

# Emily Jane McTavish

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## 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

**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 - Present

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

Humboldt Research Fellow, Scientific Computing Group

Advisor: Alexandros Stamatakis

December 2014 - August 2015

## PUBLICATIONS

*Refereed journal articles*

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.

**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.

*Manuscripts in preparation/submission*

**McTavish, E.J.**, Drew, B., Cranston K. *invited*. Philosophical and technical challenges to building a unified tree of life.

**McTavish, E.J.**, Pettengill, J., Davis, S., Rand, H., Strain, E., Allard, M., Timme R.E. *submitted*. TreesToReads: Simulating data to test phylogenetic effects of biases in SNP calling pipelines. BioRxiv preprint: <http://dx.doi.org/10.1101/037655> GitHub repository: <https://github.com/snacktavish/TreeToReads>

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

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

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 supercomputer compute time allocations.  
2011 Houston Livestock Show and Rodeo Scholarship, University of Texas.  
2010 Hartman Zoology Scholarship. University of Texas.  
2009 EcoLabs Texas Private Lands Grant.  
2008 EcoLabs Texas Private Lands Grant.

TEACHING EXPERIENCE	Molecular Evolution Workshop at the Marine Biological Laboratory:	
	<i>Faculty</i>	July 17 to July 27, 2016, Woods Hole, MA, USA
	<i>Faculty</i>	July 19 to July 29, 2015, Woods Hole, MA, USA
	<i>Faculty</i>	July 27 to August 6, 2014, Woods Hole, MA, USA
	<i>Teaching Assistant</i>	July 21 to July 31, 2013, Woods Hole, MA, USA
	<i>Teaching Assistant</i>	July 22 to August 1, 2012, Woods Hole, MA, USA
	Workshop on Quantitative Evolutionary Biology:	
	<i>Young Scientist Lecturer</i>	September 13-21, 2014, Nesin Mathematics Village, Şirince, Turkey
	Software Carpentry Workshops:	
	<i>Instructor</i> , University of Oklahoma,	April 4-5, 2014, Norman, OK, USA
	<i>Instructor</i> , University of Missouri, Kansas City,	Feb 15-16, 2014, Kansas City, KS, USA
	<i>Instructor</i> , University of Kansas,	Aug 22-23, 2013, Lawrence, KS, USA
	<i>Coordinator, Instructor</i> , UT Austin,	Dec 10-11, 2012, Austin, TX, USA
	<i>Teaching Assistant</i> , Michigan State University/UT Austin,	May 7-9, 2012, Austin, TX, USA
	Statistics and Scientific Computing Short Course (Python):	
	<i>Instructor</i>	Feb 26, 2013, Austin, TX, USA
	<i>Instructor</i>	Nov 26, 2012, Austin, TX, USA
	University of Texas Biology department:	
	<i>Teaching Assistant</i>	Introductory Biology, Fall 2007
		Evolution, Spring 2008, Spring 2009, Fall 2009
		Vertebrate Natural History (Field course), Fall 2008, Spring 2010
WORKING GROUPS	FuturePhy Interoperability Hackathon August 15-18 2016, Lawrence KS, USA	
	Futurephy/Arbor/OpenTree Clade Workshop	February 2016, Gainesville, FL, USA
	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, USA
INVITED WORKSHOP PARTICIPATION	Molecular Evolution Workshop at the Marine Biological Laboratory,	
		July 24 to August 3, 2011, Woods Hole, MA, USA
	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>Does reference genome choice affect inference?</i>	
	Bay Area Population Genomics	Sept 2016, San Francisco, CA, USA
	<i>Continually updated phylogenies</i>	
	Evolution meetings	July 2016, Austin, TX, USA
	<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	Sept 2014, Nesin Mathematics Village, Turkey
	<i>Phylesystem: a git-based data store for community curated phylogenetic estimates</i>	
	iEvoBio	June 2014, Raleigh, NC, USA

PRESENTATIONS AT SCIENTIFIC MEETINGS CONTINUED	<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	June 2013, Snowbird, UT, USA June 2013, Snowbird, UT, USA June 2013, Snowbird, UT, USA Feb 2013, Galveston, TX, USA July 2012, Ottawa, ON, Canada July 2011 Norman, OK, USA Jan 2011, San Diego, CA, USA Aug 2010, Michigan State University, MI, USA July 2010, Portland, OR, USA
PROFESSIONAL SERVICE AND OUTREACH	Society of Systematic Biologists, <i>Elected Council Member</i> Software Carpentry, <i>Instructor</i> Breaking Bio Podcast, <i>Guest</i> UT Forum, <i>Lecturer</i> Darwin Day Speaker, Texas Memorial Museum, Information Technology advisory committee, <i>Student representative</i> Science Under the Stars, <i>Presenter</i> UT Learning Activities for Mature People, <i>Lecturer</i> NPR's Science Friday, <i>Guest</i> Flying Cloud Institute Young Women In Science Program, <i>Teacher</i> UT Austin Integrative Biology Graduate Student Symposium, <i>Chairperson</i>	2016 - 2019 2011 - present September 25, 2013 March 22, 2013 February 12, 2012 Sept 2010 - Dec 2011 December 8, 2011 November 4, 2011 July 7, 2011 July, 2010 April 2009, April 2010
PROFESSIONAL EXPERIENCE	<b>Food and Drug Administration</b> <i>Consultant</i> Testing adequacy of models used for phylogenetic reconstruction of the spread of food borne diseases.  <b>Bureau of Land Management</b> <i>Conservation and land management intern</i> Live trapping of small mammals and reptiles in the field, surveying vegetation, data analysis and GIS mapping	August 2013 – present  June 2006 – August 2007
REVIEWER	NSF panelist Animal, BMC Bioinformatics, Bioinformatics, Evolutionary Applications, GigaScience, Molecular Biology and Evolution, PLoSOne, PNAS, Systematic Biology, Trends in Ecology and Evolution	