

Contact Information

Affiliation Assistant Professor of Genomics, Evolution, and Bioinformatics
School of Life Sciences
Center for Evolutionary Medicine and Informatics
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Research Interests computational evolutionary genomics, population genetics, biological theory, bioinformatics, biology education

Education

Ph.D. Genetics University of Georgia, 2006

B.S. Genetics University of Georgia, 2000, *cum laude* with honors (ΦBK)

A.B. Latin University of Georgia, 2000, *cum laude* with honors (ΦBK)

Faculty Appointments

2012–Present Assistant Professor
Genomics, Evolution, and Bioinformatics
School of Life Sciences
Arizona State University, Tempe, AZ USA

2012-Present Core Faculty
Center for Evolutionary Medicine and Informatics
The Biodesign Institute
Arizona State University, Tempe, AZ USA

2011 Huxley Faculty Fellow
Department of Ecology and Evolutionary Biology
Rice University, Houston, TX USA

Education and Training

2009–2010 Research Associate II with Dan Graur
Department of Biology and Biochemistry
University of Houston

2006–2009 Postdoctoral Research Associate with Jeffrey. L. Thorne
Bioinformatics Research Center

Department of Genetics
North Carolina State University

2001–2006

Graduate Student with Marjorie Asmussen
Department of Genetics
University of Georgia

Publications

Papers

Ramu A, Noordam MJ, Schwartz RS, Wuster A, Hurles ME, **Cartwright RA**, and Conrad DF (2013). DeNovoGear: de novo indel and point mutation discovery and phasing. *Nature Methods*, **10**:985–987.

Hufford MB, Xu X, van Heerwaarden J, Pyhäjärvi T, Chia JM, **Cartwright RA**, Elshire RJ, Glaubitz JC, Guill KE, Kaeppeler SM, Lai J, Shannon LM, Song C, Springer NM, Swanson-Wagner RA, Tiffin P, Wang J, Zhang G, Doebley J, McMullen MD, Ware D, Buckler ES, Yang S, and Ross-Ibarra J (2012). Comparative population genomics of maize domestication and improvement. *Nature Genetics*, **44**:808–811.

Cartwright RA, Hussin J, Keebler J, Awadalla P, and Stone EA (2012). A family-based probabilistic method for capturing de novo mutations from high-throughput short-read sequencing data. *Statistical Applications in Genetics and Molecular Biology*, **11**:6.

Conrad DF, Keebler JE, DePristo MA, Lindsay SJ, Zhang Y, Cassals F, Idaghdour Y, Hartl CL, Torroja C, Garimella KV, Zilvermit M, **Cartwright RA**, Rouleau G, Daly M, Stone EA, Hurles ME, and Awadalla P (2011). Variation in genome-wide mutation rates within and between human families. *Nature Genetics*, **43**:712–714.

Cartwright RA, Lartillot N, and Thorne JL (2011). History can matter: Non-Markovian behavior of ancestral lineages. *Systematic Biology*, **60**:276–290.

Cartwright RA and Graur D (2011). The multiple personalities of Watson and Crick strands. *Biology Direct*, **6**:7.

Price* N, **Cartwright RA***, Sabath N, Graur D, and Azevedo RBR (2011). Neutral evolution of robustness in *Drosophila* microRNA precursors. *Molecular Biology and Evolution*, **28**:2115–2123.

Lücking R, Hodkinson B, Stamatakis A, and **Cartwright RA** (2011). PICS-Ord: unlimited coding of ambiguous regions by pairwise identity and cost scores ordination. *BMC Bioinformatics*, **12**:10.

Cartwright RA (2011). Bards, poets, and cliques: Frequency-dependent selection and the evolution of language genes. *Bulletin of Mathematical Biology*, **73**:2201–2212.

The 1000 Genomes Project Consortium (2010). A map of human genome variation from population-scale sequencing. *Nature*, **467**:1061–1073.

Cartwright RA (2009a). Problems and solutions for estimating indel rates and length distributions. *Molecular Biology and Evolution*, **26**:473–480.

Cartwright RA (2009b). Antagonism between local dispersal and self-incompatibility systems in a continuous plant population. *Molecular Ecology*, **18**:2327–2336.

Cartwright RA (2007). Ngila: global pairwise alignments with logarithmic and affine gap costs. *Bioinformatics*, **23**:1427–1428.

Cartwright RA (2006). Logarithmic gap costs decrease alignment accuracy. *BMC Bioinformatics*, **7**:527.

Comai L and **Cartwright RA** (2005). A toxic mutator and selection alternative to the non-mendelian, RNA cache hypothesis for hothead reversion. *Plant Cell*, **17**:2856–2858.

Cartwright RA (2005). DNA assembly with gaps (Dawg): simulating sequence evolution. *Bioinformatics*, **21**(Suppl. 3):iii31–iii38.

Asmussen MA, **Cartwright RA**, and Spencer HG (2004). Frequency-dependent selection with dominance: A window onto the behavior of the mean fitness. *Genetics*, **167**:499–512.

* co-first authors.

Books **Cartwright RA** and Zivkovic B, editors (2008). *The Open Laboratory: The Best Writing on Science Blogs 2007*. Lulu.com, Chapel Hill, NC.

Blog Posts **Cartwright RA** (2012). Lab notes: The alias method for sampling from discrete distributions. The Panda's Thumb. URL <http://pandasthumb.org/archives/2012/08/lab-notes-the-a.html>.

Other Hogue LL and Ross CJ with **Cartwright RA** and Pallas SL (2005). Selman v. Cobb County: Brief of Georgia Citizens for Integrity in Science Education, et al. as amici curiae in support of appellees. United States Eleventh Circuit Court of Appeals. Nos. 05-10341-II and 05-11725-II.

Fant L with Sandefur T, **Cartwright RA**, and Pallas SL (2004). Selman v. Cobb County: Brief amicus curiae of Colorado Citizens for Science, et al. in support of plaintiffs. United States District Court, Northern District of Georgia. No. 1:02-CV-2325-CC.

Cartwright RA (2004). Ignorance excludes evolution. *Atlanta Journal-Constitution*, **Jan 28**.

Cartwright RA and Theobald DL (2003). Citing Scadding (1981) and misunderstanding vestigiality. *Talk.Origins Archive*. URL <http://www.talkorigins.org/faqs/quotes/scadding.html>.

Citations <http://scholar.google.com/citations?user=5nhJokEAAA&hl=en>

Scientific Software

Lead Developer DAWG: a simulator of related sequences. URL <http://scit.us/projects/dawg/>
 NGILA: pairwise alignment with log-affine gap costs. URL <http://scit.us/projects/ngila/>
 RED LYNX: population genetic simulation written completely in javascript. URL <http://scit.us/redlynx/>

SoFoS: rescaling of site frequency spectra. URL <http://scit.us/sofos/>

PI SISRS: SNP Identification from Short Read Sequences. URL <https://github.com/rachelss/SISRS/>

DeNovoGear: identification of de novo mutations from related individuals. URL https://github.com/reedacartwright/DNG_dev/

JAK: coalescence simulator. URL <https://github.com/reedacartwright/jak/>

Contributor SPAGeD: spatial analysis of genetic data. URL <http://ebe.ulb.ac.be/ebe/Software.html>
 Complete List See <http://scit.us/> for a complete list of available software that I have written.

Current Funding**Mutation accumulation in the ciliate *Tetrahymena thermophila***

Grant: NIH R01-GM101352-01A1 (2013–2018)

Role: ASU PI (w/ R. Zufall and R. Azevedo at UH)

Faculty Startup Funds.

Grant: ASU (2012–2014) Role: PI

Mixed infections and population genomics in malarial parasites

Grant: ASU Genomics Core / Illumina Grant Award (2013)

Role: PI/Co-PI (w/ A. Escalante)

Past Funding**Huxley Faculty Fellowship Funds**

Grant: Rice University (2011)

Role: PI

Computational Resources

Grant: TalkOrigins Foundation (2011)

Role: PI

NSF Predoctoral Fellowship

Grant: NSF (2001–2006)

Honors and Awards

2011 Nominated for the AAAS Early Career Award for Public Engagement with Science
 2010 Huxley Faculty Fellowship (Rice)
 2001–2006 NSF Predoctoral Fellowship
 2006 Scholarship to the Summer Institute in Statistical Genetics (UW)
 2005 James L. Carmon Scholarship for research reflecting state-of-the-art utilization of computer technology in the sciences or creative arts. (UGA)
 1999 Phi Beta Kappa
 Warlick-Mannion Classical Scholar (UGA)
 1998 Kossack Calculus Prize, Second Place (UGA)
 Golden Key
 1997 AP National Scholar
 1996 Cum Laude Society
 National Honor Society

Invited Seminars

2012 UNIVERSITY OF CALIFORNIA, DAVIS: Genetics Graduate Group and Genome Center
Evolutionary Models of Mutation and Variation for Genomic Data

- ARIZONA STATE UNIVERSITY: Molecular & Cellular Biology Colloquium and Genome@ASU
Joint Seminar
Evolutionary Models of Mutation and Variation for Genomic Data
- 2011 UNIVERSITY OF AUCKLAND: Department of Statistics
Studying Evolutionary Models of Mutation using Genomic Data
- UNIVERSITY OF WESTERN ONTARIO: Department of Biology
Studying Evolutionary Models of Mutation using Genomic Data
- ARIZONA STATE UNIVERSITY: School of Life Sciences
Studying Evolutionary Models of Mutation using Genomic Data
- FRED HUTCHINSON CANCER RESEARCH CENTER: Herbold Computational Biology Program
Studying Evolutionary Models of Mutation using Genomic Data
- UNIVERSITY OF ALABAMA, TUSCALOOSA: Department of Biological Sciences
Studying Evolutionary Models of Mutation using Genomic Data
- 2010 EAST CAROLINA UNIVERSITY: Department of Biology
Predicting Evolutionary Events using Biologically Robust Statistical Models
- RICE UNIVERSITY: Department of Ecology and Evolutionary Biology
Predicting Evolutionary Events from Uncertain Data
- 2007 UNIVERSITY OF NORTH CAROLINA, CHARLOTTE: Department of Bioinformatics and Genomics
Estimating the Rate and Length Distribution of Indels
- UNIVERSITY OF NORTH CAROLINA, CHAPEL HILL: C-START Undergraduate Seminar
Evolutionary Biology in 30 Minutes
- 2004 NATIONAL CENTER FOR SCIENCE EDUCATION: Activist Summit (Berkeley, CA)

Conferences and Workshops

- 2013 Society for Molecular Biology and Evolution Conference (Chicago, IL)
Poster: Probabilistic Models for De Novo Mutation Detection
*Poster: Sampling Tree-Space Effectively Using Distance Methods. Palmer ND, Schwartz RS, Cartwright RA**
Poster: Phylogenomic Investigation of the Origins and Evolutionary History of Leishmania. Harkins KM, Schwartz RS, Cartwright RA, and Stone A
- Evolution Conference (Snowbird, UT)
Talk: Sampling Tree-Space Effectively Using Distance Methods. Palmer ND, Schwartz RS, Cartwright RA
*Talk: Phylogenies from next-gen sequencing data without assembly. Schwartz RS, Cartwright RA**
- Biological Sequence Analysis and Probabilistic Models (HHMI, Janelia Farm)
Poster: Probabilistic Models for De Novo Mutation Detection
- Teaching Phylogenetics to Undergraduates, Curriculum Development Workshop (University of Texas, Austin)
- Mechanisms of Protein Evolution (University of Colorado, Denver, Anschutz Medical Campus)

- Presentation:* A mixture model for bias and error in genomic data reduces false positive identification of heterozygotes. Schwartz RS and Cartwright RA*
- Poster:* Estimating Indel Models via Simulation and Optimization. Khare A and Cartwright RA*
- Poster:* LLAMBDA: Estimating Indel Rates and Length Distributions from a Multiple Sequence Alignment. Albanese JR and Cartwright RA*
- 2012 Personal Genomes & Medical Genomics (Cold Spring Harbor Laboratory)*
Poster: Hobnail: A program for identifying transposable element families from shotgun sequencing. Smith PL and Cartwright RA.
- Society for Molecular Biology and Evolution Conference (Dublin, Ireland)
Presentation: Dawg 2.0: New Methods for Simulating Sequence Evolution
- Mathematical and Computational Evolutionary Biology (Montpellier, France; LIRMM)
Poster: Dawg 2.0: New Methods for Simulating Sequence Evolution
- SMBE Satellite Symposium on Phylomedicine (Arizona State University)
- BioQUEST/SCALE-IT Curriculum Development Workshop (University of Tennessee)
- 2011 Society for Molecular Biology and Evolution Conference (Kyoto University)
Presentation: Neutral evolution of robustness in *Drosophila* pre-microRNAs.
- Maize Genetics Conference (St. Charles, IL)*
Presentation: Genome-wide effects of domestication and improvement in landraces and modern maize. Hufford MB et al. (24 total authors)
- 2010 Evolution Conference (Portland State University)
Presentation: Extracting Phylogenetic Information from Ambiguous Regions. Cartwright RA, Lücking R, Hodkinson B, Stamatakis A
- 2009 Society for Molecular Biology and Evolution Conference (University of Iowa)
Poster: Using Population Genetics to Improve Phylogenetics and Evolutionary Inference. Cartwright RA, Lartillot N, and Thorne JL.
- Evolution Conference (University of Idaho)
Presentation: Using Population Genetics to Improve Phylogenetics and Evolutionary Inference. Cartwright RA, Lartillot N, and Thorne JL.
- Science Online Conference (Sigma Xi Center, RTP, NC)
- 2008 Evolution Conference (University of Minnesota, Twin Cities)
Presentation: Estimating the Rate and Length-Distribution of Insertions and Deletions
- North Carolina Science Blogging Conference (Sigma Xi Center, RTP, NC)
- Personal Genomes (Cold Spring Harbor Laboratory)*
Poster: Probabilistic Discovery of *de Novo* Mutations using “Next Generation” Whole Genome Sequencing of Trio and Twin Family Cohorts. Keebler J, Cartwright RA, Stone EA, and Awadalla P.
- 2007 Society for Molecular Biology and Evolution Conference (Dalhousie University)
Presentation: Estimating the Rate and Length Distribution of Indels
- North Carolina Science Blogging Conference (University of North Carolina at Chapel Hill)

- 2005 The Fifth Georgia Tech-ORNL International Conference on Bioinformatics
Proceedings: Cartwright (2005)
- Evolution Conference (University of Alaska, Fairbanks)
Presentation: DNA Assembly with Gaps (Dawg): Simulating Sequence Evolution
- Southeast Ecology & Evolution Conference (University of Georgia)
Presentation: DNA Assembly with Gaps: Simulating Sequence Evolution
- 2004 Invited participant, National Center for Science Education's Activist Summit (Berkeley, CA)
- 2004 Evolution Conference (Colorado State University)
- Southeast Ecology & Evolution Conference (Georgia Tech)
- 2002 Evolution of Language: Fourth International Conference (Harvard University)

* Did not attend and/or co-author or student presented work.

Society Memberships

Genetics Society of America
 Society for Molecular Biology and Evolution
 The Society for the Study of Evolution

External Service

Reviewer For National Science Foundation (DEB), American Journal of Botany, Bioinformatics, BMC Evolutionary Biology, Evolutionary Bioinformatics, Genetics, IEEE/ACM Transactions on Computational Biology and Bioinformatics, Molecular Biology & Evolution, Molecular Ecology, Nucleic Acids Research

FreeBSD Foundation Maintainer of MAFFT software port.

TalkOrigins Foundation Maintainer of server hosting several of the foundation's websites.

The Panda's Thumb Managing Editor

Website Admin <http://pandasthumb.org/>, <http://dererumnatura.us/>,
<http://scit.us/>, among others.

Other Skills

Programming C/C++, R, Perl, Ruby, \LaTeX , Matlab, Mathematica, Javascript

Languages Studied Classical Latin, Greek, and Sanskrit

October 23, 2013