

Emily Jane McTavish

- CONTACT INFORMATION** School of Natural Sciences
University of California, Merced
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- EDUCATION** **University of Texas**, Austin, Texas, USA
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, USA
Assistant Professor, Life and Environmental Sciences June 2016 - Present
University of Kansas, Lawrence, Kansas, USA
Postdoctoral researcher, Open Tree of Life Project, 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** *Refereed journal articles*
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., Burleigh, G., Crandall, K.A., Deng, J., Drew, B., Hibbett, D., Gazis, R., Gude, K., Katz, L.A., Laughinghouse, H.D., **McTavish, E.J.**, 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*. 93:289295.
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*. 105:445456.

PUBLICATIONS
CONTINUED

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.

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.

Manuscripts in preparation/submission

Flouri, T., **McTavish, E.J.**, Darriba, D., Kapli, P., Stamatakis, A., Holder, M.T. *in preparation*. A dynamic programming approach and tool for speed-dating and divergence time estimation.

INVITED
TALKS

Louisiana State University, Baton Rouge, Computational Biology Seminar, February 21, 2017

Society of Systematic Biologists, Baton Rouge, SSB stand alone meeting debate, January 10, 2017

Fred Hutchinson Cancer Research Center, Seattle, Computational biology seminar, November 15, 2016.

University of California, Los Angeles, Biology departmental seminar, Sept 28, 2016.

Smithsonian Natural History Museum, Frontiers in Phylogenetics Symposium, Sept 9, 2016.

Oklahoma State University, Botany departmental seminar, March 23, 2016.

The Field Museum, A. Watson Armour III Research Seminar, October 21, 2015.

École Polytechnique Fédérale de Lausanne (EPFL), Population genetics group, September 14, 2015.

Laboratoire de Biométrie et Biologie Evolutive, Lyon, September 10, 2015.

Centre d'Ecologie Fonctionnelle et Evolutive (CEFE), Montpellier, September 7, 2015.

University of Michigan, Early Career Scientists Symposium, March 29, 2014.

Michigan State University, NSF BEACON site visit, December 8, 2011.

University of Idaho, IBEST Seminar, October 6, 2011.

FUNDING
AND AWARDS

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.

FUNDING AND AWARDS CONTINUED	<p>2011 XSEDE (Extreme Science and Engineering Discovery Environment), 200,000 HPC compute time allocations.</p> <p>2011 Houston Livestock Show and Rodeo Scholarship, University of Texas.</p> <p>2010 Hartman Zoology Scholarship. University of Texas.</p> <p>2009 EcoLabs Texas Private Lands Grant.</p> <p>2008 EcoLabs Texas Private Lands Grant.</p> <p>2008 Graduate Research Funding, University of Texas.</p>
TEACHING EXPERIENCE	<p>University of California, Merced</p> <p style="text-align: right;">Phylogenetics, Spring 2018 Graduate Phylogenetics, Fall 2017 Evolution, Spring 2017</p> <p>Molecular Evolution Workshop at the Marine Biological Laboratory</p> <p><i>Faculty</i> July 20 to July 30, 2017, Woods Hole, MA, USA</p> <p><i>Faculty</i> July 17 to July 27, 2016, Woods Hole, MA, USA</p> <p><i>Faculty</i> July 19 to July 29, 2015, Woods Hole, MA, USA</p> <p><i>Faculty</i> July 27 to August 6, 2014, Woods Hole, MA, USA</p> <p><i>Teaching Assistant</i> July 21 to July 31, 2013, Woods Hole, MA, USA</p> <p><i>Teaching Assistant</i> July 22 to August 1, 2012, Woods Hole, MA, USA</p> <p>Workshop on Quantitative Evolutionary Biology</p> <p><i>Young Scientist Lecturer</i> September 13-21, 2014, Nesin Mathematics Village, Şirince, Turkey</p> <p>Software Carpentry Workshops</p> <p><i>Organizer, Instructor</i>, University of California, Merced January 10-11, 2018, Merced, CA, USA</p> <p><i>Organizer</i>, University of California, Merced August 17-18, 2017, Merced, CA, USA</p> <p><i>Instructor</i>, University of Oklahoma, April 4-5, 2014, Norman, OK, USA</p> <p><i>Instructor</i>, University of Missouri, Kansas City, Feb 15-16, 2014, Kansas City, KS, USA</p> <p><i>Instructor</i>, University of Kansas, Aug 22-23, 2013, Lawrence, KS, USA</p> <p><i>Coordinator, Instructor</i>, UT Austin, Dec 10-11, 2012, Austin, TX, USA</p> <p><i>Teaching Assistant</i>, Michigan State University/UT Austin, May 7-9, 2012, Austin, TX, USA</p> <p>Statistics and Scientific Computing Short Course (Python)</p> <p><i>Instructor</i> Feb 26, 2013, Austin, TX, USA</p> <p><i>Instructor</i> Nov 26, 2012, Austin, TX, USA</p> <p>University of Texas</p> <p><i>Teaching Assistant</i> Introductory Biology, Fall 2007 Evolution, Spring 2008, Spring 2009, Fall 2009 Vertebrate Natural History (Field course), Fall 2008, Spring 2010</p>
MENTORSHIP	<p>Graduate advisor: Jasper Toscani-Field</p> <p>Dissertation Committee member (UC Merced): Noelle Anderson, Kinsey Brock, Andy Collins-Hed, Mo Kaze, Travis Lawrence, Megha Suswaram, Jesse Wilson (graduated 2017)</p>
WORKING GROUPS	<p>Reproducible Research Hackathon January 9, 2018, Berkeley, CA, USA</p> <p>Computable evolutionary phenotype knowledge December 11-14, 2017, Durham, NC, USA</p> <p>FuturePhy/Arbor/OpenTree Clade Workshop May 4-5, 2017, Chicago, IL, USA</p> <p>FuturePhy/Arbor/OpenTree Clade Workshop October 21-23 2016, Chicago, IL, USA</p> <p>FuturePhy Interoperability Hackathon August 15-18 2016, Lawrence KS, USA</p> <p>FuturePhy/Arbor/OpenTree Clade Workshop February 2016, Gainesville, FL, USA</p> <p>Mozilla Science Lab Global Sprint July 23, 2014, Toronto, ON, Canada</p> <p>Phylotastic Hackathon at the National Center for Evolutionary Synthesis (NESCent) June 4-8, 2012, Durham, NC, USA</p>

SYMPOSIA ORGANIZED	Linking biodiversity data through phylogenetic knowledge (with Guanyang Zhang, Gaurav Vaidya, Hilmar Lapp, Nico Cellinese) TDWG Society of Systematic Biologists Mayr Award Symposium (with Tracy Heath) Evolution meetings SSB Spotlight Symposium: Uncertainty in the face of strong support (with Dave Weisrock)	Sept 1-5 2018, Dunedin, New Zealand August 22-26, 2018, Montpellier, France June 23-27 2017, Portland, OR, USA
INVITED WORKSHOP PARTICIPATION	Molecular Evolution Workshop at the Marine Biological Laboratory, Quantitative Evolutionary and Comparative Genomics: Linkage and Recombination in Genome Sequences, at the Okinawa Institute of Science and Technology (OIST)	July 24 to August 3, 2011, Woods Hole, MA, USA May 16 to June 3, 2011, Okinawa, Japan
PRESENTATIONS AT SCIENTIFIC MEETINGS	<i>Does reference genome choice affect inference?</i> Bay Area Population Genomics <i>Continually updated phylogenies</i> Evolution meetings <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 <i>Effects of ascertainment bias on population genetic inference</i> Workshop on Quantitative Evolutionary Biology <i>PhyloSystem: a git-based data store for community curated phylogenetic estimates</i> iEvoBio <i>Challenges of synthesizing divergence time information on the tree of life</i> iEvoBio <i>Estimating population histories using single-nucleotide polymorphisms sampled throughout genomes</i> Evolution meetings <i>Genomic structure of introgression in New World cattle</i> (poster) Gordon Research Conference <i>Inferring ancestry of genomic regions in cattle of hybrid origin</i> Evolution meetings <i>Tracking introgression between cattle subspecies using genomic SNP data</i> Evolution meetings <i>Using SNP data to assess population structure and hybridization in Texas Longhorn cattle</i> Plant and Animal Genome Conference <i>Impact of dispersal and sampling on inference of population structure</i> (poster) BEACON: Evolution in Action <i>Distinguishing signal from noise in phylogeographic data</i> Evolution meetings	September 2016, San Francisco State University, CA, USA July 2016, Austin, TX, USA July 2015, Vienna, Austria September 2014, Nesin Mathematics Village, Turkey June 2014, Raleigh, NC, USA June 2013, Snowbird, UT, USA June 2013, Snowbird, UT, USA February 2013, Galveston, TX, USA July 2012, Ottawa, ON, Canada July 2011 Norman, OK, USA January 2011, San Diego, CA, USA August 2010, Michigan State University, MI, USA July 2010, Portland, OR, USA

PROFESSIONAL	Society of Systematic Biologists, <i>Communications Director</i>	2018 - 2019
SERVICE	Society of Systematic Biologists, <i>Elected Council Member</i>	2016 - 2019
AND OUTREACH	Software Carpentry, <i>Instructor</i>	2011 - present
	Breaking Bio Podcast, <i>Guest</i>	September 25, 2013
	UT Forum, <i>Lecturer</i>	March 22, 2013
	Darwin Day Speaker, Texas Memorial Museum,	February 12, 2012
	Information Technology advisory committee, <i>Student representative</i>	Sept 2010 - Dec 2011
	Science Under the Stars, <i>Presenter</i>	December 8, 2011
	UT Learning Activities for Mature People, <i>Lecturer</i>	November 4, 2011
	NPR's Science Friday, <i>Guest</i>	July 7, 2011
	Flying Cloud Institute Young Women In Science Program, <i>Teacher</i>	July, 2010
	UT Austin Integrative Biology Graduate Student Symposium, <i>Chairperson</i>	April 2009, April 2010

PROFESSIONAL	Food and Drug Administration	
EXPERIENCE	<i>Consultant</i>	August 2013 – present
	Testing adequacy of models used for phylogenetic reconstruction of the spread of food borne diseases.	
	Bureau of Land Management	
	<i>Conservation and land management intern</i>	June 2006 – August 2007
	Live trapping of small mammals and reptiles in the field, surveying vegetation, data analysis and GIS mapping	

REVIEWER	NSF panelist (2014, 2015, 2016)	
	Animal, BMC Bioinformatics, Bioinformatics, Ethology Ecology & Evolution, Evolutionary Applications, GigaScience, Molecular Biology and Evolution, PLoSOne, PNAS, Systematic Biology, Trends in Ecology and Evolution	