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
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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	*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	SPAGEDI: 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.

	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:* Probabalistic 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 Charolotte, 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 Statup 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 |

February 8, 2012