

Evan McCartney-Melstad

Ecology and Evolutionary Biology
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POSITION

Postdoctoral researcher, December 13, 2016 to present. H. Bradley Shaffer laboratory, University of California, Los Angeles.

EDUCATION

University of California, Los Angeles

- PhD, Biology (December 2016)
 - Advisor: H. Bradley Shaffer
 - Dissertation title: "The Added Value of Large-Scale Genomic Data in Conservation"

Columbia University

- MA, Conservation Biology (May 2012)
 - Advisor: Martin Mendez (Wildlife Conservation Society)

Yale University

- B.S., Biology (2008)
 - Advisor: Thomas Near

REFERENCES

H. Bradley Shaffer. Professor, UCLA.

- PhD and postdoctoral advisor.
- brad.shaffer@ucla.edu; (310) 825-3836

Peter Ralph. Assistant Professor, University of Oregon.

- Collaborator on desert tortoise genomics work.
- plr@uoregon.edu; (541) 346-5530

Thomas J. Near. Associate Professor and Head of Saybrook College, Yale University.

- Undergraduate advisor and collaborator on turtle phylogenomics work.
- thomas.near@yale.edu; (203) 432-3002

PUBLICATIONS

- McCartney-Melstad E, Vu J, Shaffer HB. 2018. Genomic data recover previously undetectable fragmentation effects in an endangered amphibian. *Molecular Ecology*. 27: 4430-4443.
- McCartney-Melstad E, Gidiş M, Shaffer HB. 2018. Population genomic data reveal extreme geographic subdivision and novel conservation actions for the declining foothill yellow-legged frog. *Heredity*. 121: 112-125.
- Spinks PQ, McCartney-Melstad E, Near T, Mount G, Shaffer HB. 2017. Phylogenomic analyses of 539 highly informative loci dates a fully resolved time tree for the major clades of living turtles. *Molecular Phylogenetics and Evolution*. 115: 7-15.

- Spinks PQ, Thomson RC, McCartney-Melstad E, Shaffer HB. 2016. Phylogeny and temporal diversification of the New World pond turtles (Emydidae). *Molecular Phylogenetics and Evolution*, 103: 85-97.
- McCartney-Melstad E, Shaffer HB. 2015. Amphibian molecular ecology and how it has informed conservation. *Molecular Ecology*, 24: 5084-5109.
- McCartney-Melstad E, Mount G, Shaffer HG. 2015. Exon capture optimization in large-genome amphibians. *Molecular Ecology Resources*, 16: 1084-1094.
- Shaffer HB, Gidis M, McCartney-Melstad E, Neal K, Oyamaguchi H, Tellez M, Toffelmier E. 2015. Conservation genetics and genomics of amphibians and reptiles. *Annual Reviews of Animal Biosciences*, 3: 113-138.
- McCartney-Melstad E, Waller T, Micucci PA, Barros M, Draque J, Amato G, and Mendez M. 2012. Population structure and gene flow of the yellow anaconda (*Eunectes notaeus*) in Northern Argentina. *PLoS ONE*. 7(5): e37473.

PREPRINTS

- Wielstra, B.*, McCartney-Melstad, E*., Arntzen, J. W., Butlin, R. K., & Shaffer, H. B. (2018). Phylogenomics of the adaptive radiation of *Triturus* newts supports gradual ecological niche expansion towards an incrementally aquatic lifestyle. bioRxiv 463752. doi:10.1101/463752. *Contributed equally.
- Ashander J, Ralph P, McCartney-Melstad E, Shaffer HB. 2018. Demographic inference in a spatially-explicit ecological model from genomic data: a proof of concept for the Mojave Desert Tortoise. bioRxiv 354530. doi: 10.1101/354530. *Major revision at Molecular Ecology Resources*.
- Shaffer HB, McCartney-Melstad E, Ralph P, Bradburd G, Lundgren E, Vu J, Hagerty B, Sandmeier F, Weitzman C, Tracy CR. 2017. Desert tortoises in the genomic age: population genomics and the landscape. bioRxiv 195743. doi: 10.1101/195743.

GRANTS/AWARDS

- XSEDE Computational Research Allocation award. “Conservation Genomics of Threatened and Endangered Amphibians and Reptiles.” Co-PI. 2018-2019. (calculated value = \$33,112)
- US Department of Interior-CVPCP, “Rangewide and Landscape Genomics of the Central DPS of California Tiger Salamander”. Named Key Personnel. 2017-2019. (\$350,865)
- California Department of Transportation: “Landscape Genomics Study for California Tiger Salamander”. Named Key Personnel. 2017-2019. (\$199,985)
- Graduate Assistance in Areas of National Need (GAANN) Doctoral Fellowship. October 2013-September 2014. (\$27,631)
- Graduate Assistance in Areas of National Need (GAANN) Doctoral Fellowship. October 2012-September 2013. (\$26,984)
- Several small research grants ranging from \$1,000 to \$2,250. 2007-2013. (\$6,050)

RESEARCH EXPERIENCE

University of California, Los Angeles. Advisor: Brad Shaffer. (September 2012-present)

- Studying landscape genetics of a hybrid invasion between two salamander species. Designed and optimized a 5,000-exon capture array for the system, which we have used to enrich and sequence > 3,000 salamanders. Developed phased haplotype-based algorithm for estimating extremely low levels of hybridization.

- Using low-coverage whole-genome sequencing and mathematical modeling to predict the effects of hypothetical future placements of solar panel farms on desert tortoise population viability.
- Specialized laboratory methods include target enrichment, whole genome shotgun sequencing, RADseq experimental design and analysis, and duplex-specific nuclease genomic library normalization.
- Designed and wrote lab's data quality and analysis pipeline for short-read data.
- Constructed the lab's computational and data storage infrastructure.

American Museum of Natural History. Advisor: Martin Mendez. (2010-2012)

- Evaluated spatial genetic structuring and migration between populations of yellow anacondas (*Eunectes notaeus*) in northern Argentina using mitochondrial DNA, and investigated landscape and environmental features which could be shaping patterns of structure and gene flow (early-mid 2011).
- Microsatellite characterization and analysis.
- Laboratory work includes primer design, DNA extraction, PCR, and sequencing of several mitochondrial genes and characterization of microsatellite loci.

Yale University. Advisor: Thomas Near. (2006-2008)

- Performed a fossil-calibrated molecular clock divergence time estimate of the extant coelacanths.
- Analyzed phylogenetic signal in scored developmental characters in centrarchid fishes, including ancestral character state reconstruction.
- Performed extensive field work in rivers and streams in the American Southeast.
- Laboratory work included DNA extraction, PCR, and sequencing of freshwater fish.

ORAL PRESENTATIONS

- Genomic and geographic heterogeneity in a hybrid invasion of the endangered California tiger salamander. August 19, 2018. Evolution meetings. Montpellier, France.
- Using Genomic Data to Protect Endangered Reptiles and Amphibians in California. October 5, 2017. Invited departmental seminar at CSU Dominguez Hills. Los Angeles, CA.
- Genetic variation within the California tiger salamander (*Ambystoma californiense*) and the current extent of hybridization with the invasive barred tiger salamander (*Ambystoma mavortium*). September 20, 2017. California Tiger Salamander Conservation Science Symposium. Marina, CA (invited presentation).
- Fine-Scale Population Genomics of Protected Tiger Salamanders (*Ambystoma tigrinum*) on Long Island, NY Reveals a Highly Structured Species Impacted by Major Roads. 2017. American Society of Ichthyologists and Herpetologists. Austin, TX.
- Large-scale genomic data change our understanding of the hybridization dynamics of the endangered California tiger salamander. 2017. Evolution meetings. Portland, OR.
- Using Exon Capture Data to Measure the Tempo and Extent of Hybridization Between an Endangered Amphibian and an Introduced Congener. 2016. Eighth World Congress of Herpetology. Hangzhou, China (invited presentation).

- Complete genome sequences predict the impacts of alternative energy development scenarios on the endangered Mojave desert tortoise (*Gopherus agassizii*). 2016. Eighth World Congress of Herpetology. Hangzhou, China.
- Exon Capture Reveals Insights into the Conservation Status and Genome Organization of the Endangered California Tiger Salamander. 2016. American Society of Ichthyologists and Herpetologists. New Orleans, LA.
- Full-genome conservation genetics: Using genomic tools to evaluate the impacts of alternative energy development on the threatened Mojave desert tortoise (*Gopherus agassizii*). 2015. American Society of Ichthyologists and Herpetologists. Reno, NV. *Awarded Stoye Award for best student presentation in genetics, development, and morphology.
- Whole Genome Resequencing Provides Novel Landscape Genomic Insights for Desert Tortoise Conservation. 2015. Desert Tortoise Council 40th Annual Symposium. Las Vegas, NV.
- Conservation Genomics of the California Tiger Salamander (*Ambystoma californiense*): Past, Present, and Future. 2015. California/Nevada Amphibian Population Task Force. Malibu, CA.
- Exon Capture Optimization for a Large-Genome Amphibian. 2014. American Society of Ichthyologists and Herpetologists. Chattanooga, TN.
- A Landscape Genetic Approach to Predicting Pesticide Impacts on the California Tiger Salamander. 2013. UCLA EcoEvoPub. Los Angeles, CA.
- Fossil-calibrated Molecular Phylogenies and Divergence Time Estimates of the Two Extant Coelacanth Species (*Latimeria*). 2007. American Society of Ichthyologists and Herpetologists. St. Louis, MO.
- Freshwater fish field work and coelacanth evolution. 2008. Yale University Mellon Forum. New Haven, CT.

LANGUAGES

- R, UNIX, Perl, C++
- Spanish (intermediate), Mandarin Chinese (intermediate)

TEACHING EXPERIENCE

- University of California, Los Angeles. Teaching Associate, LS 15: Life—Concepts and Issues. Spring 2013, Winter 2016. An introductory biology course at UCLA for non-science majors. I led three discussion sections each year with roughly 20 students in each to teach concepts in biology related to the lecture material. I also helped students work through problems in office hours and graded homework assignments, quizzes, and exams.
- University of California, Los Angeles. Teaching Associate, Field Biology Quarter. Spring 2014. An intensive 16-credit, 10-week introduction to field ecology and biology. I helped students to develop field research experiments, collected data with them in field sites throughout California, and assisted them with data analysis.
- University of California, Los Angeles. Instructor, La Kretz Workshop in Conservation Genomics. Yearly, 2014-2018. Malibu, CA. I teach 25-30 students every year the basics of analyzing genomic-scale sequence data. Students are generally beginners in biological computation, and they leave the workshop with a solid basis for drawing biological inference from raw DNA sequence data.

- Columbia Science Honors Program. Instructor, Genetics and the Conservation of Biodiversity. Spring 2011, Fall 2011, and Spring 2012. The program is for high schoolers who have an interest in scientific topics outside of the realm of typical high school instruction, and tuition is free for students in the program.
- American Museum of Natural History. Mentor for NSF Research Experience for Undergraduates (REU) student. Summer 2011. One-on-one mentorship; helped a college student complete a project on genetic barcoding.
- Columbia University. Course assistant, EEEB2001: Environmental Biology. Fall 2011. Assisted students with questions they had about the material and graded homework and exams.
- Columbia University. Course assistant, EEEB4140: Ornithology. Fall 2010. Assisted instructors with class administrative duties and delivered a lecture.

MANUSCRIPT REVIEWER

- Molecular Ecology
- Molecular Ecology Resources
- Heredity
- Journal of Heredity
- Conservation Genetics
- Mitochondrial DNA