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Education

2009-2015 PhD; University of Texas at Austin, Ecology, Evolution and Behavior

2005-2009 BA; St. Olaf College, Biology

Current Appointment

Assistant Professor, Department of Biological Sciences

Southeastern Louisiana University
August 2017 - Present

Past Appointments

2016-2017: National Science Foundation Postdoctoral Fellow in Biology

Iowa State University & The Field Museum

2015 - 2016: Postdoctoral Researcher

Iowa State University & University of Kansas

2014 - 2015: Graduate Research Assistant

University of Texas at Austin

2009 - 2014: Graduate Teaching Assistant

University of Texas at Austin

Publications

Wright, AM, Wagner PJ, and Wright DE. In review. Testing character-evolution models in phylogenetic paleobiology: a case study with cambrian echinoderms. Preprint ecoevorxiv.org/ykzg5.

Harris B, McCarthy P, **Wright AM**, Schutz H, Boersma K, Shepherd S, Manning L, Malisch J, Ellington R. In Review. From panic to pedagogy: Using online active learning to promote inclusive instruction in ecology and evolutionary biology courses. Preprint: [10.22541/au.159493366.69859736](https://doi.org/10.22541/au.159493366.69859736)

Warnock RCM, **Wright AM**. Accepted. Understanding the tripartite approach to Bayesian divergence time estimation. Preprint: <https://ecoevorxiv.org/4vazh/>

Barido-Sottani J, Saupe E, Smiley TM, Soul LC, **Wright AM**, Warnock RCM. Accepted. Paleobiology. Seven rules for simulations in paleobiology.

Wright AM, Lloyd, GT. In press. Bayesian analyses in phylogenetic paleontology: Interpreting the posterior sample. *Palaeontology*.

Barido-Sottani J, Justison J, **Wright AM**, Warnock RCM, Pett WC, Heath TA. 2020. Estimating a time-calibrated phylogeny of fossil and extant taxa using RevBayes. Eds: C. Scornavacca, F. Delsuc, N. Galtier. *Phylogenetics in the Genomic Era*. No commercial publisher 5.2:1–5.2:23.

Wright AM, Schwartz RS, Oaks JM, Newman CM, and Flanagan SP. 2020. The Why, When, and How of Computing in Biology Classrooms. *F1000Research* 2020, 8:1854. <https://doi.org/10.12688/f1000research.20873.1>

Wright AM. 2019. A systematist's guide to estimating Bayesian phylogenies from morphological data. *Insect Systematics and Diversity* 3: <https://doi.org/10.1093/isd/ixz006>.

Wright AM. 2019. treesiftr: An R package and server for viewing phylogenetic trees and data *Journal of Open Source Education*, 2(11), 35, <https://doi.org/10.21105/jose.00035>

Devitt TJ, **Wright AM**, Cannatella DC, Hillis, DM. 2019. Species delimitation in endangered groundwater salamanders: Implications for aquifer management and biodiversity conservation. *Proceedings of the National Academy of Sciences* 116: 2624-2633.

Mueller UG, Kardish MR, Ishak HD, **Wright AM**, Solomon SE, Bruschi SM, Carlson AL, Bacci M. 2018. Phylogenetic patterns of ant-fungus associations indicate that farming strategies, not only a superior fungal cultivar, explain the ecological success of leafcutter ants. *Molecular Ecology* 27: 2414-2434.

Lanfear, R, **Wright AM**, Fransden PB, Senfeld T, Calcott B. 2017. PartitionFinder 2: new methods for selecting partitioned models of evolution for molecular and morphological phylogenetic analyses. *Mol. Biol. and Evol.* 34: 772-773.

Matzke NJ, **Wright AM**. 2016. Inferring node dates from tip dates in fossil Canidae: the importance of tree priors. *Biol. Lett.* 12: 8.

Bapst DW, **Wright AM** Lloyd GT, Matzke NJ. 2016. Topology, divergence dates, and macroevolutionary inferences vary between different tip-dating approaches applied to fossil theropods (Dinosauria). *Biol. Lett.* 12: 7.

Wright AM, Lloyd GT, Hillis DM. 2016. Modeling character change heterogeneity in phylogenetic analyses of morphology through the use of priors. *Syst. Biol.* 65: 602-611.

Meirelles L, Solomon S, Bacci M, **Wright AM**, Mueller, U, Rodrigues, A. 2015. Shared Escovopsis infections destabilize the tripartite co-evolution hypothesis in the higher-attine fungus-growing ant symbiosis. *R. Soc. Open Sci.* 2:9.

Wright AM, Lyons KM, Brandley MB, Hillis DM. 2015. Which Came First? Robustness in Phylogenetic Reconstruction of Ancestral States. *J Exp Zool B* 324: 504-516.

Wright AM and Hillis DM. 2014. Bayesian Analysis Using a Simple Likelihood Model Outperforms Parsimony for Estimation of Phylogeny from Discrete Morphological Data. *PLoS One* 9:10.

Li T, Hua J, **Wright AM**, Cui Y, Xie Q, Bu W, Hillis DM. 2014. Long-branch attraction and the phylogeny of true water bugs (Hemiptera: Nepomorpha) as estimated from mitochondrial genomes. *BMC Evol Biol* 14:99.

Technical Reports

Hillis DM, Devitt TJ, **Wright AM**, Cannatella DC. 2015. Genomic Assessment of Taxonomic Status of Central Texas Eurycea Salamanders. City of Austin Report.

Grants

2019-2022: Louisiana Biomedical Research Network Full Project: Integrating heterogeneous data sources to estimate phylogeny. \$294,000.

2018-2019: Louisiana Biomedical Research Network Pilot Project: Implementing a Dirichlet process for modeling complex biological data. \$50,000.

2016-2017: National Science Foundation Postdoctoral Research Fellowship in Biology, Interdisciplinary Research Using Biological Collections: Estimating a Time-Scaled Phylogenetic Tree of Ants from Combined Molecular-Morphological Data. \$136,000.

2013-2014: National Science Foundation Doctoral Dissertation Improvement Grant: Utilizing maximum likelihood estimation for phylogenetic estimation from morphological data. \$6,820.

Awards

2014: Jackson School of Geosciences: Student Travel Award. \$600.

2013: University of Texas College of Natural Sciences Outstanding Teaching Assistant. \$500

Curriculum Development

Southeastern Louisiana University

Fall 2019: Biological Data Analysis ☞

Fall 2018: Computational Biology ☞

Spring 2018: Applied Systematics [↗](#)
Spring 2018: Genomics and Transcriptomics [↗](#)
Fall 2017: Genetics

Short Courses and Other Teaching

2019: Geological Society of America Short Course: Quantitative Methods in Phylogenetic Paleobiology [↗](#)
2019: Analytical Paleobiology Workshop [↗](#)
2018: Analytical Paleobiology Workshop [↗](#)
2016 - 2019: Data Carpentry Python Ecology lesson maintainer [↗](#)
2016: Nantucket developR Course [↗](#)
2014: Society of Vertebrate Paleontology Annual Meeting. Workshop: Using fossils as tips in phylogenetic analyses.
2014: Center for Computational Biology and Bioinformatics, University of Texas at Austin. Course: Introduction to Biological Computing
2014: Center for Computational Biology and Bioinformatics Big Data in Biology Summer School, University of Texas at Austin. Course: Introduction to Python for Biologists
2014: Statistics and Data Science Department, University of Texas at Austin. Workshop: Intermediate Python.
2013: Center for Computational Biology and Bioinformatics, University of Texas at Austin. Course: Introduction to Computing with Python

Students Mentored

Basanta Khakurel, Southeastern Louisiana University
Christina Kolbmann, Southeastern Louisiana University
Courtney Grigsby, Southeastern Louisiana University
Tyler Tran, Southeastern Louisiana University
Rachael Johnson, Southeastern Louisiana University
Katherine Jenkins, Southeastern Louisiana University
Pedro Jimenez-Antenucci, Southeastern Louisiana University
Bradley Freeman, Southeastern Louisiana University
Patrick Mendoza, Iowa State University
Andre Flores, Iowa State University
Kelly Schiro, Iowa State University
Krishna Gandikota, Iowa State University

Software

tree.datatable - An R package for linking data with tips in phylogenetic trees. Roman Palacios C, **Wright AM**, Uyeda J. (developer - <https://github.com/uyedaj/treedata.table>)
treeStartR - An R package for making starting trees from combined molecular, morphological and stratigraphic data. **Wright AM**. (developer - <https://github.com/ropensci/treeStartR>)
PartitionFinder2 - Dataset partitioning selection for likelihood and Bayesian phylogenetics. Lanfear R, Frandsen PB, **Wright AM** and Calcott BC. (developer - <https://github.com/brettc/partitionfinder>)

Invited Talks

2020 **Wright AM**. Bayesian analyses in phylogenetic palaeontology: Interpreting the posterior sample. Systematics, Biogeography and Evolution meeting.
2019 **Wright AM**. Co-estimation of Phylogeny, Divergence Time, and Macroevolutionary Parameters In Formicidae. Geological Society of America Annual Meetings.

- 2019** **Wright AM.** Estimating phylogenetic trees from discrete morphological data: Modeling evolution to understand the past. Louisiana Louisiana State University Computational Biology Seminar Series.
- 2019** **Wright AM.** Modeling deep-time evolutionary processes from heterogeneous data sources. Louisiana Biomedical Research Network Annual Meeting.
- 2018** **Wright AM.** Applying a flexible model of discrete trait evolution to estimate a phylogeny of the Formicidae. Entomological Society Annual Meetings.
- 2017** **Wright AM.** Flexible Modeling of Morphology for Phylogenetic Inference. Louisiana State University Museum of Natural History.
- 2017** **Wright AM.** How did I get here: Lessons from the first in my family to go to college. BEACON Center Undergraduate Diversity Event, Evolution Meetings. Portland, OR.
- 2016** **Wright AM.** Using Phylogenetic Trees to Study Evolutionary History. Texas Women's University. Denton, TX.
- 2016** **Wright AM.** Model Misspecification: Lessons From Empirical Data. Iowa State University. Ames, IA. February 2016.
- 2014** **Wright AM,** Lyons KM, Hillis DM and Brandley M. Estimating models of character evolution with phylogenetic uncertainty. Evolution Meetings. Raleigh, NC.
- 2013** **Wright, AM** and Hillis, DM. Utilizing model-based methods for estimating phylogenetic trees from discrete morphological data with rate heterogeneity. University of Texas at Tyler.

Presentations at Scientific Meetings

* = Denotes undergraduate author

- 2019** Brown JM, **Wright, AM.** RevBayes for Teaching and Research. Society of Systematic Biologists Meeting. Gainesville, FL.
- 2019** Khakurel, B*, Grigsby, C*, **Wright, AM.** Modeling morphological state space. Society of Systematic Biologists Meeting. Gainesville, FL.
- 2019** Kolbmann, CM, Tran, TD*, Grigsby, C*, **Wright, AM.** Time heterogeneous Fossilized Birth-Death Modeling in Formicidae. Evolution Meetings. Providence, RI.
- 2019** Tran, TD*, Kolbmann, CM, Grigsby, C*, **Wright, AM.** Unifying Phenotypic and Molecular Data for Phylogenetic Estimation. Evolution Meetings. Providence, RI.
- 2019** Kolbmann, CM, Tran, TD*, Grigsby, C*, **Wright, AM.** Mechanistic Modeling of Evolution for Phylogenetic Inference. Louisiana Biomedical Research Network Bioinformatics Meeting. Baton Rouge, LA.
- 2019** Tran, TD*, Kolbmann, CM, Grigsby, C*, **Wright, AM.** Unifying Phenotypic and Molecular Data for Phylogenetic Estimation. Louisiana Biomedical Research Network Bioinformatics Meeting. Baton Rouge, LA.
- 2018** Jenkins, KM*, Johnson, R.* and **Wright, AM.** Site-heterogeneous models for morphology. South-eastern Student Research Showcase. Hammond, LA.
- 2017** **Wright AM,** Pett WC, Heath TA. Flexible Modeling of Morphological Characters for Phylogenetic Inference. Evolution Meetings. Portland, OR.
- 2016** **Wright AM** and Heath, TA. Innappropriate parameterization causes inaccurate estimation of node ages. Geological Society of America Meetings. Denver, CO.
- 2016** **Wright AM** and Heath, TA. Innappropriate parameterization causes inaccurate estimation of node ages. Evolution Meetings. Austin, TX.
- 2014** **Wright AM,** Lloyd GT, Matzke NJ, and Bapst DW. Fossils-only tip-dating of deinonychosaurian theropods: a comparison of methods and models. Society of Vertebrate Paleontology Annual Meeting. Berlin, Germany.
- 2013** **Wright AM** and Hillis DM. Utilizing model-based methods for estimating phylogenetic trees from discrete morphological data with rate heterogeneity. Evolution Meetings. Snowbird, UT.
- 2012** **Wright AM,** Brown JP, Slater GJ, and Hillis DM. On the utility of likelihood-based methods for phylogenetic estimation from binary data. Society of Vertebrate Paleontologists Annual Meeting. Raleigh, NC.
- 2011** **Wright AM,** Brown JP, Harmon LJ, and Hillis, DM. Model-based methods for paleontological phylogenetics. Annual BEACON Meeting. East Lansing, Michigan.
- 2011** **Wright AM** and Hillis DM. Effects of gene conversion on phylogenetic reconstruction. Evolution Meetings. Norman, Oklahoma.
- 2010** **Wright, AM** and Hillis, DM. Effects of gene conversion on phylogenetic reconstruction. Annual BEACON Meeting. East Lansing, Michigan.

Symposia Organized

2019: Enabling the next generation of computational biologists. iEvoBio Meeting. Moderator: **Wright AM**.
2016: New Approaches to Phylogenetic Paleobiology. Geological Society of America Annual Meetings. Moderators: Bapst DW, Hopkins M, **Wright AM**, and Wright DE
2014: Putting Fossils in Trees. Society of Vertebrate Paleontology Annual Meeting. Berlin, Germany. November 2014. Moderators: **Wright AM**, Matzke NJ, Lloyd GT and Bapst, DW.

Professional Service

Systematic Biology, Associate Editor, 2019-Present.
iEvoBio; Organization Head, 2019-Present.
Society of Systematic Biologists; Council Member, 2017-2020.
SciPy 2015 Conference Diversity Committee: Committee Member, SciPy Conference 2015
Software Carpentry Diversity Committee: Committee Member, 2014-2016
NESCent Phylotastic! Hackathon: Participant, 2013
Macroevolution Journal Club: Contributor and Organizer, 2012 - 2015
Journal reviewer for: *American Naturalist*, *BMC Evolutionary Biology*, *Ecology Letters*, *Molecular Biology & Evolution*, *Systematic Biology*, *Botany*, *Biology Letters*, *Proceedings of the Royal Society B*.
Award reviewer for: Systematic Biology Mini-ARTS Awards; SciPy Conference (2015) Diversity Travel Awards.
Society Membership: Society of Systematic Biologists, Entomological Society of America, Geological Society of America, NumFocus Foundation

Outreach

Science in the Pub: "Fungal Farmers Under Our Feet." Contributed talk, 2018.
Girls In STEM at Abby Sawyer Elementary School: Activity Leader, 2016
Girl Scouts TechGirls: Activity Leader, 2012
GirlStart Girl Congress, Activity Leader, 2011
Travis County High School Science Fair: Judge, 2010
Blog Owner: Paleontology