April Marie Wright

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Education

September 2009 - May 2015 PhD; University of Texas at Austin, Ecology, Evolution and Behavior
September 2005 - May 2009 BA; St. Olaf College, Biology

Current Appointment

Program Officer, Systematics and Biodiversity Science
National Science Foundation
January 2025 - Present
Dyson Associate Professor, Department of Biological Sciences
Southeastern Louisiana University
August 2022 - Present

Past Appointments

August 2023 - December 2024: Assistant Dean, College of Science and Technology
Southeastern Louisiana University

August 2017 - July 2022: Assistant Professor, Department of Biological Sciences
Southeastern Louisiana University
July 2016 - July 2017: National Science Foundation Postdoctoral Fellow in Biology
Iowa State University & The Field Museum
August 2015 - June 2016: Postdoctoral Researcher
Iowa State University & University of Kansas
August 2014 - May 2015: Graduate Research Assistant
University of Texas at Austin
August 2009 - May 2014: Graduate Teaching Assistant
University of Texas at Austin

In Review

Wynd BM, Khakurel B, Kammerer CF, Wagner PJ, and **Wright AM**. In Review. Incorporating continuous characters in joint estimation of dicynodont phylogeny.
Preprint: https://www.biorxiv.org/content/10.1101/2025.03.03.641281v1

Phifer E, Wright DF, Wagner PJ, and **Wright AM**. Testing Character Evolution Models in Phylogenetic Paleobiology with Reversible Jump Markov-Chain Monte Carlo.

Wynd BM, and **Wright AM**. In Review. Modeling of Rate Heterogeneity in Datasets Compiled for Use With Parsimony.
Preprint: https://doi.org/10.1101/2024.06.26.600858

Wagner PJ, and **Wright AM**. In Review. Quantitative Models for Distinguishing Punctuated and Continuous-Time Models of Character Evolution and Their Implications for Macroevolutionary Theory.
Preprint: https://www.biorxiv.org/content/10.1101/2024.04.09.588788v1.abstract

Publications

Italics indicate undergraduate author

Gross, CP, **Wright AM**, and Daru BH. 2025. A global biogeographic regionalization for butterflies. Philosophical Transactions B: 380.1917: https://doi.org/10.1098/rstb.2023.0211

Mulvey L, May MR, Brown JM, Höhna S, **Wright AM**, Warnock RCM. 2024. Assessing the Adequacy of Morphological Models used in Palaeobiology. Systematic Biology: 74(1): 34–52. https://doi.org/10.1093/sysbio/syae055

Khakurel B, *Grigsby C, Zariwala J, Tran TD*, Höhna S, and **Wright AM**. 2024. The fundamental role of character coding in Bayesian morphological phylogenetics. Systematic biology: 73(5), 861-871. https://doi.org/10.1093/sysbio/syae033

Barido-Sottani J, Schwery O, Warnock RCM, Zhang C, **Wright AM**. 2024. Practical guidelines for Bayesian phylogenetic inference using MCMC. Open Res Europe 2024, 3:204 https://open-research-europe.ec.europa.eu/articles/3-204/v2

Khakurel B, Nikolakis ZL, Crother BI, and **Wright AM**. 2023. Species delimitation in Eastern Pine Snakes (*Pituophis melanolucus*). Bulletin of the Society of Systematic Biologists: 1–14. https://doi.org/10.18061/bssb.v2i1.9423

Duhamel A, Benoit J, Wynd BM, **Wright AM**, and Rubidge B. 2023. Redescription of three basal anomodonts: a phylogenetic reassessment of the holotype of *Eodicynodon oelofseni* (NMQR 2913). Frontiers in Earth Science. https://doi.org/10.3389/feart.2023.1220341

Simões TR, Vernygora OV, de Medeiros BA, & **Wright AM.** 2023. Handling Character Dependency in Phylogenetic Inference: Extensive Performance Testing of Assumptions and Solutions Using Simulated Data. Systematic Biology 72: 662–680. https://doi.org/10.1093/sysbio/syad006

Wright AM, Barido-Sottani J, Warnock RCM and Bapst DW. 2022. Integrating Fossil Observations Into Phylogenetics Using the Fossilized Birth–Death Model. Annual Reviews in Ecology, Evolution and Systematics. 53:12.1–12.2. http://doi/10.1146/annurev-ecolsys-102220-030855

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. 2022. Lessons learned from organizing and teaching virtual phylogenetics workshops. Bulletin of the Society of Systematic Biologists: 1:2. https://doi.org/10.18061/bssb.v1i2.8425

Charpentier CP, **Wright AM**. 2022. Revticulate: An R framework for interaction with RevBayes. Methods in Ecology and Evolution: https://doi.org/10.1111/2041-210X.13852

Ward SJ, McMahan CD, *Khakurel B*, **Wright AM**, Piller KR. 2022. Next Generation Sequence data supports the taxonomic validity of *Poeciliopsis gracilis* and *Poeciliopsis pleurospilus* (Cyprinodontiformes: Poeciliidae). PLoS: 10.1371/journal.pone.0262687

Román Palacios C, **Wright AM**, Uyeda J. 2021. treedata.table: A wrapper for data.table that enables fast manipulation of phylogenetic trees matched to data. PeerJ 9:e12450 https://doi.org/10.7717/peerj.12450

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. https://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. https://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. https://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. https://doi:10.1017/pab.2020.30

Wright AM, Lloyd, GT. 2020. Bayesian analyses in phylogenetic paleontology: Interpreting the posterior sample. Palaeontology. https://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. https://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. https://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. https://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. https://doi.org: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. https://doi.org: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. https://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. https://doi.org: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. https://doi.org: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.
https://doi.org: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. https://doi.org: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.
https://doi.org: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. https://doi.org: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

2023 - 2025: Linux Servers for Scientific Computing: Promoting Computational Literacy. Louisiana Board of Regents. $66,873

2021-2026: CAREER: Quantitative assessment of models for phylogenetic data. National Science Foundation. $1,150,905.

2021-2024: Collaborative Research: phyloregion, computational infrastructure for biogeographic regionalization and macroecology in the R computing environment. National Science Foundation. $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. Louisiana Biomedical Research Network. $294,000.

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

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

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

Awards

2018: Louisiana Biomedical Research Network Outstanding New PI Award.
2014: Jackson School of Geosciences: Student Travel Award. $600.

Curriculum Development

Southeastern Louisiana University

Spring 2020:   Introductory Biology II
Fall 2019:   Biological Data Analysis ⌧
Fall 2018:   Computational Biology ⌧
Spring 2018:   Applied Systematics ⌧
Fall 2017:   Genetics

Short Courses and Other Teaching

2024:   Biogeography in R Workshop ⌧
2019:   Nantucket developeR Course ⌧
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

Ashley Canas, Southeastern Louisiana University
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)
datelife: Scientific Data on Time of Lineage Divergence for Your Taxa. O'Meara B, Sanchez-Reyes LL, Eastman J, Heath TA, **Wright AM**, Schliep K, Chamberlain S, Midford P, Harmon LJ, Brown JW, Pennell M, Alfaro MJ, McTavish EJ. (developer - http://phylotastic.org/datelife/index.html)
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

2023   **Wright AM**. Model Selection: A Biological Perspective. Tulane University
2023   **Wright AM**. Model Selection in Phylogenetic Paleobiology. American Museum of Natural History.
2023   **Wright AM**. Model Selection in Biology. St. Catherine university.
2022   **Wright AM**. Models, Meaning and the Middle Cambrian. Yale University.
2021   **Wright AM**. Finding confidence among infinite possibilities: Lessons from paleontological phylogenetics. Southeastern Louisiana University.
2021   **Wright AM**. The fossilized birth-death process: An overview. Phyloseminar.
2021   **Wright AM**. Paleontological Phylogenetics and Deep Time Evolution. Mississippi University for Women.
2021   **Wright AM**. 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 AM**. 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

2023. 	**Wright, AM**. The burst of divergence-time estimation methods: a conversation on the how and why. Society of Systematic Biologists Meeting. Ciudad Mèxico, MX.

2023 	Khakurel, B, **Wright, AM**. Data-based PPS to compare Mk and SHDM models for morphological data. Society of Systematic Biologists Meeting. Ciudad Mèxico, MX.

2022 	Wagner, PJ, **Wright, AM**. The importance of considering punctuated change when assessing macroevolutionary scenarios in the context of phylogenies. Geological Society of America Meetings. Denver, CO.

2022 	Schwery, O, Khakurel, B, **Wright, AM**. Adequacy of Fossilised Birth-Death models: a test case in ants. Evolution Meetings. Cleveland, OH.

2022 	Khakurel, B, **Wright, AM**. Species delimitation on Eastern Pine snakes. Evolution Meetings. Cleveland, OH.

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

Evolution Meetings, Assistant Meeting Organizer, 2022-Present
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

STEMFest. Southeastern Louisiana University. Activity, 2021. 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