April Marie Wright

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Current Appointments

Assistant Professor, Department of Biological Sciences
Southeastern Louisiana University
August 2017 - Present

Past Appointments

National Science Foundation Postdoctoral Fellow in Biology
July 2016 - Present
Iowa State University & The Field Museum
Supervisors: Dr. Tracy Heath & Dr. Corrie Moreau

Postdoctoral Researcher
Iowa State University
September 2015 - July 2016
Ecology, Evolution and Organismal Biology
Supervisor: Dr. Tracy Heath

Postdoctoral Researcher
University of Kansas
July 2015 - July 2016
Ecology and Evolutionary Biology
Supervisor: Dr. Mark Holder

Education

2009-2015   PhD in Biology; University of Texas at Austin

Ecology, Evolution and Behavior
Award Date: April 14, 2015
Supervisor: Dr. David Hillis

2005-2009   BA in Biology; St. Olaf College

Publications

Mueller UG, Kardish MR, Ishak HD, **Wright AM**, Solomon SE, Bruschi SM, Carlson AL, Bacci M. In press. 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.

Wright, AM 2017. Editor's note on 'Putting fossils in trees' special issue. Biol. Lett. 13: 1.

Lanfear, R, **Wright AM**, Fransden PB, Senfeldova 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

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

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. Awarded: 2016.

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

Awards

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

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

Curriculum Development

July 2016 - March 2017: Data Carpentry Python Ecology lesson maintainer.

- Published Lesson Materials: 10.5281/zenodo.570050

August 2016: Nantucket developeR Course. Workshop Materials: Developing Phylogenetic Methods in R

February 2016: Bodega Bay Marine Lab Intermediate Bioinformatics Training workshop. Workshop Session: Reduced-Representation Sequencing for Population History Inference

October 2014: Society of Vertebrate Paleontology Annual Meeting. Workshop: Using fossils as tips in phylogenetic analyses.

Spring 2013 & 2014: Center for Computational Biology and Bioinformatics, University of Texas at Austin. Course: Introduction to Biological Computing

Spring 2014: Center for Computational Biology and Bioinformatics Big Data in Biology Summer School, University of Texas at Austin. Course: Introduction to Python for Biologists

Fall 2014: Statistics and Data Science Department, University of Texas at Austin. Workshop: Intermediate Python.

Teaching Assistant Experience

July 2014, July 2016: Woods Hole Workshop on Molecular Evolution; Woods Hole Marine Biological Laboratory.

September 2009 — May 2014: School of Biological Sciences, University of Texas at Austin.
Courses: Advanced Systematics, Evolution, Evolution and Diversity, Lab Experience in Genetics, Human Biology, Genetics.

Fall 2011 — Spring 2012: Statistics and Data Science Department, University of Texas at Austin. Courses: Beginning Python.

September 2006 — May 2008: St. Olaf College. Courses: Genetics (lab section), Evolution and Diversity (lab section).

Students Mentored

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

Software

PartitionFinder2 (Python) - 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

2017

Wright AM. Flexible Modeling of Morphology for Phylogenetic Inference. Louisiana State University Museum of Natural History.

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.

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

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.

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. Poster Presentation.

Wright AM and Hillis DM. Effects of gene conversion on phylogenetic reconstruction. Evolution Meetings. Norman, Oklahoma. Poster presentation.

2010

Wright AM and Hillis, DM. Effects of gene conversion on phylogenetic reconstruction. Annual BEACON Meeting. East Lansing, Michigan. August 2010. Poster presentation.

Symposia Organized

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

SciPy 2015 Conference Diversity Committee: Committee Member, SciPy Conference 2015

Software Carpentry Diversity Committee: Committee Member, 2014-

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

Outreach

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: http://wrightaprilm.github.io/, Paleantology