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## Rachel S Schwartz

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Cartwright Lab  
Center for Evolutionary Medicine and Informatics  
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### EDUCATION

Ph.D. Ecology, University of California, Davis, 2008  
B.A. Biology, Bryn Mawr College, 2001

### PROFESSIONAL APPOINTMENTS

2013 – present Assistant Research Scientist, The Biodesign Institute, Arizona State University  
2012 – 2013 Postdoctoral Researcher, The Biodesign Institute, Arizona State University  
2009 – 2011 NSF Bioinformatics Fellow, Department of Biology, Colorado State University  
2008 – 2009 Postdoctoral Researcher, Department of Biology, Colorado State University  
2001 – 2003 Research Technician, Department of Biology, University of Notre Dame

### PUBLICATIONS

#### Preprints and Submissions

**Schwartz, R.S.**, A.L. Merry\*, M.M. Howell\*, and R.A. Cartwright. Strong selection is necessary for repeated evolution of blindness in cavefish. *Available on BioRxiv at* <http://dx.doi.org/10.1101/031872>

Wu, S., **R.S. Schwartz**, D. Winter, R.A. Cartwright, and D.F. Conrad. A novel method to model read counts in genomic data to reduce false positive identification of heterozygotes. *Available on BioRxiv at* <http://dx.doi.org/10.1101/031724>

Rankin, A., **R.S. Schwartz**, C. Floyd, and B. May. Population dynamics of the yellow-bellied marmot (*Marmota flaviventris*) contrast with other alpine mammals. *Available on BioRxiv.*

Huang, N., K.A. Vigh-Conrad, **R.S. Schwartz**, R.A. Cartwright, and D.F. Conrad. Joint mutation calling and cell lineage inference from genome sequencing of single cells. *Submitted to Genome Research.*

#### Peer-Reviewed

2015 Harkins, K.M., **Schwartz, R.S.**, A.C. Stone, and R.A. Cartwright. Phylogenomic reconstruction supports supercontinent origins for *Leishmania*. *Infection, Genetics and Evolution*. Accepted pending minor revision. *Available on BioRxiv at* <http://dx.doi.org/10.1101/028969>

- Winter, D.J., M. Andreina Pacheco, A.F. Vallejo, **R.S. Schwartz**, M. Arevalo-Herrera, S. Herrera, R.A. Cartwright, and A.A. Escalante. Whole genome sequencing of field isolates reveals extensive genetic diversity in *Plasmodium vivax* from Colombia. *PLoS Neglected Tropical Diseases*. In press. Available on BioRxiv at <http://dx.doi.org/10.1101/025338>
- Schwartz, R.S.**, K.M Harkins, A.C. Stone, and R.A. Cartwright. A composite genome approach to identify phylogenetically informative data from next-generation sequencing. *BMC Bioinformatics*. 16:193.
- 2014 Lavretsky, P.\* , **R.S. Schwartz**, M.R. Baerwald, and B. May. Developing Major Histocompatibility markers in a species of concern: the Sacramento Perch (*Archoplites interruptus*). *Journal of Fish Biology*. 85:1766-1776.
- 2013 Ramu, A., M.J. Noordam, **R.S. Schwartz**, A. Wuster, M.E. Hurles, R.A. Cartwright, and D.F. Conrad. DeNovoGear: *de novo* indel and point mutation discovery and phasing. *Nature Methods*. 10: 985–987.
- O’Neill, E.M., **R. Schwartz**, C.T. Bullock, J.S. Williams, H.B. Shaffer, X. Aguilar-Miguel, G. Parra-Olea, and D.W. Weisrock. Parallel tagged amplicon sequencing reveals major lineages and phylogenetic structure in the North American tiger salamander (*Ambystoma tigrinum*) species complex. *Molecular Ecology*. 22: 111-129.
- 2010 **Schwartz, R.S.** and R.L. Mueller. Variation in DNA substitution rates among lineages erroneously inferred from simulated clock-like data. *PLoS ONE*. 5(3): e9649.
- Schwartz, R.S.** and R.L. Mueller. Limited effects of among-lineage rate variation on the phylogenetic performance of molecular markers. *Molecular Phylogenetics and Evolution*. 54: 849–856.
- Schwartz, R.S.** and R.L. Mueller. Branch length estimation and divergence dating: estimates of error in Bayesian and maximum likelihood frameworks. *BMC Evolutionary Biology*. 10:5.
- 2008 **Schwartz, R.S.** and B. May. Genetic evaluation of isolated populations for use in reintroductions reveals significant genetic bottlenecks in potential stocks of Sacramento perch. *Transactions of the American Fisheries Society*. 137: 1764–1777.
- 2004 **Schwartz, R.S.** and B. May. Characterization of microsatellite loci in Sacramento perch (*Archoplites interruptus*). *Molecular Ecology Notes*. 4:694-697.

\* undergraduate student

## FUNDING AND AWARDS

- 2014 – 2017 ABI Innovation: Identifying phylogenetically informative data from next-generation sequencing (PI: R. Cartwright) [NSF DBI-1356548; \$686,240]
- 2009 – 2011 Bioinformatics Postdoctoral Fellowship [NSF #0906004; \$123,000]
- 2008 University Instructional Improvement Grant [UC Davis; \$5,315]
- 2005 – 2008 Ecology Graduate Group Block Grant Fellowship [UC Davis; \$29,400]
- 2005 – 2007 Jastro-Shields Research Grant [UC Davis; \$1,800]
- 2006 – 2007 Graduate K-12 Fellowship [NSF; \$40,000]

- 2005 – 2007 Amendment to Restoration of Sacramento Perch to San Francisco Estuary (PI: B. May) [California Bay Delta Authority (CALFED); \$96,421]
- 2005 Department of Animal Science Cole Fellowship [UC Davis; \$3,000]
- 2004 Graduate Research Fellowship Honorable Mention [NSF]

### **SUBMITTED PROPOSALS**

- 2013 Identification of pathogen evolution using whole-genome sequence data (with co-PIs R. Cartwright and S. Kumar) [NIH; \$275,000; Funded by NSF ABI (see above)]

### **INVITED SEMINARS**

- 2015 *Phylogenomics: Big Data Meets Evolutionary Biology*  
University of Maryland, Baltimore County, Department of Biology
- Developing computational methods to understand evolution using genomic data*  
University of New Hampshire, College of Life Sciences and Agriculture
- 2014 *Inferring Phylogenies from Next-Generation Sequence Data*  
University of Alabama, Department of Biology
- 2013 *Inferring Phylogenies from Next-Generation Sequence Data*  
American University, Department of Biology
- 2012 *Understanding Populations with Genomic Data*  
California State University-Monterey Bay, Division of Environmental Science and Policy
- Phylogeography with Whole-Genome Sequence Data*  
Susquehanna University, Department of Biology
- Building the Tree of Life in an -omics World: Phylogenetics with Whole Genome Sequence Data*  
West Virginia University, Department of Biology
- 2008 Colorado State University, Biology Department  
University of Minnesota, Community Genetics Seminar
- 2006 University of Wisconsin, Eau Claire, Department of Biology
- 2005 Point Reyes Seashore, Pacific Coast Science and Learning Center Seminar Series  
California Parks Monitoring and Genetics Workshop

### **PRESENTATIONS AT SCIENTIFIC MEETINGS**

#### **Talks**

- 2015 *Orthologous loci for phylogenomics from raw NGS data*  
Society for Systematic Biology, Ann Arbor, MI
- Rapid identification of phylogenetically informative data from next-gen sequencing*

- Society for Molecular Biology and Evolution, Vienna, Austria
- 2014 *Inferring phylogenies from next-generation sequencing data*  
Society for the Study of Evolution, Raleigh, NC
- 2013 *Phylogenies from next-gen sequencing data without assembly*  
Society for the Study of Evolution, Snowbird, UT
- A mixture model for bias and error in genomic data reduces false positive identification of heterozygotes*  
Mechanisms of Protein Evolution, Denver, CO
- 2009 *Impacts of mutational dynamics on phylogeny estimation*  
Society for the Study of Evolution, Moscow, ID
- 2007 Ecological Society of America, San Jose, CA
- 2005 Conservation Genetics Symposium, Pacific Grove, CA  
Bay Area Conservation Biology Symposium, Davis, CA

### **Posters**

- 2014 *Phylogenies from next-generation sequencing*  
Society for Molecular Biology and Evolution, San Juan, PR
- 2007 Evolutionary Change in Human-altered Environments Summit, Los Angeles, CA
- 2006 CALFED Science Conference, Sacramento, CA  
Interagency Ecological Program Workshop, Pacific Grove, CA
- 2004 CALFED Science Conference, Sacramento, CA
- 2001 American Society of Limnology and Oceanography, Albuquerque, NM

### **TEACHING EXPERIENCE**

#### **Arizona State University Guest Lecturer**

Genomic Analysis (2 classes, spring 2015)

Genetics (1 class, fall 2012)

#### **Software Carpentry Instructor**

ASU Workshop (April 18-19, 2015)

#### **University of Wisconsin – Eau Claire, Adjunct Instructor**

Biology Senior capstone (spring 2012)

Introduction to Ecology and Evolution labs (spring 2012)

#### **University of California, Davis, Co-Instructor**

Ecology for non-science majors (spring 2008)

#### **NSF GK-12 Fellowship**

Genetics and Evolution for 7<sup>th</sup> graders (2006-2007)

**University of California, Davis, Teaching Assistant**

Ecology (spring 2006)

Human Heredity (spring 2005)

**Scientific / Textbook Consultant**

California State Education and Environment Roundtable (2008)

Thomson Higher Education (2006 – 2007)

13 undergraduate students supervised (2006 – present)

**SERVICE**

Volunteer, Ask-A-Biologist, ASU (2013 – present)

Volunteer mentor, Girls in STEM, Arizona Science Center (Nov. 14, 2015)

Student representative, Conservation AOE, Graduate Group in Ecology, UC Davis (2008)

Chair Selection Committee, Graduate Group in Ecology, UC Davis (2008)

Reviewer, Applications to the Graduate Group in Ecology, UC Davis (2008)

Organizer, education outreach workshop, Ecological Society of America meeting (2007)

Volunteer mentor, Center for Land Based Learning (2005-2008)

Picnic Day Committee, Animal Science Department, UC Davis (2006 – 2007)

Volunteer, UC Davis Society of Conservation Biology outreach program (2005 – 2006)

Co-chair session of American Fisheries Society Cal-Neva Annual Meeting (2005)

Volunteer intern, Science Outreach, Cooper Elementary, Vacaville, CA (2005)

Reviewer for: American Journal of Botany; BMC Bioinformatics; BMC Evolutionary Biology;  
Canadian Journal of Fisheries and Aquatic Sciences; Conservation Genetics;  
Fisheries; Infection, Genetics and Evolution; PLoS ONE

**SOCIETY MEMBERSHIPS**

Society for the Study of Evolution

Society for Molecular Biology and Evolution

Society of Systematic Biologists

**PROGRAMMING LANGUAGES**

Python, Perl, Shell, R, C++

## REFERENCES

Reed Cartwright, Assistant Professor  
The Biodesign Institute  
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Rachel Mueller, Associate Professor  
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