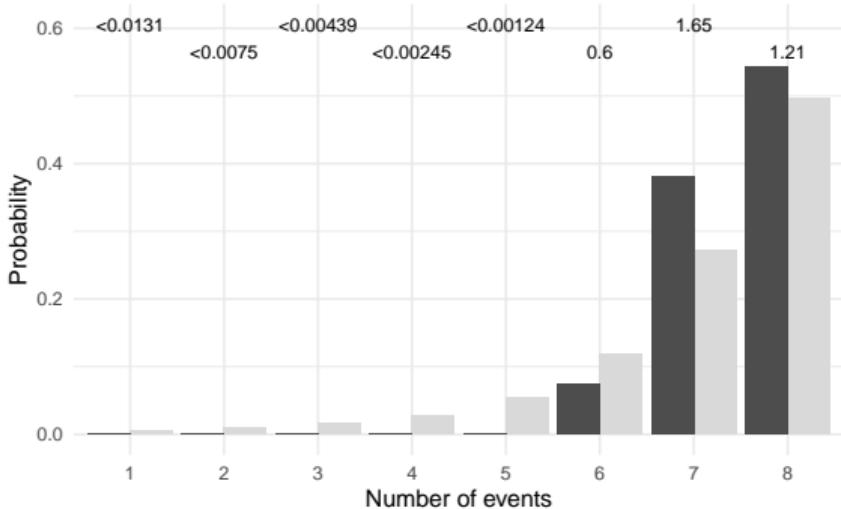


Strong support for independent divergences

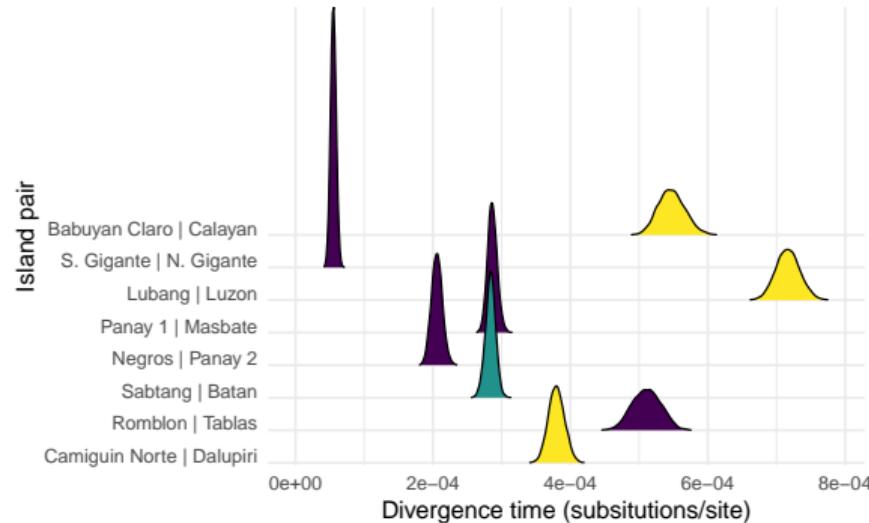
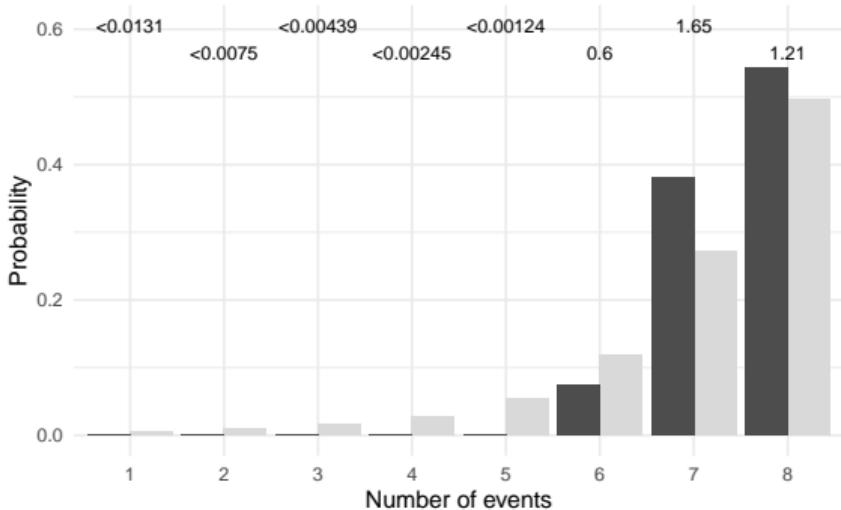
Results: Gekko



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Weak support for independent divergences

Take home points

- ▶ Support against the “species-pump” hypothesis

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

Caveats

- ▶ Too few island pairs to rule out climate-driven vicariant speciation
- ▶ Variation in fragmentation times among island pairs
- ▶ Variation in mutation rates

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 - ▶ Variation in fragmentation times among island pairs
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-
- ▶ Seems safe to conclude that the “species-pump” is not the rule for Philippine gekkonids

Everything is on GitHub...

Software:

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

Open-Science Notebooks:

- ▶ Ecoevolity testing: <https://github.com/phyletica/ecoevolity-experiments>
- ▶ Gecko RADseq: <https://github.com/phyletica/gekgo>

Acknowledgments

Ideas and feedback:

- ▶ Phyletica Lab (the Phyleticians)
- ▶ David Bryant, Mark Holder, Adam Leaché, and Vladimir Minin; Editors Laura Kubatko, Mohamed Noor, and David Weisrock; and five anonymous

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- ▶ Patrick Monnahan and John Kelly for their help with the MSG libraries

Computation:

- ▶ Alabama Supercomputer Authority
- ▶ Auburn University Hopper Cluster

Funding:



DEB 1656004

Photo credits:

- ▶ Rafe Brown and Cam Siler
- ▶ [PhyloPic!](#)

Thanks to ASN, SSE, SSB, and all organizers of Evolution 2019!

Questions?

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