

Reed A. Cartwright, PhD

Research Statement

I use computational and statistical approaches to study evolutionary processes using genomic data. My research is species neutral, and I currently work on data from both model and non-model organisms, including humans, chimps, angiosperms, *E. coli*, and pathogenic and non-pathogenic eukaryotic microbes. Most of my research involves developing and applying novel software to estimate diversity and mutation processes in populations. I am also interested in pedagogy and develop web-based simulations to improve biology teaching.

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)

Appointments (Current)

- 2012–Present** Assistant Professor and Barrett Honors Faculty
Genomics, Evolution, and Bioinformatics
School of Life Sciences
Arizona State University, Tempe, AZ USA
- 2016–Present** Virginia G. Piper Center for Personalized Diagnostics
The Biodesign Institute
Arizona State University, Tempe, AZ USA

Appointments (Previous)

- 2014–2016** Human and Comparative Genomics Laboratory
The Biodesign Institute
Arizona State University, Tempe, AZ USA
- 2012–2014** 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
- 2009–2010** Research Associate II with Dan Graur
Department of Biology and Biochemistry
University of Houston, Houston, TX USA
- 2006–2009** Postdoctoral Research Associate with Jeffrey. L. Thorne
Bioinformatics Research Center and Department of Genetics
North Carolina State University, Raleigh, NC USA
- 2001–2006** Graduate Student with Marjorie Asmussen
Department of Genetics
University of Georgia, Athens, GA USA

Publications

* co-first or co-last authors ^P supervised postdoc ^S supervised grad student ^U supervised undergrad

Preprints and Drafts

30. **Cartwright RA**, Schwartz RS^P, Merry AL^U, and Howell MM^U (2016) Strong selection is necessary for evolution of blindness in cave dwellers. *bioRxiv*. doi:10.1101/031872. Preprint available at bioRxiv.
29. Roos B^U, Wilson Sayres M, and **Cartwright RA** (2016) Genie: A population genetics simulation built with JavaScript. *Draft Prepared*.
28. Huang N, Vigh-Conrad KA, Schwartz RS^P, **Cartwright RA**, and Conrad DF (2015) Joint variation discovery and lineage inference from single cell sequencing reveals two developmental phases of mutation. *Under Revision*.
27. Palmer ND^U and **Cartwright RA** (2015) Strong episodic selection for natural competence due to host-pathogen dynamics. *Draft Prepared*.
26. Wu SH^P, Schwartz RS^P, Winter DJ^P, Conrad DF, and **Cartwright RA** (2015) A novel method to model read counts in genomic data to reduce false positive identification of heterozygotes. *bioRxiv*. doi:10.1101/031724. Preprint available at bioRxiv.

Peer-Reviewed Papers

25. Long H*, Winter DJ^{P*}, Chang AY, Sun W, Wu SH^P, Balboa M, Azevedo RB, **Cartwright RA**, Lynch M, and Zufall RA (2017) Low base-substitution mutation rate in the ciliate *Tetrahymena thermophila*. *Genome Biology and Evolution*. Accepted.
24. Furstenau TN^S and **Cartwright RA** (2016) The effect of the dispersal kernel on isolation-by-distance in a continuous population. *PeerJ*, 4:e1848. doi:10.7717/peerj.1848.
23. Harkins K, Schwartz RS^P, **Cartwright RA**, and Stone AC (2016) Phylogenomic reconstruction supports supercontinent origins for *Leishmania*. *Infection, Genetics, and Evolution*, 38:101–109. doi:10.1016/j.meegid.2015.11.030.
22. Lofgren ET, Collins K, Smith TC, and **Cartwright RA** (2016) Equations of the end: Teaching mathematical modeling using the zombie apocalypse. *Microbiology and Biology Education*, 17:137–142. doi:10.1128/jmbe.v17i1.1066.
21. Crusoe M, Alameldin H, Awad S, Boucher E, Caldwell A, **Cartwright RA**, Charbonneau A, Constantinides B, Edvenson G, Fay S, Fenton J, Fenzl T, Fish J, Garcia-Gutierrez L, Garland P, Gluck J, Gonzalez I, Guermond S, Guo J, Gupta A, Herr J, Howe A, Hyer A, Harpfer A, Irber L, Kidd R, Lin D, Lippi J, Mansour T, McAnulty P, McDonald E, Mizzi J, Murray K, Nahum J, Nanlohy K, Nederbragt A, Ortiz-Zuazaga H, Ory J, Pell J, Pepe-Ranney C, Russ Z, Schwarz E, Scott C, Seaman J, Sievert S, Simpson J, Skennerton C, Spencer J, Srinivasan R, Standage D, Stapleton J, Steinman S, Stein J, Taylor B, Trimble W, Wiencko H, Wright M, Wyss B, Zhang Q, zyme e, and Brown C (2015) The khmer software package: enabling efficient nucleotide sequence analysis. *F1000Research*, 4:900. doi:10.12688/f1000research.6924.1.
20. Karin EL, Rabin A, Ashkenazy H, Shkedy D, Avram O, **Cartwright RA**, and Pupko T (2015) Inferring indel parameters using a simulation-based approach. *Genome Biology and Evolution*, 7:3226–3238. doi:10.1093/gbe/evv212.
19. Schwartz RS^P, Harkins K, Stone AC, and **Cartwright RA** (2015) A composite genome approach to identify phylogenetically informative data from next-generation sequencing. *BMC Bioinformatics*, 16:193. doi:10.1186/s12859-015-0632-y.
18. Winter DJ^P, Pacheco MA, Vallejo AF, Schwartz RS^P, Arevalo-Herrera M, Herrera S, **Cartwright RA***, and Escalante AA* (2015) Whole genome sequencing of field isolates reveals extensive genetic diversity in *Plasmodium vivax* from Colombia. *PLoS Negl Trop Dis*, 9:e0004252. doi:10.1371/journal.pntd.0004252.
17. Ramu A, Noordam MJ, Schwartz RS^P, Wuster A, Hurler ME, **Cartwright RA**, and Conrad DF (2013) DeNovoGear: de novo indel and point mutation discovery and phasing. *Nature Methods*, 10:985–987. doi:10.1038/nmeth.2611.
16. **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. doi:10.2202/1544-6115.1713. *Paper began before ASU*.
15. Hufford MB, Xu X, van Heerwaarden J, Pyhäjärvi T, Chia JM, **Cartwright RA**, Elshire RJ, Glaubitz JC, Guill KE, Kaepler 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. doi:10.1038/ng.2309. *Paper began before ASU*.

14. **Cartwright RA** (2011) Bards, poets, and cliques: Frequency-dependent selection and the evolution of language genes. *Bulletin of Mathematical Biology*, 73:2201–2212. doi:10.1007/s11538-010-9619-z.
13. **Cartwright RA** and Graur D (2011) The multiple personalities of Watson and Crick strands. *Biology Direct*, 6:7. doi:10.1186/1745-6150-6-7.
12. **Cartwright RA**, Lartillot N, and Thorne JL (2011) History can matter: Non-Markovian behavior of ancestral lineages. *Systematic Biology*, 60:276–290. doi:10.1093/sysbio/syr012.
11. 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. doi:10.1038/ng.862.
10. 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. doi:10.1186/1471-2105-12-10.
9. 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. doi:10.1093/molbev/msr029.
8. The 1000 Genomes Project Consortium (2010) A map of human genome variation from population-scale sequencing. *Nature*, 467:1061–1073. doi:10.1038/nature09534.
7. **Cartwright RA** (2009) Problems and solutions for estimating indel rates and length distributions. *Molecular Biology and Evolution*, 26:473–480. doi:10.1093/molbev/msn275.
6. **Cartwright RA** (2009) Antagonism between local dispersal and self-incompatibility systems in a continuous plant population. *Molecular Ecology*, 18:2327–2336. doi:10.1111/j.1365-294X.2009.04180.x.
5. **Cartwright RA** (2007) Ngila: global pairwise alignments with logarithmic and affine gap costs. *Bioinformatics*, 23:1427–1428. doi:10.1093/bioinformatics/btm095.
4. **Cartwright RA** (2006) Logarithmic gap costs decrease alignment accuracy. *BMC Bioinformatics*, 7:527. doi:10.1186/1471-2105-7-527.
3. **Cartwright RA** (2005) DNA assembly with gaps (Dawg): simulating sequence evolution. *Bioinformatics*, 21:iii31–iii38. doi:10.1093/bioinformatics/bti1200.
2. 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. doi:10.1105/tpc.105.036293.
1. 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. doi:10.1534/genetics.167.1.499.

Books

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

Other

5. **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>.
4. Hogue LL and Ross CJ with Reed A Cartwright 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.
3. **Cartwright RA** (2004) Ignorance excludes evolution. *Atlanta Journal-Constitution*, Jan 28.
2. Fant L with Sandefur T, Reed A Cartwright, 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.
1. **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>

5535 citations and h-index of 13 (as of 2016/01/26)

Scientific Software

accMulate	estimation of mutation rates from mutation accumulation lines URL https://github.com/dwinter/accMulate/ first release: 2015
Dawg	simulation of molecular evolution using complex indel models URL https://github.com/reedacartwright/dawg/ first release: 2005; last update: 2015
DeNovoGear	identification of de novo mutations from related individuals. URL https://github.com/denovogear/denovogear/ first release: 2013; last update: 2015
DFE	fitting, simulating and generally exploring the distribution of fitness effects from MA studies URL https://github.com/dwinter/dfe/ first release: 2015
Emdel	estimation of indel rate and length parameters using expectation-maximization URL https://github.com/reedacartwright/emdel/ first release: 2009; last update: 2014
MDM	simulating and fitting mixtures of Dirichlet-multinomials in R URL https://github.com/dwinter/mdm/ first release: 2015
NbMCL	Neighborhood size inference using marginal composite likelihood URL https://github.com/tfursten/NbMCL/ first release: 2015
Nbmcmc	Bayesian inference of neighborhood size using composite marginal likelihood URL https://github.com/tfursten/nbmcmc/ first release: 2015
Ngila	pairwise alignment with log-affine gap costs URL http://scit.us/projects/ngila/ first release: 2007; last update: 2013
PICS-Ord	extract phylogenetic information from ambiguously aligned regions URL http://scit.us/projects/ngila/wiki/PICS-Ord first release: 2011
Relrates	calculation of relative rates for phylogenetic analysis URL https://github.com/rachelss/rrelrates/ first release: 2015
SISRS	SNP identification from short read sequences. URL https://github.com/rachelss/SISRS/ first release: 2014; last update: 2015
SoFoS	rescaling of site frequency spectra URL http://scit.us/sofos/ first release: 2010; last update 2012

Educational Software

- Genie** individual-based, spatially-explicit simulation of population evolution on a landscape
URL <http://cartwrig.ht/apps/genie/>
first release: 2015
- RandomCall** implementation of randomized call for classroom exercises
URL <http://cartwrig.ht/apps/randomcall/>
first release: 2015
- RedLynx** population genetic simulation
URL <http://cartwrig.ht/apps/redlynx/>
first release: 2009; last update 2015
- WhiteZed** epidemiological modeling and zombie apocalypse simulation
URL <http://cartwrig.ht/apps/whitezed/>
first release 2015

Funding

Current Awards

Estimating insertions and deletions across the tree of life

Grant: BSF 2015247 (2016–2020)
Role: PI — w/ T Pupko PI (Tel Aviv U.); Award: \$172,000 (ASU: \$86,400)

ABI Innovation: Identifying phylogenetically informative data from next-generation sequencing

Grant: NSF DBI-1356548 (2014–2017)
Role: PI; Award: \$686,240

Mutation accumulation in the ciliate *Tetrahymena thermophila*

Grant: NIH R01-GM101352 (2013–2018)
Role: ASU PI — w/ R Zufall PI and R Azevedo Co-I (U. Houston); Award: \$1,442,528 (ASU: \$733,790)

Analysis of “de novo” mutation from sequencing of related individuals and cells

Grant: NIH R01-HG007178 (2014–2019)
Role: ASU PI — w/ D Conrad PI (Washington University in St. Louis); Award: \$2,500,000 (ASU: \$1,281,295)

DNA and Human Origins at ASU

Grant: Office of the President, Arizona State University to the Institute of Human Origins (2015)
Role: Co-I — w/ A Stone PI, I Gilby, M Rosenberg, and M Wilson Sayres (ASU); Award: ~\$100,000

Previous Awards

Mixed infections and population genomics in malarial parasites

Grant: ASU Genomics Core / Illumina Grant Award (2013)
Role: PI— w/ A. Escalante PI (ASU); Award: \$3000

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

- 2014** Nominated for CLAS teaching award at ASU
- 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

Student and Postdoc Awards

- 2016** Sunny Mahesh — Internship with Bioinformatics Research and Interdisciplinary Training Experience (BRITE) in Analysis and Interpretation of Information-Rich Biological Data Sets Program at Boston University
Dominic Nicacio — University of Washington Tuition Award (full fellowship to med school)
Dominic Nicacio — ASU Moeur Award
- 2015** Diana Arroyo — Internship with the Summer Multicultural Access to Research Training (SMART) Program in the University of Colorado at Boulder.
Melissa Ip — Fulton Undergraduate Research Initiative (Spring)
Melissa Ip — Travel award to the Society of Molecular Biology and Evolution annual conference (Vienna)
Dominic Nicacio — Hispanic Scholarship Foundation Scholarship Award
Dominic Nicacio — Fred Holmes Memorial Scholarship
Rachel Schwartz — Travel award to attend the Phylogenomics Symposium and Software School (Ann Arbor)
- 2014** Melissa Ip — Fulton Undergraduate Research Initiative (Spring and Fall)
Adam Orr — Joyce Foster Larson Scholarship
- 2013** Nathan Palmer — Travel award to the Society of Molecular Biology and Evolution annual conference (Chicago)
Jessica Albanese — Gustave Malécot poster award for the best undergraduate poster at the Mechanisms of Protein Evolution II Conference for her poster “LAMBDA: Estimating Indel Rates and Length Distributions from a Multiple Sequence Alignment.”
Akash Khare — Gustave Malécot poster award for the best undergraduate poster at the Mechanisms of Protein Evolution II Conference for his poster “Estimating Unbiased Indel Models via Simulation and Optimization.”

Invited Seminars

- 2016** THE UNIVERSITY OF GEORGIA: Bioinformatics Seminar Series
Detecting Mutations with Short-Read Sequencing
- AUSTRALIAN NATIONAL UNIVERSITY: Research School of Biology Seminar Series
Detecting Mutations with Short-Read Sequencing
- ARIZONA STATE UNIVERSITY: Biomedical Informatics Seminar Series
Detecting Mutations with Short-Read Sequencing
- 2014** ARIZONA STATE UNIVERSITY: SoLS Departmental Seminar Series
Strong selection is necessary for repeated evolution of blindness in cavefish.
- 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

Pedagogical Conferences and Workshops

- 2015** Software Carpentry Instructor Training (University of California, Davis)
- 2013** Teaching Phylogenetics to Undergrads, Curriculum Development Workshop (University of Texas, Austin)
- 2012** BioQUEST/SCALE-IT Curriculum Development Workshop (University of Tennessee, Knoxville)
- 2009** Science Online Conference (Research Triangle Park, NC)
- 2008** North Carolina Science Blogging Conference (Research Triangle Park, NC)
- 2007** North Carolina Science Blogging Conference (Chapel Hill, NC)
- 2004** National Center for Science Education's Activist Summit (Berkeley, CA)

Scientific Conferences

* presenter ^P supervised postdoc ^S supervised grad student ^U supervised undergrad ^T supervised technician or programmer

- 2016**
- Society for Molecular Biology and Evolution Conference (Gold Coast, Australia)
Keynote: Getting Phylogenetically Informative Data. Schwartz RS^{P*} and **Cartwright RA**
Talk: The Molecular Evolution of Human Breasts. **Cartwright RA*** and Winter DJ^P
Poster: Ciliates have extremely low mutation rates, why?
Winter DJ^{P*}, Chang A, Azevedo R, Zufall R, and **Cartwright RA**
Poster: Phylogenies derived from somatic mutations agree with physical topologies in *Eucalyptus*
Orr AJ^{S*}, Lanfear R, and **Cartwright RA**
- Evolution Conference (Austin, Texas)
Poster: Joint modeling of error processes from whole genome sequencing using mixtures of Dirichlet multinomial distributions
Wu SH^{P*}, Schwartz RS^P, Winter DJ^P, Conrad DF, **Cartwright RA**
- 2015**
- Probabilistic Modeling in Genomics (Cold Spring Harbor Laboratory)
- Society for Molecular Biology and Evolution Conference (Vienna)
Talk: Bayesian estimation of neighborhood size using composite marginal likelihoods. Furstenau TN^{S*} and **Cartwright RA**
Talk: Rapid identification of phylogenetically informative data from next-gen sequencing
Schwartz RS^{P*} and **Cartwright RA**
Talk: Adaptive convergence and quasi-heterozygous advantage after experimental evolution of *Escherichia coli*.
Sievert CJ^{P*}, Loeffler T, Panyon L, Morris C, Winter DJ^P, Dai KB^T, Wang X, and **Cartwright RA**
Poster: Estimating Trio Model Parameters to Improve Detection of De Novo Mutations. Ip M^{U*} and **Cartwright RA**
Poster: Designing molecular diagnostics from shotgun sequencing data: a case study using *Leishmania*. Harkins KM*, Schwartz RS^P, Fehren-Schmitz L, **Cartwright RA**, and Stone AC
- Evolution Conference (Guarujá, Brazil)
Talk: Migration-Selection Balance and the Unlikely Evolution of Blindness in Cavefish
- SMBE Satellite Meeting on DNA Mutation, Repair, and Evolution (Indiana University Bloomington)
Talk: AccMUlate: Estimating Spontaneous Mutation Rates in MA Lines
Poster: DFE: An R package for estimating the distribution of fitness effects from Mutation Accumulation experiments. Winter DJ^{P*}, **Cartwright RA**, and Azevedo R
- Biology of Genomes (Cold Spring Harbor Laboratory)
Poster: Population genomic analysis of *Plasmodium vivax* from Colombia reveals substantial genetic diversity and a selective sweep associated with drug resistance. Winter DJ^{P*}, Pacheco MA, Schwartz RS^P, **Cartwright RA**, and Escalante AA
Poster: Directly measuring the rate of spontaneous mutation in *Tetrahymena thermophila*. Wu SH^{P*}, Winter DJ^P, Chang A, Azevedo R, Zufall R, and **Cartwright RA**
- The Human Mutation Rate Meeting (Max Planck Institute for Evolutionary Anthropology)
Poster: DeNovoGear: Estimating de novo mutations from related individuals and cells. **Cartwright RA***, Dai KB^T, Schwartz RS^P, Winter DJ^P, Wu SH^P, Huang N, Ramu A, and Conrad DF
- 2014**
- Southern California Evolutionary Genetics & Genomics (University of California, Los Angeles)
Talk: Strong Selection is Necessary for Repeated Evolution of Blindness in Cavefish.
- Society for Molecular Biology and Evolution Conference (San Juan, Puerto Rico)
Symposium: Mutation: the Ultimate Source of Molecular Variation. Co-Organized by **Cartwright RA** and Wilson

Sayres MA.

Poster: Phylogenies from Next-Generation Sequence without Assembly or Alignment. Schwartz RS^P and **Cartwright RA^{*}**

Poster: Directly measuring the rate of spontaneous mutation in *Tetrahymena thermophila*. Winter DJ^{P*}, Chang A, Azevedo R, Zufall R, and **Cartwright RA**

Evolution Conference (Raleigh, NC)

Talk: Accurate Detection of Mutations from Short-Read Sequencing. Winter DJ^{P*}, Chang A, Azevedo R, Zufall R, and **Cartwright RA**

Talk: Inferring Phylogenies from Next-Generation Sequence Data. Schwartz RS^{P*} and **Cartwright RA**

Poster: The Effect of the Dispersal Distribution on Isolation-by-Distance in a Continuous Population. Furstenau TN^{B*} and **Cartwright RA**

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^{U*}, Schwartz RS^P, **Cartwright RA**

Poster: Phylogenomic Investigation of the Origins and Evolutionary History of *Leishmania*. Harkins KM^{*}, Schwartz RS^P, **Cartwright RA**, and Stone A

Evolution Conference (Snowbird, UT)

Talk: Sampling Tree-Space Effectively Using Distance Methods. Palmer ND^U, Schwartz RS^P, **Cartwright RA^{*}**

Talk: Phylogenies from next-gen sequencing data without assembly. Schwartz RS^{P*}, **Cartwright RA**

Biological Sequence Analysis and Probabilistic Models (HHMI, Janelia Farm)

Poster: Probabilistic Models for De Novo Mutation Detection

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^{P*} and **Cartwright RA**

Poster: Estimating Indel Models via Simulation and Optimization. Khare A^{U*} and **Cartwright RA**

Poster: LLAMBDA: Estimating Indel Rates and Length Distributions from a Multiple Sequence Alignment. Albanese JR^{U*} 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^{G*} 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)

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.
- 2008** Evolution Conference (University of Minnesota, Twin Cities)
Presentation: Estimating the Rate and Length-Distribution of Insertions and Deletions
- 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
- 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** Evolution Conference (Colorado State University)
- Southeast Ecology & Evolution Conference (Georgia Tech)
- 2002** Evolution of Language: Fourth International Conference (Harvard University)

Society Memberships

- Society for Molecular Biology and Evolution (lifetime member)
- The Society for the Study of Evolution (lifetime member)

External Service

- Journals** PeerJ (Academic Editor)
- SWC** Certified Software Carpentry Instructor (<http://software-carpentry.org/>)
- Grant Reviewer** Leakey Foundation (ad hoc), NSF (ad hoc and panelist)
- Manuscript Reviewer** 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, PeerJ, Systematic Biology
- FreeBSD** Maintainer of software ports: biology/mafft, biology/samtools, biology/htslib, biology/bcftools
- TalkOrigins** Maintainer of server hosting several of the foundation’s websites.
- Panda’s Thumb** Managing Editor, <http://pandasthumb.org/>

Reed A. Cartwright, PhD
Assistant Professor, School of Life Sciences
cartwright@asu.edu @MinionLab
<http://cartwrig.ht/>

Human and Comparative Genomics Laboratory
The Biodesign Institute at Arizona State University
PO Box 875301, Tempe, AZ 85287-5301, USA
Ph: 480-965-9949 Fax: 480-727-6947

Other Skills

Programming C/C++, R, Perl, Shell, Ruby, \LaTeX , Matlab, Mathematica, JavaScript, Python

Languages Studied Classical Latin, Greek, and Sanskrit

Generated on September 15, 2016