Emily Jane McTavish

Contact Information

School of Natural Sciences
University of California, Merced
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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., Wetzer, 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, Arcta, CA
Seminar	January 4, 2019, Instituto Gulbenkian de Ciência, Oieras, 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

Organizer, Instructor, University of California, Merced	January 10-11, 2018, Merced, CA
Organizer, University of California, Merced	August 17-18, 2017, Merced, CA
Instructor, University of Oklahoma,	April 4-5, 2014, Norman, OK
Instructor, University of Missouri, Kansas City,	Feb 15-16, 2014, Kansas City, KS
Instructor, University of Kansas,	Aug 22-23, 2013, Lawrence, KS
Coordinator, Instructor, UT Austin,	Dec 10-11, 2012, Austin, TX
Teaching Assistant, Michigan State University/UT Austin,	May 7-9, 2012, Austin, TX

Statistics and Scientific Computing Short Course (Python)

Instructor	Feb 26, 2013, Austin, TX
Instructor	Nov 26, 2012, Austin, TX

University of Texas

Teaching Assistant	Introductory Biology, Fall 2007 Evolution, Spring 2008, Spring 2009, Fall 2009 Vertebrate Natural History (Field course), Fall 2008, Spring 2010

Working Groups

Phyloref/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
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 (NESCent)	June 4-8, 2012, Durham, NC

Symposia Organized

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)
American Geophysical Union (AGU) December 9-13 2019, San Francicso, CA

Linking biodiversity data through phylogenetic knowledge (with Guanyang Zhang, Gaurav Vaidya, Hilmar Lapp, Nico Cellinese)
TDWG September 1-5 2018, Dunedin, New Zealand

Society of Systematic Biologists Mayr Award Symposium (with Tracy Heath)
Evolution meetings August 22-26, 2018, Montpelier, France

SSB Spotlight Symposium: Uncertainty in the face of strong support (with Dave Weisrock)
Evolution meetings June 23-27 2017, Portland, OR

Invited Workshop Participation

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

Linking Biodiversity Data Using Evolutionary History
Biodiversity Next — October 2019, Leiden, Netherlands

Nurturing a sustainable Open Tree of Life
TDWG — September 2018, Dunedin, New Zealand

Cultivating community collaboration to build a sustainable Open Tree of Life
Evolution Meetings — August 2018, Montpelier, France

Does reference genome choice affect inference?
Bay Area Population Genomics — September 2016, San Francisco State University, CA

Continually updated phylogenies
Evolution meetings — July 2016, Austin, TX

The Open Tree of Life - Curating, synthesizing, and updating phylogenetic information across 1.8 million taxa (poster)
Society for Molecular Biology and Evolution — July 2015, Vienna, Austria

Effects of ascertainment bias on population genetic inference
Workshop on Quantitative Evolutionary Biology — September 2014, Nesin Mathematics Village, Turkey

Phylesystem: a git-based data store for community curated phylogenetic estimates
iEvoBio — June 2014, Raleigh, NC

Challenges of synthesizing divergence time information on the tree of life
iEvoBio — June 2013, Snowbird, UT

Estimating population histories using single-nucleotide polymorphisms sampled throughout genomes
Evolution meetings — June 2013, Snowbird, UT

Genomic structure of introgression in New World cattle (poster)
Gordon Research Conference — February 2013, Galveston, TX

Inferring ancestry of genomic regions in cattle of hybrid origin
Evolution meetings — July 2012, Ottawa, ON, Canada

Tracking introgression between cattle subspecies using genomic SNP data
Evolution meetings — July 2011 Norman, OK

Using SNP data to assess population structure and hybridization in Texas Longhorn cattle
Plant and Animal Genome Conference — January 2011, San Diego, CA

Impact of dispersal and sampling on inference of population structure (poster)
BEACON: Evolution in Action — August 2010, Michigan State University, MI

Distinguishing signal from noise in phylogeographic data
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 committtee*	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

Postdoctoral scholars

Luna Luisa Sánchez Reyes	August 2019 - August 2023
Martha Kandziora	September 2017 - May 2019

Doctoral student advisees (Quantitative and Systems Biology - QSB)

Graduated with PhD

Lesly Lopez Fang	August 2023
Jasper Toscani-Field	October 2022

Active (advanced to candidacy)

Lucia Bazan-Williamson	Fall 2020 - present

Active (not yet advanced to candidacy)

Josue Duque	Fall 2022 - present

Graduate student committee membership (QSB unless otherwise noted)

Active

Clarence Le	March 2023 - present
Brooke Weinstein	August 2020 - present
Nattanon Wutthituntisil	August 2020 - present

Completed

Jordan Collignon (Math)	May 2024
Karly Higgins-Polling,	May 2024
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, *Guest editor*	Fall 2023
Systematic Biology, *Editorial board*	2017 - 2019
Proceedings of The Royal Society B, *Associate editor*	Jan 2019 - 2022

Reviewer

NSF Committee of Visitors (2020)
NSF panelist (2014, 2015, 2016, 2018)
French National Research Agency, reviewer

Peer reviewer: 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