April Marie Wright

Address
403 Biology Building
Southeastern Louisiana University
2400 N. Oak St
Hammond, LA 70401

Phone (512) 940-5761
Email wright.aprilm@gmail.com
Website https://paleantology.com/the-wright-lab/

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

** = denotes undergraduate co-author

Charpentier, CP**, **Wright AM**. In review. Revticulate: An R framework for interaction with RevBayes. Preprint: https://ecoevorxiv.org/rsf85/
Ward SJ, McMahan CD, Khakurel B**, **Wright AM**, Piller KR. In review. Next Generation Sequence data supports the taxonomic validity of *Poeciliopsis gracilis* and *Poeciliopsis pleurospilus* (Cyprinodontiformes: Poeciliidae)
Barido-Sottani J, Justison JA, Borges R, Brown JM, Dismukes W, do Rosario Petrucci B, Fabreti G, Höhna S, Landis MJ, Lewis PO, May MR, Mendes FK, Pett W, Redelings BD, Tribble CM, **Wright AM**, Zenil-Ferguson R, Heath TA. Accepted. Lessons learned from organizing and teaching virtual phylogenetics workshops.
Román Palacios C, **Wright AM**, Uyeda J. Accepted. treedata.table: A wrapper for data.table that enables fast manipulation of phylogenetic trees matched to data. Preprint: https://ropensci.github.io/treedata.table/articles/E_Preprint.html
Wright AM, Wagner PJ, and Wright DF. 2021. Testing character-evolution models in phylogenetic paleobiology: a case study with Cambrian echinoderms. Cambridge: Cambridge University Press. doi:10.1017/9781009049016
Warnock RCM, **Wright AM**. 2020. Understanding the tripartite approach to Bayesian divergence time estimation. Elements of Paleontology. Cambridge: Cambridge University Press. doi:10.1017/9781108954365

Harris B, McCarthy P, **Wright AM**, Schutz H, Boersma K, Shepherd S, Manning L, Malisch J, Ellington R. 2020. From panic to pedagogy: Using online active learning to promote inclusive instruction in ecology and evolutionary biology courses. Ecology and Evolution 10: 12581-12593. doi:10.1002/ece3.6915
Barido-Sottani J, Saupe E, Smiley TM, Soul LC, **Wright AM**, Warnock RCM. 2020. Seven rules for simulations in paleobiology. Paleobiology, 1-10. doi:10.1017/pab.2020.30
Wright AM, Lloyd, GT. 2020. Bayesian analyses in phylogenetic paleontology: Interpreting the posterior sample. Palaeontology. doi:10.1111/pala.12500
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. doi:10.12688/f1000research.20873.1
Wright AM. 2019. A systematist's guide to estimating Bayesian phylogenies from morphological data. Insect Systematics and Diversity 3. doi: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, doi.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. doi.org:10.1073/pnas.1815014116.
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. doi: 10.1111/mec.14588.
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. doi: 10.1093/molbev/msw260.
Matzke NJ, **Wright AM**. 2016. Inferring node dates from tip dates in fossil Canidae: the importance of tree priors. Biol. Lett. 12: 8. doi.org:10.1098/rsbl.2016.0328
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. doi:10.1098/rsbl.2016.0237
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. doi:10.1093/sysbio/syv122
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. doi: 10.1098/rsos.150257
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. doi:10.1002/jez.b.22642
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. doi:10.1371/journal.pone.0109210
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. doi: 10.1186/1471-2148-14-99.

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

2021-2026: CAREER: Quantitative assessment of models for phylogenetic data. $1,150,905.
2021-2024: Collaborative Research: phyloregion, computational infrastructure for biogeographic regionalization and macroecology in the R computing environment. $193,747. **Supplement:** Research Experience for Post-Baccalaureate Students in the Biological Sciences. $52,570
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 developeR 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

Anisha Neupane, Southeastern Louisiana University
Simran Baruwal, Southeastern Louisiana University
Amere Roussell, Southeastern Louisiana University
Caleb Charpentier, Southeastern Louisiana University
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

Revticulate - An R package for accessing RevBayes from an R session. Charpentier CP, **Wright AM**. (developer - https://paleantology.github.io/Revticulate/index.html)
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

2021 **Wright AMW**. Finding confidence among infinite possibilities: Lessons from paleontological phylogenetics. University of California, Berkeley.
2021 Breanna Harris, **Wright AM**, and Shepherd SL. From Panic to Pedagogy – tips and resources for making online teaching more active and inclusive.
2021 **Wright AMW**. Finding confidence among infinite possibilities: Lessons from paleontological phylogenetics. University of Idaho.
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. Southeastern 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 DF.
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*, *PLoS One*.
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: Paleantology