

Contact Information

Affiliation Assistant Professor of Genomics, Evolution, and Bioinformatics
School of Life Sciences
Center for Evolutionary Medicine and Informatics
The Biodesign Institute
Arizona State University

Mailing Address Center for Evolutionary Medicine and Informatics
The Biodesign Institute at Arizona State University
PO Box 875301
Tempe, Arizona 85287-5301

Phone 1-480-965-9949 (office)

Fax 1-480-727-6947

Email cartwright@asu.edu, reed@scit.us

Research Interests computational evolutionary genomics, population genetics, biological theory, bioinformatics, biology education

Education

Ph.D. Genetics University of Georgia, 2006

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

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

Faculty Appointments

Jan. 2012– Assistant Professor of Genomics, Evolution, and Bioinformatics
School of Life Sciences
Center for Evolutionary Medicine and Informatics
The Biodesign Institute
Arizona State University, Tempe, AZ USA

Jan. 2011–Jan. 2012 Huxley Faculty Fellow
Department of Ecology and Evolutionary Biology
Rice University, Houston, TX USA

Education and Training

Aug. 2009–Jan. 2011 Research Associate II with Dan Graur
Department of Biology and Biochemistry
University of Houston

Aug. 2006–Aug. 2009 Postdoctoral Research Associate with Jeffrey. L. Thorne
Bioinformatics Research Center
Department of Genetics
North Carolina State University

Aug. 2001–Aug. 2006 Graduate Student with Marjorie Asmussen
Department of Genetics
University of Georgia

| | |
|---------------------|---|
| Spring 2006 | Graduate Lab Assistant BIOL 1108L—Principles of Biology II Lab |
| Fall 2006 | Graduate Teaching Assistant GENE 3000—Evolutionary Biology |
| Fall 2002 | Graduate Teaching Assistant GENE 3200—Genetics |
| Jan. 2001–Aug. 2001 | Research Technician with Marjorie Asmussen Department of Genetics University of Georgia |

Publications

- Active Papers Hufford MB, Xu X, van Heerwaarden J, Pyhäjärvi T, Chia JM, **Cartwright RA**, Elshire RJ, Glaubitz JC, Guill KE, Kaeppler S, Lai J, Shannon LM, Song C, Springer NM, Swanson-Wagner RA, Tiffin P, Wang J, Zhang G, Doebley J, McMullen MD, Buckler ES, Ware D, Yang S, and Ross-Ibarra J (submitted). Genome-wide effects of domestication and improvement in landraces and modern maize.
- Papers **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, Zilversmit 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.

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>.

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/>

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.

Honors and Awards

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

Conferences and Presentations

- 2012 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.
 University of Auckland, Department of Statistics
 Presentation: Studying Evolutionary Models of Mutation using Genomic Data
 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)
 University of Western Ontario, Department of Biology
 Presentation: Studying Evolutionary Models of Mutation using Genomic Data
 Arizona State University, School of Life Sciences
 Presentation: Studying Evolutionary Models of Mutation using Genomic Data
 Fred Hutchinson Cancer Research Center, Herbold Computational Biology Program
 Presentation: Studying Evolutionary Models of Mutation using Genomic Data
 The University of Alabama, Department of Biological Sciences
 Presentation: Studying Evolutionary Models of Mutation using Genomic Data
- 2010 Evolution Conference (Portland State University)
 Presentation: Extracting Phylogenetic Information from Ambiguous Regions. Cartwright RA, Lücking R, Hodkinson B, Stamatakis A
 East Carolina University, Department of Biology
 Presentation: Predicting Evolutionary Events using Biologically Robust Statistical Models
 Rice University, Department of Ecology and Evolutionary Biology
 Presentation: Predicting Evolutionary Events from Uncertain Data
- 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.

- 2008 Science Online Conference (Sigma Xi Center, RTP, NC)
 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 UNC Charlotte, Department of Bioinformatics and Genomics
Presentation: Estimating the Rate and Length Distribution of Indels
 Society for Molecular Biology and Evolution Conference (Dalhousie University)
Presentation: Estimating the Rate and Length Distribution of Indels
 Invited speaker, Undergraduate Honors “C-START” Seminar (University of North Carolina at Chapel Hill)
Presentation: Evolutionary Biology in 30 Minutes
 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)
 Evolution Conference (Colorado State University)
 Southeast Ecology & Evolution Conference (Georgia Tech)
- 2002 Evolution of Language: Fourth International Conference (Harvard University)

* Did not attend; co-author presented work.

Society Memberships

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

Funding History

Jan. 2011–Present Huxley Faculty Fellowship Startup Funds
 Jan. 2011 TalkOrigins Foundation Support

Aug. 2009–Jul. 2011 NLM grant LM010009-01 to D Graur and G Landan
Aug. 2006–Aug. 2009 NIH grant GM070806 to JL Thorne
Aug. 2001–Aug. 2006 NSF Predoctoral Fellowship
Aug. 2005–Aug. 2006 Graduate Teaching Assistantship
Aug. 2003–Aug. 2004 Graduate Research Assistantship, NIH Grant 5R01 GM48528-06 to MA Asmussen

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

Websites Administered <http://pandasthumb.org/>, <http://talkorigins.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

January 17, 2012