

# Emily Jane McTavish

---

## CONTACT INFORMATION

School of Natural Sciences  
University of California, Merced  
5200 N. Lake Rd, Merced CA 95343  
ejmctavish@ucmerced.edu

## EDUCATION

**University of Texas**, Austin, Texas

*Ph.D*, Ecology, Evolution and Behavior

May 2013

Advisor: David M. Hillis

Dissertation: *Estimating population histories using single-nucleotide polymorphisms sampled throughout genomes*

**McGill University**, Montreal, Quebec, Canada *BS*, Honours Biology

April 2006

## PROFESSIONAL APPOINTMENTS

**University of California, Merced**, Merced, CA

Associate Professor, Life and Environmental Sciences

July 2023 - Present

Assistant Professor, Life and Environmental Sciences

June 2016 - July 2023

**University of Kansas**, Lawrence, Kansas

Postdoctoral researcher, Department of Ecology and Evolutionary Biology

Advisor: Mark T. Holder

May 2013 - June 2016

**Heidelberg Institute for Theoretical Studies**, Heidelberg, Germany

Humboldt Research Fellow, Scientific Computing Group

Advisor: Alexandros Stamatakis

December 2014 - August 2015

## PUBLICATIONS

^ indicates a postdoctoral or graduate student advisee

*Submitted*

**McTavish, E.J.**, Gerbracht, J.A., Holder, M.T., Iliff, M.J., Lepage, D., Rasmussen, P.C. Redelings, B., Sanchez-Reyes, L.L., Miller, E.T. *in review*. A complete and dynamic tree of birds. Preprint: <https://doi.org/10.1101/2024.05.20.595017>

Guo, J., **McTavish, E.J.**, Rosindell, J. *in review*. Phylogenetic Diversity Across the Complete Tree of Life. Preprint: <https://www.researchsquare.com/article/rs-4397985/v1>

Miller, E.T., Auer, T., Barry, J., Davis, C.L., Dokter, A.M., Farnsworth, A., Hochachka, W.M., Johnston, A., LaSorte, F., Robinson, O.J., Rodewald, A. D., Stillman, A.N., Strimas-Mackey, A., **McTavish, E.J.** Wood, C., Fink, D. *in review*. Systematically pruning the avian tree of life: Citizen science offers insights into worrisome population losses.

*Refereed journal articles*

Mikryukov, V., Abarenkov, K., Laffan, S., Robertson, T., **McTavish, E.J.**, Stjernegaard Jeppesen, T., Waller, J., Blissett, M., Köljalg, U., Miller, J. *accepted*. PhyloNext: a pipeline for phylogenetic diversity analysis of GBIF-mediated data. *BMC Evolutionary Biology*

^Lopez Fang, L., Ortega-Del Vecchyo, D., **McTavish, E.J.**, Huerta-Sanchez, E. 2024. Leveraging shared ancestral variation to detect local introgression. *PLoS Genetics* <https://doi.org/10.1371/journal.pgen.1010155>

^Sánchez Reyes, L.L., **McTavish, E.J.**, O'Meara, B. *accepted*. DateLife: leveraging databases and analytical tools to reveal the dated Tree of Life. *Systematic Biology*, <https://doi.org/10.1101/782094>

PUBLICATIONS  
CONTINUED

- ^Sánchez Reyes, L.L., **McTavish, E.J.** (2022) Approachable case studies support learning and reproducibility in data science: An example from evolutionary biology, *Journal of Statistics and Data Science Education*, 10.1080/26939169.2022.2099487
- ^Toscani Field, J., Abrams, J., Cartee, J., **McTavish, E.J.** 2022. Rapid Alignment Updating with Extensiphy. *Methods in Ecology and Evolution* 13:682–693 GitHub repository: <https://github.com/McTavishLab/Extensiphy>
- ^Sánchez Reyes, L.L., ^Kandziora, M., **McTavish, E.J.** 2021. Physcraper: a python package for continual update of evolutionary estimates using the Open Tree of Life. *BMC Bioinformatics* 22:355 Software package reviewed and accepted by *pyOpenSci*. GitHub repository: <https://github.com/McTavishLab/Physcraper>
- Brock, K., **McTavish, E.J.**, Edwards, D. 2022. Color Polymorphism is a Driver of Diversification in the Lizard Family Lacertidae. *Systematic Biology* 7:24-39
- McTavish, E.J.**, ^Sánchez Reyes, L.L., Holder, M.T. 2021. OpenTree: A Python package for Accessing and Analyzing data from the Open Tree of Life *Systematic Biology* 6:1295–1301. GitHub repository: <https://github.com/OpenTreeofLife/python-opentree>
- Lin, M., Simons, A.L., Curd, E.E., Harrigan, R.J., Schneider, F.D., Ruiz-Ramos, D.V., Gold, Z., Osborne, M.G., Shirazi, S., Schweizer, T.M., Moore, T.N., Fox, E.A., Turba, R., Garcia-Vedrenne, A.E., Helman, S.K., Rutledge, K., Mejia, M.P., Munguia Ramos, M.N., Wetzter, R., Pentcheff, D., **McTavish, E.J.**, Dawson, M.N., Shapiro, B., Wayne, R.K., Meyer, R.S., 2021. Landscape analyses using eDNA metabarcoding and Earth observation predict community biodiversity in California. *Ecological Applications* 31(6):e02379
- McTavish, E.J.**, Drew, B.T., Cranston K. 2017. How and why to build a unified tree of life. *BioEssays* 39:1700114.
- McTavish, E.J.**, Pettengill, J., Davis, S., Rand, H., Strain, E., Allard, M., Timme R.E. 2017. TreesToReads: Simulating data to test phylogenetic effects of biases in SNP calling pipelines. *BMC Bioinformatics* 18:178. GitHub repository: <https://github.com/snacktavish/TreeToReads>
- Hinchliff, C., Smith, S.A., Allman, J.A., Burleigh, G., Chaudhary, R., Coghill, L.M., Crandall, K.A., Deng, J., Drew, B.T., Gazis, R., Gude, K., Hibbett, D., Katz, L.A., Laughinghouse, H.D., **McTavish, E.J.**, Mitford, P., Owen, C., Ree, R., Soltis, D., Williams, T., Cranston, K.A. 2015. Synthesis of phylogeny and taxonomy into a comprehensive tree of life. *Proceedings of the National Academy of Sciences USA*. 112:12764-1276
- McTavish, E.J.**, Holder M.T., Steel, M. 2015. Twisted trees and inconsistency of tree estimation when gaps are treated as missing data – two examples of inconsistency caused by non-linear distance corrections. *Molecular Phylogenetics and Evolution*. 93:289–295
- McTavish, E.J.**, Hinchliff, C., Allman, J.F., Brown, J., Cranston, K.A., Holder M.T., Rees, J. A., Smith, S. A. 2015. Phylesystem: a git-based data store for community curated phylogenetic estimates. *Bioinformatics*. 17:2794-800
- McTavish, E.J.**, Hillis, D.M. 2015. How does ascertainment bias in SNP analyses affect inferences about population history? *BMC Genomics*. 16:266
- McTavish, E.J.**, Hillis, D.M. 2014. A genomic approach for distinguishing between recent and ancient admixture in cattle. *Journal of Heredity*. 105:445–456
- McTavish, E.J.**, Decker, J.E., Schnabel, R.D., Taylor, J.F., Hillis, D.M. 2013. New World cattle show ancestry from multiple independent domestication events. *Proceedings of the National Academy of Sciences USA*. 110:E1398-E1406

PUBLICATIONS  
CONTINUED

Stoltzfus, A., Lapp, H., Matasci, N., Deus, H., Sidlauskas, B., Zmasek, C.M., Vaidya, G., Pontelli, E., Cranston, K., Vos R., Webb, C.O., Harmon, L.J., Pirrung, M., O'Meara, B., Pennell, M.W., Mirarab, S., Rosenberg, M.S., Balhoff, J.P., Bik, H.M., Heath, T., Midford, P., Brown J.W., **McTavish E.J.**, Sukumaran J., Westneat M., Alfaro M.E., Steele A. 2013. Phylotastic! Making Tree-of-Life Knowledge Accessible, Re-usable and Convenient. *BMC Bioinformatics*. 14:1-1

**McTavish\*, E.J.**, Smith\*, G., Guerrero, R., Gering, E. 2012. Flight morphology variation in a damselfly with female limited polymorphism. *Evolutionary Ecology Research*. 14:325-341

Brown, J. Savidge, K. **McTavish, E.J.** 2010. DIM SUM: Demography and Individual Migration Simulated Using a Markov chain. *Molecular Ecology Resources*. 11:358-363

Smith, G., Gering, E. R. Guerrero, **McTavish, E.J.**, Lydgate, T. 2009. *Theobroma cacao* L. (Malvaceae) agroecology in Kauai: a case study. *Pacific Agriculture and Natural Resources* 1:21-26

*Book chapters*

Holder, M. T. and **McTavish, E.J.** 2016. Hypothesis tests for comparing trees. *Encyclopedia of Evolution*, Elsevier.

*Non-refereed publications*

Klott, J. S., M. C. Whitfield, M. Cota, **McTavish, E.J.** 2007. 2006-2007 wildlife inventory in the Jarbidge field office. BLM ID Tech. Bull. 2007-003.

*Refereed conference proceedings*

Holder, M.; Cranston, K. A.; **McTavish, E. J.**, 2019 The Need for Semantically Rich Notions of “Taxa” for Interoperability in Biodiversity Informatics. *American Geophysical Union*,

**McTavish, E.J.** 2019. Linking Biodiversity Data Using Evolutionary History. (Biodiversity\_Next). *Biodiversity Information Standards*,

**McTavish, E.J.**, Holder, M. T., Cranston, K. A. 2018. Nurturing a sustainable Open Tree of Life (TDWG). *Biodiversity Information Standards*, e25727,

INVITED  
TALKS

Seminar	Jan 25, 2024, Center for the Evolutionary Origins of Human Behavior, Inuyama, Japan
Seminar	October 13, 2023, Cornell Lab of Ornithology, Cornell University, Ithaca, NY
Seminar	May 19, 2023, EMBO Satellite Workshop on Biodiversity Informatics, Hellenic Center for Marine Research, Heraklion, Crete
Seminar	October 16, 2020, Cornell Lab of Ornithology, Cornell University, Ithaca, NY
Seminar	October 16, 2019, Humboldt State University, Arcata, CA
Seminar	January 4, 2019, Instituto Gulbenkian de Ciência, Oeiras, Portugal
Integrative Biology seminar	November 29, 2018, UC Berkeley, Berkeley, CA
Integrative Biology seminar	October 31, 2018, University of Minnesota, Minneapolis, MN
Computational Biology seminar	February 21, 2017, Louisiana State University, Baton Rouge, LA
Debate	January 10, 2017, Society of Systematic Biologists, Baton Rouge, LA
Computational Biology seminar	November 15, 2016, Fred Hutchinson Cancer Research Center, Seattle, WA
Biology seminar	September 28, 2016, University of California, Los Angeles, CA
Frontiers in Phylogenetics Symposium	September 9, 2016, Smithsonian Natural History Museum, Washington, DC
Botany seminar	March 23, 2016, Oklahoma State University, Stillwater, OK
A. Watson Armour III Research Seminar	October 21, 2015, The Field Museum, Chicago, IL
Population genetics group	September 14, 2015, École Polytechnique Fédérale de Lausanne (EPFL), Lausanne, Switzerland
Seminar	September 10, 2015, Laboratoire de Biométrie et Biologie Evolutive, Lyon, France

INVITED TALKS CONTINUED	Seminar September 7, 2015, Centre d'Ecologie Fonctionnelle et Evolutive (CEFE), Montpellier, France Early Career Scientists Symposium March 29, 2014, University of Michigan, Ann Arbor, MI NSF BEACON site visit December 8, 2011, Michigan State University, East Lansing, MI IBEST Seminar October 6, 2011, University of Idaho, Moscow, ID
FUNDING AND AWARDS	2023 CC* Regional Computing: CENVAL-ARC: Central Valley Accessible Research and Computational Hub at UC Merced, NSF OAC (~\$1,000,000) 2022 U-RISE at UC Merced (Senior Personnel) NIH URISE 2022 Supplemental funding "Cultivating a Sustainable Open Tree of Life" NSF DBI (~\$53,000) 2021 GEO-Microsoft Planetary Computer Programme "Phylogenetic Diversity in the cloud" (\$60,000 & Microsoft Azure cloud credits in the amount of \$60,000, with Co-PI's J. Miller, M.T. Holder, S.Laffan) 2021 Supplemental funding "Elucidating and Detecting Adaptive Introgression" NSF DEB (~\$60,000) 2019 Full proposal invited - NSF "Evolutionarily informed eco-inference from large data sets" 2019 Invited participant- NSF "Harnessing the Data Revolution" Ideas Lab, May 2019, Tysons Corner, VA. 2018 PI "Cultivating a Sustainable Open Tree of Life" NSF ABI (~\$435,000) 2017 UC Merced, Committee on Research award. 2014 Humboldt Postdoctoral Fellowship, Alexander von Humboldt foundation. Germany. 2014 Invited Speaker, Early Career Scientists Symposium. University of Michigan. 2014 Travel award, National Evolutionary Synthesis Center (NESCent). 2012 Research funding (~\$40,000 co-author with J. Sullivan, B. Sarver and D. M. Hillis), BEACON Center for the study of Evolution in Action. 2011 Research funding (~\$150,000, co-author with J. Sullivan, J. Foster and D. M. Hillis), BEACON Center for the study of Evolution in Action. 2011 XSEDE (Extreme Science and Engineering Discovery Environment), 200,000 HPC compute time allocations.
TEACHING EXPERIENCE	University of California, Merced Graduate Phylogenetics, Fall 2017, Spring 2020, Spring 2022 Introductory Biology, Fall 2018, Fall 2019 Evolution, Spring 2017, Spring 2019, Fall 2022, Spring 2023, Fall 2023 Phylogenetics, Spring 2018  Computational Molecular Evolution Workshop July 19-27, 2022, Hinxton, UK Molecular Evolution Workshop at the Marine Biological Laboratory  Faculty May 30-June 3, 2024, Woods Hole, MA Faculty May 26-June 5, 2023, Woods Hole, MA Faculty May 27-June 6, 2022, Woods Hole, MA Faculty August 1-11, 2019, Woods Hole, MA Faculty July 18-28, 2018, Woods Hole, MA Faculty July 20-30, 2017, Woods Hole, MA Faculty July 17-27, 2016, Woods Hole, MA Faculty July 19-29, 2015, Woods Hole, MA Faculty July 27-August 6, 2014, Woods Hole, MA Teaching Assistant July 21-31, 2013, Woods Hole, MA Teaching Assistant July 22-August 1, 2012, Woods Hole, MA  Trees in the Desert, Large Scale Phylogenetics Workshop April 12-14, 2019, Biosphere 2, AZ Workshop on Quantitative Evolutionary Biology  Young Scientist Lecturer September 13-21, 2014, Nesin Mathematics Village, Şirince, Turkey

TEACHING EXPERIENCE CONTINUED	Software Carpentry Workshops	
	<i>Organizer, Instructor</i> , University of California, Merced	January 10-11, 2018, Merced, CA
	<i>Organizer</i> , University of California, Merced	August 17-18, 2017, Merced, CA
	<i>Instructor</i> , University of Oklahoma,	April 4-5, 2014, Norman, OK
	<i>Instructor</i> , University of Missouri, Kansas City,	Feb 15-16, 2014, Kansas City, KS
	<i>Instructor</i> , University of Kansas,	Aug 22-23, 2013, Lawrence, KS
	<i>Coordinator, Instructor</i> , UT Austin,	Dec 10-11, 2012, Austin, TX
	<i>Teaching Assistant</i> , Michigan State University/UT Austin,	May 7-9, 2012, Austin, TX
	Statistics and Scientific Computing Short Course (Python)	
	<i>Instructor</i>	Feb 26, 2013, Austin, TX
WORKING GROUPS	<i>Instructor</i>	Nov 26, 2012, Austin, TX
	University of Texas	
	<i>Teaching Assistant</i>	Introductory Biology, Fall 2007
		Evolution, Spring 2008, Spring 2009, Fall 2009
		Vertebrate Natural History (Field course), Fall 2008, Spring 2010
	Phylotref/OpenTree/Phenoscape	April 3-5, 2019, Durham, NC
	Next Generation Phenomics Tools for the Tree of Life	May 24-25, 2018, Portland, ME
	Reproducible Research Hackathon	January 9, 2018, Berkeley, CA
	Computable Evolutionary Phenotype Knowledge	December 11-14, 2017, Durham, NC
	FuturePhy/Arbor/OpenTree Clade Workshop	May 4-5, 2017, Chicago, IL
SYMPOSIA ORGANIZED	FuturePhy/Arbor/OpenTree Clade Workshop	October 21-23 2016, Chicago, IL
	FuturePhy Interoperability Hackathon	August 15-18 2016, Lawrence KS
	FuturePhy/Arbor/OpenTree Clade Workshop	February 2016, Gainesville, FL
	Mozilla Science Lab Global Sprint	July 23, 2014, Toronto, ON, Canada
	Phylotastic Hackathon at the National Center for Evolutionary Synthesis (NESCen)	June 4-8, 2012, Durham, NC
	Putting 'Dark Matter' Biodiversity on the Map: Crosslinking Metagenomics, Phylogenetics and Specimen Occurrence Data Infrastructures to Advance Scientific Understanding and Policy Relevance of Cryptic Biodiversity (with Kyle Copas)	
	<i>American Geophysical Union (AGU)</i>	December 9-13 2019, San Francisco, CA
	Linking biodiversity data through phylogenetic knowledge (with Guanyang Zhang, Gaurav Vaidya, Hilmar Lapp, Nico Cellinese)	
	<i>TDWG</i>	September 1-5 2018, Dunedin, New Zealand
	Society of Systematic Biologists Mayr Award Symposium (with Tracy Heath)	
INVITED WORKSHOP PARTICIPATION	<i>Evolution meetings</i>	August 22-26, 2018, Montpellier, France
	SSB Spotlight Symposium: Uncertainty in the face of strong support (with Dave Weisrock)	
	<i>Evolution meetings</i>	June 23-27 2017, Portland, OR
	National Workshop on Data Science Education	
		June 27-30, 2022, Berkeley, CA
	Molecular Evolution Workshop at the Marine Biological Laboratory,	
		July 24 to August 3, 2011, Woods Hole, MA
	Quantitative Evolutionary and Comparative Genomics: Linkage and Recombination in Genome Sequences, at the Okinawa Institute of Science and Technology (OIST)	
		May 16 to June 3, 2011, Okinawa, Japan

PRESENTATIONS AT SCIENTIFIC MEETINGS	<i>Linking Biodiversity Data Using Evolutionary History</i>	
	Biodiversity Next	October 2019, Leiden, Netherlands
	<i>Nurturing a sustainable Open Tree of Life</i>	
	TDWG	September 2018, Dunedin, New Zealand
	<i>Cultivating community collaboration to build a sustainable Open Tree of Life</i>	
	Evolution Meetings	August 2018, Montpellier, France
	<i>Does reference genome choice affect inference?</i>	
	Bay Area Population Genomics	September 2016, San Francisco State University, CA
	<i>Continually updated phylogenies</i>	
	Evolution meetings	July 2016, Austin, TX
	<i>The Open Tree of Life - Curating, synthesizing, and updating phylogenetic information across 1.8 million taxa</i> (poster)	
	Society for Molecular Biology and Evolution	July 2015, Vienna, Austria
	<i>Effects of ascertainment bias on population genetic inference</i>	
	Workshop on Quantitative Evolutionary Biology	
		September 2014, Nesin Mathematics Village, Turkey
	<i>Phylesystem: a git-based data store for community curated phylogenetic estimates</i>	
	iEvoBio	June 2014, Raleigh, NC
	<i>Challenges of synthesizing divergence time information on the tree of life</i>	
	iEvoBio	June 2013, Snowbird, UT
	<i>Estimating population histories using single-nucleotide polymorphisms sampled throughout genomes</i>	
	Evolution meetings	June 2013, Snowbird, UT
	<i>Genomic structure of introgression in New World cattle</i> (poster)	
	Gordon Research Conference	February 2013, Galveston, TX
	<i>Inferring ancestry of genomic regions in cattle of hybrid origin</i>	
	Evolution meetings	July 2012, Ottawa, ON, Canada
	<i>Tracking introgression between cattle subspecies using genomic SNP data</i>	
	Evolution meetings	July 2011 Norman, OK
	<i>Using SNP data to assess population structure and hybridization in Texas Longhorn cattle</i>	
	Plant and Animal Genome Conference	January 2011, San Diego, CA
	<i>Impact of dispersal and sampling on inference of population structure</i> (poster)	
	BEACON: Evolution in Action	August 2010, Michigan State University, MI
	<i>Distinguishing signal from noise in phylogeographic data</i>	
	Evolution meetings	July 2010, Portland, OR
PROFESSIONAL SERVICE AND OUTREACH	Society of Systematic Biologists, Treasurer	Nov 2021 - Dec 2024
	UC Merced Faculty Advisory Committee on IT (FACIT) Co-Chair	2019 - present
	UC Committee on Academic Computing and Communications (UCACC)	
	UCM representative	2019 - present
	Society of Systematic Biologists, Awards committee	2017 - present
	Society of Systematic Biologists, Communications Director	2018 - 2019
	Society of Systematic Biologists, Elected Council Member	Jan 2016 - Dec 2018
	JupyterCon, Program committee	March-September, 2018
	Software Carpentry, Instructor	2011 - present
	Breaking Bio Podcast, Guest	September 25, 2013
	UT Forum, Lecturer	March 22, 2013
	Darwin Day Speaker, Texas Memorial Museum,	February 12, 2012
	Information Technology advisory committee, Student representative	Sept 2010 - Dec 2011
	Science Under the Stars, Presenter	December 8, 2011
	UT Learning Activities for Mature People, Lecturer	November 4, 2011
	NPR's Science Friday, Guest	July 7, 2011
	Flying Cloud Institute Young Women In Science Program, Teacher	July, 2010
	UT Austin Integrative Biology Graduate Student Symposium, Chairperson	April 2009, April 2010

ADVISING ACTIVITIES	<b>Postdoctoral scholars</b>	
	Luna Luisa Sánchez Reyes	August 2019 - August 2023
	Martha Kandziora	September 2017 - May 2019
	<b>Doctoral student advisees (Quantitative and Systems Biology - QSB)</b>	
	<i>Graduated with PhD</i>	
	Lesly Lopez Fang	August 2023
	Jasper Toscani-Field	October 2022
	<i>Active (advanced to candidacy)</i>	
	Lucia Bazan-Williamson	Fall 2020 - present
	<i>Active (not yet advanced to candidacy)</i>	
	Josue Duque	Fall 2022 - present
	<b>Graduate student committee membership (QSB unless otherwise noted)</b>	
	<i>Active</i>	
	Clarence Le	March 2023 - present
	Brooke Weinstein	August 2020 - present
	Karly Higgins-Polling,	March 2017 - present
	Nattanon Wutthituntisil	August 2020 - present
	Jordan Collignon (Math)	April 2019 - present
	<i>Completed</i>	
	Yumary Vasquez	August 2023
	Noelle Anderson	July 2023
	Megha Suswaram	October 2022
	Kinsey Brock	May 2021
	Robert Boria	May 2021
	Danaan Deneve Weeks	December 2020
	Travis Lawrence	June 2018
	Jesse Wilson (ES)	August 2017
EDITORIAL SERVICE	pyOpenSci, <i>Guest editor</i>	Fall 2023
	Systematic Biology, <i>Editorial board</i>	2017 - 2019
	Proceedings of The Royal Society B, <i>Associate editor</i>	Jan 2019 - 2022
REVIEWER	NSF Committee of Visitors (2020)	
	NSF panelist (2014, 2015, 2016, 2018)	
	French National Research Agency, reviewer	
	<i>Peer reviewer:</i> Animal; BMC Bioinformatics; BMC Genomics; Bioinformatics; Ethology, Ecology & Evolution; Evolutionary Applications; G3:Genes-Genomes-Genetics; GigaScience; Methods in Ecology and Evolution; Molecular Biology and Evolution; Molecular Ecology; Molecular Ecology Resources; PLoSOne; PNAS; pyOpenSci; Biology; Trends in Ecology and Evolution	