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Education and Appointments

2020–present Postdoctoral scholar, UC Davis
2019–present Postdoctoral scholar, UC Berkeley
2011–2019 PhD, Population Biology, UC Davis
2008–2010 BS, Evolution, Ecology and Biodiversity, UC Davis (Highest Honors)

Publications

18. **May, M. R.** & Rothfels, C. J. (2021). *Mistreating birth-death models as priors in phylogenetic analysis compromises our ability to compare models.* [bioRxiv](#). [Link](#). [Slides](#).
17. Tribble, C. M., Freyman, W. A., Landis, M. J., Lim, J. Y., Barido-Sottani, J., Kopperud, B. T., Höhna, S. & **May, M. R.** (2021). *RevGadgets: an R Package for visualizing Bayesian phylogenetic analyses from RevBayes.* [bioRxiv](#). [Link](#).
16. Höhna, S., Freyman, W. A., Nolen, Z., Huelsenbeck, J. P., **May, M. R.**, & Moore, B. R. (2021). *A Bayesian approach for estimating branch-specific speciation and extinction rates.* [bioRxiv](#). [Link](#).
15. Gao, J., **May, M. R.**, Rannala, B. & Moore, B. R. (2021). *Phylogenetic insights on the early spread of the COVID-19 pandemic and the efficacy of intervention measures.* [bioRxiv](#). [Link](#).
14. Barido-Sottani, J., Justison, J. A., Borges, Rui., Brown, J. M., Dismukes, W., do Rosario, P., ..., **May, M. R.**, ..., & Heath, T. A. (2021). *Lessons learned from organizing and teaching virtual phylogenetics workshops.* [In review](#).
13. **May, M. R.**, Contreras, D. L., Sundue, M. A., Nagalingum, N. S., Looy, C. V., & Rothfels, C. J. (2021). *Inferring the total-evidence timescale of Marattialean fern evolution in the face of model sensitivity.* *Systematic Biology*, in press. [Link](#). [Slides](#).

12. Thompson A., **May M. R.**, Moore, B. R. & Kopp A. (2020). *A hierarchical Bayesian mixture model for inferring the expression state of genes in transcriptomes*. Proceedings of the National Academy of Sciences 117(32), 19339–19346. [Link](#).
11. **May, M. R.** & Moore, B. R. (2020). *A Bayesian approach for inferring the impact of a discrete character on rates of continuous-character evolution in the presence of background-rate variation*. Systematic Biology 69(3), 530–544. [Link](#).
10. Turelli, M., Cooper, B. S., Richardson, K. M., Ginsberg, P. S., Peckenpaugh, B., Antelope, C. X., ..., **May, M. R.**, ... & Hoffmann, A. A. (2018). *Rapid global spread of wRi-like Wolbachia across multiple Drosophila*. Current Biology 28(6), 963–971. [Link](#).
9. Jiao, Y., Peluso, P., Shi, J., Liang, T., Stitzer, M. C., Wang, B., ..., **May, M. R.**, ... & Ware, D. (2017). *Improved maize reference genome with single-molecule technologies*. Nature 546(7659), 524–527. [Link](#).
8. **May, M. R.**, S. Höhna, & B. R. Moore (2016). *A Bayesian approach for detecting the impact of mass-extinction events on molecular phylogenies when rates of lineage diversification may vary*. Methods in Ecology and Evolution 7(8), 947–959. [Link](#).
7. Moore, B. R., Höhna, S., **May, M. R.**, Rannala, B. & Huelsenbeck, J. P. (2016). *Critically evaluating the theory and performance of Bayesian analysis of macroevolutionary mixtures*. Proceedings of the National Academy of Sciences 34(113), 9569–9574. [Link](#).
6. **May, M. R.** & Moore, B. R. (2016). *How well can we detect lineage-specific diversification-rate shifts? A simulation study of sequential AIC methods*. Systematic Biology 6(65), 1076–1084. [Link](#).
5. Höhna, S., **May, M. R.**, & Moore, B. R. (2016). *TESS: an R package for efficiently simulating phylogenetic trees and performing Bayesian inference of lineage diversification rates*. Bioinformatics 32(5), 789–791. [Link](#).
4. Magee, A. F., **May, M. R.**, & Moore, B. R. (2014). *The dawn of open access to phylogenetic data*. PLoS One 9(10), e110268. [Link](#).
3. Brandvain, Y., Pauly, G. B., **May, M. R.**, & Turelli, M. (2014). *Explaining Darwin's corollary to Haldane's rule: the role of mitonuclear interactions in asymmetric postzygotic isolation among toads*. Genetics 197(2), 743–747. [Link](#).
2. Melters, D. P., Bradnam, K. R., Young, H. A., Telis, N., **May, M. R.**, Ruby, J. G., ... & Chan, S. W. (2013). *Comparative analysis of tandem repeats from hundreds of species reveals unique insights into centromere evolution*. Genome Biology 14(1), 1–20. [Link](#).
1. **May, M. R.**, Provance, M. C., Sanders, A. C., Ellstrand, N. C., & Ross-Ibarra, J. (2009). *A Pleistocene clone of Palmer's oak persisting in southern California*. PLoS One 4(12), e8346. [Link](#).

Presentations

8. **May, M. R.** & Rothfels, C. J. (2021). *Mistreating birth-death models as priors in phylogenetic analysis compromises our ability to compare models.* Botanical Society of America Conference. (Invited.)
7. **May, M. R.**, Contreras, D. L., Sundue, M. A., Nagalingum, N. S., Looy, C. V., & Rothfels, C. J. (2021). *Inferring the total-evidence timescale of marattialean fern evolution in the face of model sensitivity.* Joint Annual Evolution Meeting.
6. **May, M. R.** & Moore, B. R. (2017). *A Bayesian method for inferring discrete-state dependent rates of continuous-trait evolution.* Joint Annual Evolution Meeting; Portland, Oregon.
5. **May, M. R.**, Moore, B. R., Höhna, S., Huelsenbeck, J. P., & Rannala, B. (2016). *Towards a correct Bayesian method for inferring lineage-specific rates of speciation and extinction.* Joint Annual Evolution Meeting; Austin, Texas.
4. **May, M. R.** (2016). *Problems and solutions for inferring lineage-specific rates of speciation and extinction.* Center for Population Biology seminar series; UC Davis.
3. **May, M. R.** & Moore, B. R. (2014). *Inferring lineage-specific rates of continuous-trait evolution.* Botanical Society of America Conference; Boise, Idaho.
2. **May, M. R.** (2013). *Mostly Bayesian methods for inferring heterogeneous evolutionary processes across phylogenies.* Center for Population Biology seminar series; UC Davis.
1. **May, M. R.** & Moore, B. R., (2013). *Assessing the reliability of MEDUSA using simulation.* Joint Annual Evolution Meeting; Snowbird, Utah.

Fellowships and Awards

UC Davis Outstanding Graduate Student Teaching Award (2017)
NSF GRFP Predoctoral Fellowship (2011–2016)

Societies and Services

Member of: *Society of Systematic Biologist, Society for the Study of Evolution, Botanical Society of America.*

Peer review for: *Systematic Biology, Proceedings of the National Academy of Sciences, Proceedings of the Royal Society B, Methods in Ecology and Evolution, Frontiers in Plant Science, Functional Ecology, Molecular Biology and Evolution, PLoS One, PeerJ.*

Teaching

- 2021 Instructor for Stay-At-Home RevBayes Workshop.
- 2019 Instructor for Madrid Phylogenetics Workshop.
- 2019 Organizer and instructor for Bodega Applied Phylogenetics Workshop.
- 2018 Instructor for Madrid Phylogenetics Workshop.
- 2018 Teaching assistant for EVE 103: Phylogeny and Macroevolution (UC Davis).
- 2017 Organizer and instructor for Bodega Applied Phylogenetics Workshop.
- 2016 Teaching assistant for EVE 103: Phylogeny and Macroevolution (UC Davis). *Awarded UC Davis Outstanding Graduate Student Teaching Award 2017.*
- 2015 Organizer and teaching assistant for Bodega Applied Phylogenetics Workshop.
- 2014 Organizer and teaching assistant for Bodega Applied Phylogenetics Workshop.
- 2013 Organizer and teaching assistant for Bodega Applied Phylogenetics Workshop.
- 2012 Teaching assistant for EVE 103: Phylogeny and Macroevolution (UC Davis).

Software Tutorials

- 13. **May, M. R.** & Höhna, S. *Rev Language Syntax: A very short introduction to the Rev language.* [Link.](#)
- 12. Tribble, C. M. & **May, M. R.** *Introduction to RevGadgets: Plotting the output of RevBayes analyses in the R package RevGadgets.* [Link.](#)
- 11. **May, M. R.**, Moore, B. R., & Höhna, S. *Introduction to MCMC using RevBayes: Introduction to MCMC simulation using a simple binomial model.* [Link.](#)
- 10. **May, M. R.** & Höhna, S. *Model Selection of Partition Models: Comparing relative model fit with Bayes factors.* [Link.](#)
- 9. **May, M. R.** & Höhna, S. *Model Averaging of Substitution Models: Reversible-jump MCMC over substitution models.* [Link.](#)
- 8. Höhna, S. & **May, M. R.** *Branch-Specific Diversification Rate Estimation: How to estimate branch-specific shifts in diversification rates.* [Link.](#)
- 7. Höhna, S., Freyman, W. A., & **May, M. R.** *Diversification Rate Estimation with Missing Taxa: How to estimate diversification rates with incomplete taxon sampling.* [Link](#)
- 6. **May, M. R.** *Simple Brownian Rate Estimation: Estimating rates of Brownian-motion evolution.* [Link.](#)

5. **May, M. R.** *Relaxed Brownian Rate Estimation: Estimating branch-specific rates of Brownian-motion evolution.* [Link](#).
4. **May, M. R.** *State-Dependent Brownian Rate Estimation: Estimating state-dependent rates of Brownian-motion evolution.* [Link](#).
3. **May, M. R.** *Multivariate Brownian Motion: Accounting for correlations among continuous traits.* [Link](#).
2. **May, M. R.** *Simple Ornstein-Uhlenbeck Models: Estimating optima under Ornstein-Uhlenbeck evolution.* [Link](#).
1. **May, M. R.** *Relaxed Ornstein-Uhlenbeck Models: Estimating lineage-specific optima under Ornstein-Uhlenbeck evolution.* [Link](#).