,

CURRICULUM VITAE

JONATHAN ARNOLD

Date & Place of Birth: November 27, 1953; New York City

- **Field of Endeavor: Systems Biology**

- **Video of Research: http://www.nsf.gov/news/special_reports/science_nation/biologicalclocks.jsp**

- **International Leadership**

    - Fungal Genome Initiative Steering Committee
    - *Neurospora* Genomics Working Group
    - *Pneumocystis* Genome Project Steering Committee
    - *Aspergillus fumigatus* Genomics Steering Committee
    - Advisor to Burroughs-Wellcome Fund on Fungal Genomics
    - NIH Genome Study Section (ad hoc)
    - NIH Genetics Study Section (ad hoc)
    - NIH GCAT Study Section (ad hoc)
    - Charter Member of NIH Genetic Variation and Evolution (GVE) study section, 2005-2008

- **Academic degrees**

Ph.D.	1982	Statistics	Yale University
M.Phil.	1978	Statistics	Yale University
B.S.	1975	Mathematics	Yale University

- **Title of doctoral dissertation**

    Statistics of Natural Populations: Seasonal Variation in Inversion Frequencies of Mexican *Drosophila pseudoobscura*.
    Thesis Advisor: I. R. Savage, deceased

- **Faculty positions**

2002-Present	Professor	Departments of Genetics, Statistics, and Physics/Astronomy, UGA
1997-Present	Professor	Departments of Genetics and Statistics, UGA
1992-1997	Associate Professor	Departments of Genetics and Statistics, UGA
1988- 1992	Associate Professor	Department of Genetics, UGA
1982-1987	Assistant Professor	Department of Statistics/ Computer Science and Genetics, UGA
1981-1982	Adjunct Instructor	Department of Statistics, Rutgers University

- **Areas of Research**

    - Systems Biology
    - Fungal Genomics
    - Computational Genomics
    - Molecular Evolutionary Genetics
    - Theoretical Population Genetics
    - Chromosomal Evolution

- **Grants Received**

    "Measuring and Modeling how Clocks in Single Cells Communicate: an interdisciplinary approach". MCB-SSB/PHY-POLS-1713746, 08/01/2017-07/31/2020, $830,000 (PI: Jonathan Arnold, Co-PI, H. Bernd Schuttler, Leidong Mao, and Art Edison). This is two separate awards combined administratively into one NSF award.

    "EAGER: ALICE, MCB-1645325, "Adaptive Learning for Interdisciplinary Collaborative Environments", 7/10/2016-7/09/2018, $299,899 (PI: Juan Gutierrez, Co-PI: Jonathan Arnold, Pedro Portes

    "REU site: Interdisciplinary research experiences in Nanotechnology and Biomedicine", NSF EEC-1659525, 2017-2020, $411,338 (PI: Leidong Mao, Co-PI: Jonathan Arnold)

    "REU site: collaborative research: genomics and computational biology", NSF DBI-1426834, 3/18/2014-3/17/2019, $538,095 (PI: Jonathan Arnold, Co-PI: Richard B. Meagher, PI: David A. Logan)

    "REU site: Interdisciplinary research experiences in Nanotechnology and Biomedicine", NSF EEC-1359095, 2014-2017, $359,998 (PI: Leidong Mao, Co-PI: Jonathan Arnold)

    "REU site: genomics and computational biology", NSF DBI-1062213, 2011-2014, $379,000 (PI: Jonathan Arnold, Co-PI: Richard B. Meagher)

    "Creativity Extension Award to DBI-0646315", NSF DBI-01041715, 2010-2011, $91,350 (PI: Jonathan Arnold, Co-PI: D.A. Logan).

    "Workshop on Mathematical Biology and Numerical Analysis", NSF DMS-0906557, 2009-2010, $30,000 (PI: T. Taha, Co-PIs: J. Arnold, J. Prestegard, & A Summers).

    "Genomics and Computational Biology, an REU site", NSF DBI-0646315, 2007-2011, $318,012+$91,350 (PI: J. Arnold, Co-PIs: D.A. Logan, C. Teare Ketter).

    "CAA: Identification of genetic networks in *Neurospora crassa*: a systems biology approach", NSF MCB-0542915, Mar 1, 2006- Feb 29, 2008, $157,115, (PI: D. A. Logan and Co-PI: J. Arnold)

    "Computing Life and the Kinetics of the Cell", NSF QSB-0425762, 2004-2008, $499,994, (PI: J. Arnold and Co-PI: H.-B. Schuttler)

"A population based, multi-disciplinary study of Centenarians", NIH 5P01 AG017553-03, 2003-2009, $159,720 (PI: L. Poon and Co-PIs: J. Arnold, R. Green, M. Jazwinski, M.A. Johnson, W. Markesbery, and W. Rogers)

"Genomics and Computational Biology, an REU site", NSF DBI-0243754, 2003-2007, $337,000 (PI: J. Arnold, Co-PIs: D.A. Logan, C. Teare Ketter, & S. Datta).

"Novel statistical methods for generation of integrated genomics maps", USDA-2002-35300-12475, 2002-2007, $280,000 (Co-PIs: S. Bhandarkar and J. Arnold)

"3rd International Symposium on Fungal Genomics and Computational Biology", Burroughs-Wellcome Fund 1001657, 2000-2001, $5,000 (PI: J. Arnold)

"3rd International Symposium on Fungal Genomics and Computational Biology", DOE- 021463, 2000-2001, $10,000 (PI: J. Arnold)

"*Pneumocystis* Genome Project", NIH 018275-01, 1999-2004, $206,440, (subcontract from Dr. M. T. Cushion, University of Cincinnati).

"Parallel computing of physical maps for fungal genomes," USDA-9710389, 1997-2000, $200,000 (Co-PIs, S. Bhandarkar and J. Arnold).

" *In vitro* reconstruction of fungal chromosomes", NSF, 1996-2000, $467,917, 11/01/96-10/31/00, Microbial Genetics, MCB-9630910 (PI: J. Arnold)

" Robotics system for physical mapping fungal genomes", NSF, 1996-1998, $107,150, 3/15/96-3/15/98, BIR-9512887 (PI: J. Arnold)

" Development of fungal-resistant peanut varieties", Georgia Research Alliance, 1996-1997, $350,000, 7/01/96-6/30/97 (Co-PIs: L. Ljungdahl, J. Arnold, and P. Ozias-Akins).

" Parallel computing of physical maps", NSF, 1994-1995, $50,000, 11/15/94 - 11/15/95, BIR-9422896.

" Novel data parallel algorithms and neural networks for computer vision, image processing, and genetics on the MasPar MP-2, MASPAR Corp., 1993-1994, $420,656.

" *In vitro* reconstruction of fungal chromosomes", NIH grant, W. E. Timberlake and J. Arnold, 8/1/89-7/31/94, $837,037.

" Instrumentation for a biological sequence/structure computational facility (BS/SCF), NSF grant, J. Arnold, 1989-1990, 2 years, $188,090.

" Mitochondrial-nuclear interactions in hybrid zones", NSF grant, J. Arnold, 1988-1991, 3 years, $130,000.

" Statistical problems in population genetics", NSF grant, J. Arnold, 1983-1987, 3 years, $125,000.

" Statistical computing and genetic engineering", Army Research Office (ARO) training grant,

J. Arnold and R. Bradley, 1983-1986, 3 years, $60,000.

- **Awards and Honors**

  The UGA Excellence in undergraduate research mentoring award, 2002

  National Science Foundation Creativity Extension Award for work on the biological clock, 2010.

  AAAS Fellow, 2011

  Franklin Diversity Leadership Development Award, 2013

- **Undergraduate Instruction**

  - "Genomics and Society" 12-credit core cluster course for freshmen with new Genomics laboratory for undergraduates in partnership with Drs. Celeste Condit, William Barstow, Scott Kleiner, and Nelson Hilton in the Departments of Speech Communication, Botany, Philosophy, and English, respectively, 2001-2005

  - 10-week NSF-funded summer institute for undergraduates from underrepresented groups in fungal genomics and computational biology in partnership with Clark Atlanta University, Fort Valley State University. and Georgia State University in partnership with Drs. David Logan, Richard B. Meagher, William Seffens, Susmita Datta and Catherine Teare-Ketter. 2000-2009

  - Introductory Genetics (60$\rightarrow$350+ students each fall) for last 23 years. 1985-2008

  - Annual Academic Affairs Faculty Symposium, "Why do I need to learn this: Science and Math for the Non-Science Majors"

- **Graduate Instruction**

  - Genomics
  - Genomic Analysis
  - Nucleic Acids
  - Advanced Molecular Genetics
  - Genetic Data Analysis (Statistical Genetics)
  - Advanced Population Genetics
  - Bioethics
  - C++

- **Past Courses Taught**

  - Molecular Evolution
  - Theoretical Population Genetics
  - Nucleic Acids
  - Advanced Molecular Genetics

- Advanced Population Genetics
- Advanced Ecological Genetics
- Statistical Methods
- Statistical Theory
- Regression Methods
- Data Analysis
- Experimental Design
- Statistical Computing with APL
- Bioinformatics
- Genetics
- Systems biology
- Mathematical Biology

- **Departmental Committees**

  - Head Search, Statistics, 2001 – 2003
  - Bioinformatics faculty search, Statistics, 2000-2002
  - Graduate Affairs Committee, 2000 – 2003
  - IOB Graduate Affairs Committee – 2012-2016
  - Undergraduate Affairs Committee, 1997 – 2016
  - Complex Traits Search, 2006
  - Systems Biology Search, 2006
  - Computational Biology Search, 2008
  - Genetics Department Executive Committee, 2009-present
  - Web page committee, 2010-present
  - Awards Committee – 2011-2016

- **University Committees**

  - Executive Committee of Institute of Bioinformatics
  - Institute of Bioinformatics Advisory Board
  - University Wide Genome Committee,
  - University Computing Advisory Committee
  - University Computational Science Program Advisory Committee
  - Carmon Fellowship Selection Committee
  - 3 recruiting committees in computational biology
  - Georgia Advanced Computing Resource Center Advisory Committee 2011-2014
  - College Promotion and Tenure – 2013-2014

- **Other University Services**

  - Graduate Coordinator, Institute of Bioinformatics, University of Georgia, 2013-
    Director, NSF REU site in Fungal Genomics & Computational Biology, 2000-2019
  - Director, Fungal Genome Resource, UGA, 1995-present.
  - Founding Director, Biological Sequence/Structure Computational Facility (BS/SCF), UGA, 1988-1992.

- **Federal Services**

  - NSF Computational Biology Panel, 1997-1999

- DOE Genome Panel, 1993-1994
- NIH Genomics Study Section (ad hoc), 2003
- NIH Genetics Study Section (ad hoc), 2004-2005
- NIH Genetic Variation and Evolution Study Section, charter member, 2005-2008
- NIH GCAT Study Section (ad hoc), 2010

- **Editorships**

  - Associate editor, *Frontiers in Genetics of Aging*, 2011-
  - Editor, Special issue of *Genetics* 157 devoted to Fungal Genomics and Computational Biology, March, 2001
  - Genome Editor, *Fungal Genetics & Biology*, 1997
  - Associate Editor, *Evolution*, 1988-1991

- **Journal volume edited**

  - *Fungal Genetics and Biology*, vol. 21 (Genome Issue), 1997
  - *Genetics*, vol. 157, March, 2001
  - Xiong, M, Z Zhao, J Arnold, and F Yu (2010). Next-generation sequencing. *Journal of Biomedicine and Biotechnology*, Hindawi Publishing Corporation.
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- **Journal articles**

  All of the following manuscripts were peer-reviewed prior to acceptance and publication.

  - JR Powell, WJ Tabachnick, and J Arnold (1980). Genetics and the origin of a vector population*: Aedes aegypti*, a case study. *Science* 201: 1385-1387.

  - J Arnold, (1981). Statistics of natural populations, I: estimating an allele probability in cryptic fathers with a fixed number of offspring. *Biometrics* 37: 495-504.

  - J Arnold, and DR Kankel (1981). Fate mapping multi-focus phenotypes. *Genetics* 99: 211-229.

  - RG Harrison, and J Arnold (1982). A narrow hybrid zone between closely related cricket species. *Evolution* 36: 535-552.

  - WW Anderson, and J Arnold (1983). Genotypic interactions in a model of density-regulated selection. *American Naturalist* 121: 649-655.

  - J Arnold, and WW Anderson (1983). Density-regulated selection in a heterogeneous environment. *American Naturalist* 121: 656-668.

  - JC Avise, JE Neigel, and J Arnold (1984). The demographics of mitochondrial lineage survivorship. *Journal of Molecular Evolution* 20: 99-105.

  - J Arnold, and ML Morrison (1985). Statistics of natural populations. II. Estimating an allele probability in cryptic mothers with a fixed number of offspring. *Genetics* 109: 785-798.

- VK Eckenrode, J Arnold, and RB Meagher (1985). Comparison of the 18s rRNA with the sequence of other ribosomal small subunit rRNAs. *Journal of Molecular Evolution* 21:259-269.

- WW Anderson, J Arnold, SA Sammons, and DG Yardley (1986). Frequency-dependent viabilities of *Drosophila pseudoobscura* karyotypes, *Heredity* 56: 7-17.

- IF Goldman, J Arnold, and BC Carlton (1986). Selection for resistance to *Bacillus thuringiensis* subspecies *israelensis* in field and laboratory populations of the mosquito *Aedes aegypti*, *Journal of Invertebrate Pathology* 47: 317-324.

- J Arnold, VK Eckenrode, K Lemke, GJ Phillips, and SW Schaeffer. (1986). A comprehensive package for DNA sequence analysis in Fortran-IV for the PDP-11. *Nucleic Acids Research* 14: 239-254.

- MJ Sobel, J Arnold, and M Sobel (1986). Statistics of natural populations. III. Sequential sampling plans for the estimation of gene frequencies. *Biometrics* 42: 45-65.

- MA Asmussen, J Arnold, and JC Avise (1987). Statistics of natural populations. IV. Definition and properties of disequilibrium statistics for associations between nuclear and cytoplasmic genotypes. *Genetics*115: 755-768.

- GJ Phillips, J Arnold, and R Ivarie (1987). Mono- through hexanucleotide composition of the *Escherichia coli* genome: a Markov chain analysis. *Nucleic Acids Research* 15: 2611-2626.

- GJ Phillips, J Arnold, and R Ivarie (1987). The effect of codon usage on the oligonucleotide composition of the *E. coli* genome and identification of over- and underrepresented sequences by Markov chain analysis. *Nucleic Acids Research* 15: 2627-2638.

- JC Avise, J Arnold, RM Ball, E Bermingham, T Lamb, JE Neigel, CA Reeb, and N. C. Saunders (1987). Intraspecific phylogeography: the mitochondrial DNA bridge between population genetics and systematics. *Annual Review of Ecology and Systematics* 18: 489-522.

- SG Wellso, DJ Howard, JL Adams, and J Arnold (1988). Electrophoretic monomorphism in six biotypes and two populations of the Hessian fly (*Diptera*: *cedidouryiidae*). *Annals of Entomological Society of America* 80 (1): 50-53.

- J Arnold, MA Asmussen, and JC Avise (1988). An epistatic mating system model can produce permanent cytonuclear disequilibria in a hybrid zone. *Proceedings of the National Academy of Sciences USA* 85: 1893-1896.

- JC Avise, RM Ball, and J Arnold (1988). Current versus historical population sizes in vertebrate species with high gene flow: a comparison based on mitochondrial DNA lineages and inbreeding theory for neutral mutations. *Molecular Biology and Evolution* 5: 331-344.

- J Arnold, AJ Cuticchia, DA Newsome, WW Jennings III, and R Ivarie (1988).

Mono- through hexanucleotide composition of the sense strand of yeast DNA: a Markov chain analysis. *Nucleic Acids Research* 16: 7145-7157.

- PA Adams, A Falek, and J Arnold (1988). Huntington's Disease in Georgia: Age at onset. *American Journal of Human Genetics* 43: 695-704.

- RB Meagher, MD McLean, and J Arnold (1988). Recombination within a subclass of restriction fragment polymorphisms may help link classical and molecular genetics. *Genetics* 120: 809-818.

- MA Asmussen, J Arnold, and JC Avise (1989). The effects of assortative mating and migration on cytonuclear associations in hybrid zones", *Genetics* 122, 923-934.

- CJ Williams, WW Anderson, CJ Brown, and J Arnold (1989). An analysis of density-dependent viability selection, *Journal of the American Statistical Association* 84, September, 84, 662-668.

- CJ Williams, WW Anderson, and J Arnold (1990). Generalized linear modeling methods for selection component experiments. *Theoretical Population Biology* 35 (2): 389-423.

- JC Avise, WS Nelson, J Arnold, RK Koehn, GC Williams, and V Thorsteinsson (1990). The evolutionary genetic status of Icelandic eels. *Evolution* 44: 1254-1262.

- SE Surles, J Arnold, A Schnabel, JC Hamrick, and BC Bongarten (1990). Genetic relatedness in open-pollinated families of two leguminous tree species, *Robinia pseudoacacia L.* and *Gleditsia tricanthos L.*, *Theoretical and Applied Genetics* 80: 49-56.

- MA Asmussen, and J Arnold (1991). The effects of admixture and population subdivision on cytonuclear disequilibria, *Theoretical Population Biology* 39: 273-300.

- Y-X Fu, and J Arnold (1991). On the association of RFLP's across species boundaries. *Proceedings of the National Academy of Sciences USA* 88: 3967-3971.

- H Brody, J Griffith, AJ Cuticchia, J Arnold, and WE Timberlake (1991). Chromosome-specific recombinant DNA libraries from the fungus *Aspergillus nidulans*. *Nucleic Acids Research* 19: 3105-3109.

- WW Anderson, J Arnold, DG Baldwin, AT Beckenbach, CJ Brown, SH Bryant, JA Coyne, LG Harshman, WB Heed, DE Jeffrey, LB Klaczko, BC Moore, JM Porter, JR Powell, T Prout, SW Schaeffer, JC Stephens, CE Taylor, ME Turner, GO Williams, JA Moore (1991). Four decades of inversion polymorphism in *Drosophila pseudoobscura*. *Proceedings of the National Academy of Sciences USA* 88: 10367-10371.

- JM Brewer, J Arnold, GG Beach, WL Ragland, and JK Wunderlich. (1991). Comparison of the amino acid sequences of tissue-specific parvalbumins from chicken muscle and thymus and possible evolutionary significance. *Biochemical and Biophysical Research Communications* 181: 226-231.

- Y-X Fu, and J Arnold (1992). Dynamics of cytonuclear disequilibria in finite

populations   and a comparison with a two-locus nuclear system. *Theoretical Population Biology* 41, No. 1, 1-25.

- Y-X Fu, and J Arnold (1992). A table of exact sample sizes for use with Fisher's exact test for 2 x 2 tables. *Biometrics* 48 (December) 48: 1103-1112.

- AJ Cuticchia, J Arnold, and WE Timberlake (1992). The use of simulated annealing in chromosome reconstruction experiments based on binary scoring of clones. *Genetics* 132: 591-601.

- AJ Cuticchia, J Arnold, H Brody, and WE Timberlake (1992) CMAP: Contig mapping and analysis package: a relational database for chromosome reconstruction, *CABIOS* 8: 467-474.

- Y-X Fu, WE Timberlake, and J Arnold (1992). On the design of genome mapping experiments using short synthetic oligonucleotides. *Biometrics* 48: 337-359.

- AJ Cuticchia, R Ivarie, and J Arnold (1992). The application of Markov chain analysis to oligonucleotide frequency prediction and physical mapping of *Drosophila melanogaster*. *Nucleic Acids Research* 20: 3651-3657.

- AJ Cuticchia, J Arnold, and WE Timberlake (1993). ODS: Ordering DNA sequences, a physical mapping algorithm based on simulated annealing. *CABIOS* 9, 2, 215-219.

- AJ Cuticchia, J Arnold, and WE Timberlake (1993). PCAP: Probe choice and analysis package: a set of programs to aid in choosing synthetic oligomers for contig mapping, *CABIOS* 9, 2, 201-203.

- ML Cellino, and J Arnold (1993). The effects of male sterility on cytonuclear disequilibria in hybrid zones. *Genetica* 88: 37-50.

- J Arnold. (1993). Cytonuclear disequilibria in hybrid zones. *Annual Review of Ecology and Systematics* 24: 521-554.

- SK Hollingshead, J Arnold, T Readdy, and DE Bessen (1994). Molecular evolution of a multi-gene family in group A *streptococci*, *Molecular Biology and Evolution* 11: 208-219.

- Y Wang, RA Prade, J Griffith, WE Timberlake, and J Arnold (1994). A fast random cost algorithm for physical mapping. *Proc. Natl. Acad. Sci. USA* 91: 11094-11098.

- Y Wang, RA Prade, J Griffith, WE Timberlake, and J. Arnold (1994). ODS_BOOTSTRAP: Assessing the statistical reliability of physical maps by resampling. *CABIOS* 10: 625-634.

- M Xiong, HJ Chen, RA Prade, Y Wang, J Griffith, WE Timberlake, and J. Arnold (1996). On the consistency of a physical mapping algorithm to reconstruct a chromosome. *Genetics* 142: 267-284.

- R Dean and J Arnold (1996). Cytonuclear disequilibria in hybrid zones using RAPD markers. *Evolution* 50(4): 1702-1705.

- S Datta, Y-X Fu, and J Arnold (1996). Dynamics and equilibrium behavior of cytonuclear disequilibria under genetic drift, mutation, and migration. *Theoretical Population Biology* 50: 298-324.

- R Dean and J. Arnold (1996). Small sample properties for estimators of cytonuclear disequilibria. *Heredity* 77: 396-399.

- SM Bhandarkar, S Chirravuri, and J Arnold (1996). Parallel computing of physical maps--a comparative study in SIMD and MIMD parallelism. *J. Computational Biology* 3: 503-528.

- S Datta and J Arnold (1996). Diagnostics and a statistical test of neutrality hypotheses using the dynamics of cytonuclear disequilibria, *Biometrics* 52: 1042-1054.

- SM Bhandarkar, S Chirravuri, and J Arnold (1996). PARODS - A study of parallel algorithms for ordering DNA sequences. *CABIOS* 12, No. 4, 269-280.

- K Wollenberg, J Arnold, and JC Avise (1996). Recognizing the forest for the trees: testing temporal patterns of cladogenesis using a null model of stochastic diversification. *Molecular Biology and Evolution* 13: 833-849.

- S Datta, M Kiparsky, DM Rand, and J Arnold (1996). A statistical test of a neutral model using the dynamics of cytonuclear disequilibria. *Genetics* 144: 1985-1992.

- RA Prade, J Griffith, K Kochut, J Arnold, and WE Timberlake (1997). *In vitro* reconstruction of the *Aspergillus (=Emericella) nidulans* genome. *Proc. Natl. Acad. Sci. USA* 94: 14564-14569

- R Dean and J Arnold (1997). The effects of unidirectional incompatibility on cytonuclear disequilibria in a hybrid zone. *Genetica* 101: 215-223

- M Sanchez, J Arnold, and MA Asmussen (1997). Effects of vertical transmission rates on the survival, maintenance of genetic variability and association of viral parasite and host genotypes. *Gibier Faune Sauvage* 14: 477-492

- J Arnold and MT Cushion (1997). Constructing a physical map of the *Pneumocystis* genome, *J. Euk. Microbiol.* 44:8s

- MT Cushion, and J Arnold (1997). Proposal for a *Pneumocystis* Genome Project, *J. Euk. Microbiol* 44: 7s

- SM Bhandarkar, S Machaka, S Chirravuri, and J Arnold (1998). Parallel computing for chromosome reconstruction via ordering of DNA sequences. *Parallel Computing* 24: 1177-1204.

- S Datta and J Arnold (1998). Dynamics of cytonuclear disequilibria in subdivided populations. *J. Theor. Biol.,* 192: 99-111

- KT Scribner, S Datta, J Arnold and JC Avise (1999). Empirical evaluation of cytonuclear models incorporating genetic drift and tests for neutrality of mtDNA variants: data from experimental *Gambusia* hybrid zones, *Genetica* 105: 101-108

- TJ Lott, BP Holloway, DA Logan, R Fundyga, and J Arnold (1999).
  Towards understanding the evolution of the human commensal yeast, *Candida albicans*.
  Microbiology 145: 1137-1143

- MS Sanchez, J Arnold, and MA Asmussen (2000). Symbiont survival and
  host-symbiont disequilibria under differential vertical transmission. *Genetics* 154: 1347-1365

- Kelkar, HS, J Griffith, ME Case, S Covert, R D Hall, C Keith, JS Oliver, MJ Orbach,
  MS Sachs, J Wagner, MJ Weise, J Wunderlich, and J Arnold. (2001). The
  Neurospora crassa genome: cosmid libraries sorted by chromosome. *Genetics* 157 (March
  issue), 979-990

  Hoyer, LL, R Fundyga, JE Hecht, JC Kapetyn, FM Klis, and J Arnold. (2001).
  Characterization of ALS genes from non-albicans *Candida* and phylogenetic analysis of the
  ALS family, *Genetics* 157 (April issue), 1555-1567

- RD Hall,, SM Bhandarkar, J. Arnold, and T. Jiang (2001). Physical mapping with
  automatic capture of hybridization data. *Bioinformatics* 17 (3): 205-213

- Zhang, Y, H Tian, E Kraemer, and J Arnold (2002). Visualization of protein
  interaction mapping using Java 3D. *Bioinformatics*, submitted

- Kraemer, E, J Wang, J Guo, S Hopkins, and J Arnold (2001). An analysis
  of gene-finding approaches for *Neurospora crassa*. *Bioinformatics* 17: 901-912

- Fang, X, JA Miller, and J Arnold (2002). J3DV: a Java-based 3D database visualization tool.
  Software – *Practice and Experience* 32: 443-463

- Battogtokh, D, DK Asch, ME Case, J Arnold, & H-B Schuttler (2002). An ensemble method
  for identifying regulatory circuits with special reference to the *qa* gene cluster of *Neurospora
  crassa*. *PNAS USA* 99: 16904-16909

- Fundyga, R, TJ Lott, and J Arnold (2002). Population structure of *Candida albicans*, a
  member of the human flora, as determined by microsatellite loci, *Infection, Genetics, and
  Evolution* 2: 57-68.

- Kochut, KJ, J Arnold, A Sheth, J Miller, E Kraemer, B Arpinar, and J Cardoso. (2003).
  INTELLIGEN: a distributed workflow system for discovering protein-protein interactions.
  Parallel and Distributed Databases 13, 43-72

- Xu, Z, B Lance, C Vargas, B Arpinar, S Bhandarkar, E Kraemer, KJ Kochut, JA Miller, JR
  Wagner, MJ Weise, JK Wunderlich, J Stringer, G Smulian, MT Cushion, & J Arnold (2003).
  Mapping by sequencing the Pneumocystis genome using the ODS3 tool. *Genetics* 163: 1299-
  1313

- Cardoso, J, A Sheth, JA Miller, J Arnold, and KJ Kochut (2004). Quality of service for
  workflows and web service processes. *J. Web Semantics: Science, Services, and Agents on the
  World Wide Web* 1: 281-308

- Strobel, G. and J. Arnold (2004). Essential eukaryotic core. *Evolution* 58, No. 2, 441-446

- Lott, TJ, RE Fundyga, RJ Kuykendall, and J Arnold (2005). The human commensal yeast, *Candida albicans*, has an ancient origin. *Fungal Genetics and Biology* 42: 444-451

- Sanchez, MS., CJ Basten, AM Ferrenberg, MA Asmussen, and J Arnold (2006). Exact sample sizes needed to detect dependence in 2 x 3 tables. *Theoretical Population Biology* 69: 111-120

- Icenhour, CR, J Arnold, M Medvedovic, and MT Cushion (2006). Competitive coexistence of two *Pneumocystis* species, *Infection, Genetics, and Evolution* 6: 177-186

- Dai, J, A Davey, IC Siegler, J Arnold, and LW Poon (2006). GCSDB: an integrated database system for the Georgia Centenarian Study. *Bioinformation* 1: 214-219

- Dai, J, L. Li, S. Kim, B. Kimball, M. Jazwinski, and J Arnold for the Georgia Centenarian Study (2007). Exact sample size needed to detect dependence in 2 x 2 x 2 tables. *Biometrics* 63: 1245-1253

- Tewari, S, SM Bhandarkar, and J Arnold (2007). Design and analysis of an efficient recursive linking algorithm for constructing likelihood based genetic maps for a large number of markers. *Journal of Bioinformatics and Computational Biology* 5 (No 2), 201-250

- Yu, Y, W Dong, C Altimus, X Tang, J Griffith, M Morello, L Dudek, J Arnold, and H-B Schuttler (2007). A genetic network for the clock of *Neurospora crassa*. *PNAS USA* 104: 2809-2814

- Logan, DA, AL Koch, W Dong, J Griffith, R Nilsen, ME Case, H-B Schuttler and J Arnold (2007). Genome-wide expression analysis of genetic networks in *Neurospora crassa*. *Bioinformation* 1 (10), 390-395

- Cushion, MT, AG Smulian, BE Slaven, T Sesterhenn, J Arnold, C Staben, A Porollo, R Adamczyk, and J Meller. (2007). Transcriptome of *Pneumocystis carinii* during fulminate infection: carbohydrate metabolism and the concept of a compatible parasite, *PloS one 2(5):* e423. doi:10.1371/journal.pone.0000423

- Dong, W, X Tang, Y Yu, J Griffith, R Nilsen, D Choi, J Baldwin, L Hilton, K Kelps, J McGuire, R Morgan, M Smith, M Case, J Arnold, H-B Schuttler, Q Wang, J Liu, J Reeves, and D Logan (2007). Systems biology of the Neurospora biological clock, *IET Systems Biology* 1 (No 5): 257-265

- Dong, W, X Tang, Y Yu, R. Nilsen, J Griffith, R Kim, J Arnold, and H.-B. Schuttler (2008). Systems biology of the clock in *Neurospora crassa*, *PLoS ONE* **3**: e3105, http://dx.plos.org/10.1371/journal.pone.0003105

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- Aguar, K., C C Sanchez, D. Boada Beltran, S Safaei, M Asefi, J Arnold, P Portes, H R Arabnia, J Gutierrez 2017. Considerations on Interdisciplinary Instruction and Design influenced by Adaptive Learning. SAIL-SB: A case study involving Biology, Computer Science, Mathematics, and Statistics. *Computers and Education*, submitted, https://arxiv.org/submit/1831769

- **Invited journal article or chapter; not refereed**

  - Arnold, J (1997). Editorial. *Fungal Genetics and Biology*, 21: 254-57.

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- **Convention papers and book chapters that were refereed and published in proceedings**

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- Kececioglu, J, S Shete, and J Arnold (2000). Reconstructing order and distance in physical maps using non-overlapping probes. RECOMB 2000, 183-192

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- Hall, RD, SM Bhandarkar, SA Machaka, SS Shete, and J Arnold (2000). Parallel computation for chromosome reconstruction on a cluster of workstations. *Proc. Intl. Parallel and Distributed Processing Symposium (IPDS)*, Cancun, Mexico, May 2000, p. 63-70

- Bhandarkar, SM, SA Machaka, SS Shete, and J Arnold (2000). Parallel computation for chromosome reconstruction on a cluster of workstations. *Proc. Intl Parallel and Distributed Processing Symposium (IPDS)*, Cancun, Mexico, May 1-5, 2000. pp. 63-70

Bhandarkar, SM, J Huang, and J Arnold (2002). Parallel Monte Carlo methods for physical mapping of chromosomes. *Proc. IEEE Computer Society Bioinformatics Conference*, Stanford University, Palo Alto, CA Aug 14-16, pp. 64-75.

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Arnold, J, H-B Schuttler, D A Logan, D Battogtokh, J Griffith, B Arpinar, S Bhandarkar, S Datta, K J Kochut, E. Kraemer, J A Miller, A Sheth, G Strobel, T Taha, B Aleman-Meza, J Doss, L Harris, and A Nyong (2004). Chapter 22 in Metabolomics. In *Handbook of Industrial Mycology*. 597-634 Marcel-Dekker, NY, NY

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Bhandarkar, SM, J Huang, and J Arnold (2006). An Information theoretic approach to genome reconstruction. Chapter 11 in *Handbook of Computational Molecular Biology*. 11-1-11-26 CRC Press, Boca Raton, FL

Tewari, S, J Arnold and SM Bhandarkar (2006) "Efficient Recursive Linking Algorithm for Computing the Likelihood of an Order of a Large Number of Genetic Markers" *Proc. of the IEEE LSS Computational Systems Bioinformatics Conference* (CSB 2006), Aug. 14-18, 2006, Stanford University, Palo Alto, CA., P Markstein and Y. Xu (ed.s), Imperial College Press, London. Pp. 191-198

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Xiong, M and J Arnold (2006). Do genetic networks obey Kirchhoff's and Ohm's Laws? *Proc. IASTED International Conf. on Comp. & Systems Biology*, Dallas, TX, November 13-14, 2006, pp. 13-19.

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Deng, Z, S Arsenault, L Mao, & J Arnold 2016. Measuring synchronization of stochastic oscillators in Biology. *J. Physics Conference Series* 750: 012001, doi:10.1088/1742-6596/750/1/012001

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Deng, Z, J. Arnold, & L Mao (2017). Light entrainment of single cell circadian oscillator measured by a high-throughput microfluidic droplet platform. *Proc. of the 21st International Conference on Miniaturized Systems for Chemistry and Life Sciences (MicroTAS)*. Savannah, GA October 22-26, 2017.

- **Invited seminars and symposiums (1993-present)**

  - Colloquium talk on "Towards a map of the human genome," Dept. of Statistics, UC Santa Barbara, April 8, 1993

  - "*In vitro* reconstruction of *A. nidulans* chromosome IV," June 8-11, 1994, NIH Mycology Workshop, Flagstaff, AZ. Symposium.

  - "*In vitro* reconstruction of fungal chromosomes," seminar speaker, Bristol-Meyer, Princeton, NJ, June 25, 1994.

  - "*In vitro* reconstruction of fungal chromosomes," seminar speaker, National Science Foundation, Arlington, VA, Sept. 8, 1994.

  - "*In vitro* reconstruction of fungal chromosomes,", seminar speaker, Department of Energy, Germantown, MD, October 19, 1994.

  - "*In vitro* reconstruction of fungal chromosomes and genomes," Fungal Genetics meeting, Asilomar, CA, March 21-26, 1995.

  - "*In vitro* reconstruction of fungal genomes," Georgia Institute of Technology, May 23,1995.

- "*In vitro* reconstruction of fungal chromosomes," seminar speaker, School of Biological Sciences, Georgia Tech., Spring, 1995.

- "*In vitro* reconstruction of fungal chromosomes," seminar speaker, Dept. of Biological Sciences, Clark Atlanta University, November, 1995.

- "*In vitro* reconstruction of fungal chromosomes," symposium speaker, First Fungal Genome Workshop, Stillwater, OK, August 19, 1996.

- "Fungal Genomics," symposium speaker, Plant Molecular Biology Retreat, December, 1996.

- " Fungal Genomics", seminar, University of Cincinnati Medical Center, August, 1997.

- " Fungal Genomics", Second International Symposium on Fungal Genomics, Athens, GA, March 26-27, 1998.

- "Statistical Genomics", Sixth International Symposium/Statistics, Purdue, Lafayette, IN, June 21-23, 1998.

- "*Neurospora crassa* physical mapping project", Gordon Conference on Cellular and Molecular Mycology, Holderness School, Plymouth, NH, July 19 – 24, 1998.

- "Statistical Genomics", Part II, Fall Colloquia, Purdue, Lafayette, IN, Oct. 21-23, 1998.

- "Genomics", Human Genetics Center, University of Texas at Houston, March 16- 18, 1999.

- "Fungal Genomics", 20th Fungal Genetics Conference, Asilomar Conference, Pacific Grove, CA, March 23 – 25, 1999.

- "Physical mapping of *Pneumocystis carinii*", Society of Protozoologists, Raleigh, NC May 26-29, 1999.

- "Physical Mapping", Burroughs Wellcome Meeting following the American Society of Microbiology, Chicago, IL June 3 – 4, 1999.

- " Fungal Genomics", International Botanical Congress, St. Louis, MI, August 1-7, 1999

- " Microsatellite variation in *Candida albicans*", invited talk, General Society of Microbiology, University of Warwick, Warwick, England, April 13, 2000.

- "*In vitro* reconstruction of fungal chromosomes", Clark Atlanta University, Spring 2000.

- "Computing Life", Joint Statistical Meetings (JSM) 2001, Atlanta, GA, August 9, 2001

- "Metabolomics", North Carolina State University, ,Raleigh, NC, Feb 19, 2002

- "Fungal Genomics", Centers for Disease Control, Atlanta, GA, May 15, 2002

- "Computing Life", Purdue University, April, 2003

- "Computing Life", National Science Foundation Workshop on

"Computational Resources for Microbial Systems, Arlington, VA, October 27-29, 2003

- "Computing Life", University of Minnesota, Bioinformatics: Building Bridges, April 16, 2004

- "Genetic Networks", Dept. Biochemistry & Molecular Biology, Louisiana Health Science Center, January 13, 2006, rescheduled, New Orleans.

- "Systems Biology of the Biological Clock", keynote address, First International Conference on Computational Systems Biology, July 20-23, 2006, Shanghai, China.

- "Design of Case-Control studies of Centenarians", invited talk, International Conference on Centenarians, October 18, 2006, Sunchang, Korea

- "Systems Biology of the Biological Clock", Yale Department of Ecology and Evolutionary Biology, November 14, 2007, New Haven, CT

- "Biological clock and aging", 20th Anniversary Celebration of the Georgia Centenarian Study, August 12, 2008, Atlanta, GA

- "Biological Clock and Aging, IAGG Meeting, July 8, 2009, Paris, France

- "Systems Biology of the Clock", Yale Systems Biology Symposium, October 15, 2010, New Haven, CT

- "Systems Biology of the Clock", seminar, Department of Organismal and Evolutionary Biology, Harvard University, March 21, 2012, Cambridge, MA

- "Systems Biology of the Clock", seminar, Department of Bioinformatics and Biostatistics, University of Louisville, March 27, 2015, Louisville, KY

- "Measuring synchronization of stochastic oscillators in biology", in *Recent Developments in Computer Simulation Studies in Condensed Matter Physics*. UGA. February 22-26, 2016, Center for Simulational Physics.

- "ALICE: New approaches to undergraduate and graduate education education in systems biology, March 12, 2016, Spelman College, NSF Quantitative Biology Workshop

- "Are there clocks in single cells that synchronize?", Laboratory of Genetics, University of Wisconsin – Madison, January 25, 2017

- "Are there clocks in single cells that synchronize?", Georgia Scientific Computing Symposium, University of Georgia, February 25, 2017

- **Recognitions and outstanding achievements**

  - Member of Sigma Xi

  - Yale University Graduate Fellowship

- Yale Stanley Prize in Mathematics (undergraduate)

- NSF Creativity Extension Award, 2010

- **Current Postdoctoral Fellows**

- **Current students**

  Krach, Emily, PhD candidate, Genetics Department, "Single cell gene expression in fungal filaments"

  Montenegro, Tito Pena, PhD candidate (joint with Mandy Joye), Institute of Bioinformatics, "Identifying the network of ^{1}C metabolism for a microbial ecosystems perturbed by an oil spill in the Caribbean"

  Caranica, Cristian PhD candidate, Department of Statistics, "Ensemble Methods for Stochastic Cellular Networks in single cells"

  Judge, Michael, PhD candidate, Genetics Department, "Systems biology of clock signaling in *Neurospora crassa*"

  Deng, Zhaojie, PhD candidate, College of Engineering, "Measuring and modeling oscillators in single cells of *Neurospora crassa*

  Cheong, Jia Hwei, PhD candidate, Chemistry Department, "FRQ-less oscilators in single cells"

- **Past postdoctoral fellows**

  Dong, Wubei, Genetics, UGA, "Systems biology of Neurospora" –Professor, Huazhong Agricultural University, Wuhan, China

  Dai, Jianliang "Sample size problem for 2 x 2 x 2 table" – M. D. Anderson Cancer Center, Research Statistical Analyst, Houston, TX.

  Arpinar, B. "Adaptive workflows for protein-protein interaction mapping" – UGA, now associate professor, Computer Science Department, University of Georgia

  Hall, D., "Fungal Genome Database", Assistant Computational Biologist – UGA, now Computational Biology at Research Triangle Institute (RTI), Research Triangle Park

  Kelkar, H., "*In vitro* reconstruction of the *Neurospora crassa* and *Aspergillus flavus* genomes.", now Bioinformatics Scientist, University of North Carolina – Chapel Hill

  Prade, R., (1995). "Physical mapping of *Aspergillus nidulans*". Associate Professor, Dept. Microbiology and Molecular Genetics, Oklahoma State University, Stillwater, OK.

  Wang, Y., (1994). "Neural Networks for physical mapping". Bioinformatics Department, Merck , Inc.

Fu, Y.-X. (1990). "Cytonuclear disequilibria in finite populations". Professor, University of Texas   at Houston Human Genetics Center, University of Texas at Houston, Houston, TX.

- **Past students**
  Al-Omari, Ahmad, Ph.D (2015), Institute of Bioinformatics, "Discovering a regulatory network topology by Markov Chain Monte-Carlo on GPGPUs with special reference to the biological clock of *Neurospora crassa*", assistant professor, Yarmouk University, Jordan

  Manzourolajdad, Amirhossein, Ph.D. (2014), Institute of Bioinformatics, UGA: *Ab initio* Identification of regulatory RNAs using information-theoretic uncertainty. postdoctoral fellow, NLM

  Bouffier, Amanda M., M.S. (2013), Institute of Bioinformatics, UGA: A MINE alternative to D-optimal designs for the linear model.

  Arte, Ankit, M.S (2011), Computer Science, UGA: HiDEW: High-Speed Determination of epigenetic code rendered through a Web Application. Web developer, University of Georgia

  Tang, Xiaojia, Ph.D. (2009), Physics and Astronomy, UGA: The Computational Systems Biology for the Biological Clock of *Neurospora crassa*. Postdoctoral fellow, Mayo Clinic with Dr. Krishna Kalari

  Tewari, Susanta, Ph.D. (2008), Statistics, UGA: Construction of high-resolution likelihood-based integrated genetic and physical map of *Neurospora crassa*. Postdoctoral fellow, Markey Cancer Center, University of Kentucky-Lexington

  Koch, Allison, B.S., Genetics, UGA: Systems Biology of the *qa* gene cluster in *Neurospora crassa*, Regulatory Affairs manager at Astra/Zeneca

  Morello, M., B.S., Genetics, UGA: Half-life of the *wc-1* mRNA in *Neurospora crassa*". Medical College of Georgia physician training program.

  Altimus, Cara, B.S. Honors, Genetics, UGA "What makes a Biological clock in tick?" Honors Thesis. Johns Hopkins University postdoctoral fellow

  Whitworth, C., Honors, Genetics, UGA, "Integrated genomic and proteomic analysis of the *qa* gene cluster of *Neurospora crassa*". Postdoctoral fellow, National Institutes of Health.

  Xu, Zheng, M.S. (2001), Computer Science, UGA, "Mapping by Sequencing using ODS". University of Chicago Business School

  Fundyga, R., Ph.D. (2001), Genetics, UGA, "The population genetics of pathogenic fungi: empirical and theoretical studies. ASM postdoctoral fellow", CDC, now veterinarian, Plymouth, MASS

  Hall, D., Ph.D. (1999), Genetics, UGA, "New computational tools for genome mapping". Rho, principal investigator.

  Sanchez, M., Ph.D. (1999), Genetics, UGA, "Coevolutionary models of host/pathogen systems." Postdoctoral fellow, Dr. Alan Hastings, University of California - Davis

  Shete, S., Ph.D. (1998), Statistics, UGA, "Methods for physical mapping." Professor. University of Texas M.D. Anderson Cancer Center, Houston, Texas.

Wollenberg, K., Ph.D. (1997), Genetics, UGA, "Testing for nonrandomness in phylogenetic trees." Assistant Professor, Tufts University, now NIH

Dean, R., Ph.D. (1996), Genetics, UGA, "Three models for cytonuclear disequilibria". Statistical Geneticist. National Plant Germplasm System, Griffin, GA.

Datta, S., Ph.D. (1995), Statistics, UGA, "Dynamics of cytonuclear disequilibria and related statistical tests for the neutrality of mitochondrial DNA markers for hybrid zone data". Professor, Department of Biostatistics, University of Florida, Gainesville, FL.

Xiong. M., Ph.D. (1993), Statistics, UGA, co-sponsored with H.J. Chen, "Mathematical theory of neural learning and its applications to statistics and molecular biology". Professor, University of Texas at Houston Human Genetics Center, University of Texas at Houston, Houston, TX.

Cellino, M. J., M. S. (1992), Genetics, UGA, "The effects of cytoplasmic male sterility on Cytonuclear Disequilibria in hybrid zones". Networking Professional, NetCom, Inc, Washington, D.C.

Cuticchia, A. J., Ph.D. (1992). Genetics, UGA. "Computational advances in the physical mapping of small eukaryotic genomes". instructor, North Carolina Central University and AJC Legal Services.

Williams, C. J., Ph.D. (1988). Statistics, UGA. "Statistical problems in selection component analysis". full professor, Department of Mathematics & Statistics, University of Idaho.

Phillips, G. J., Ph.D. (1987). Genetics, UGA, Co-sponsored with S. R. Kushner. "Structural and functional characterization of the Exonuclease I (*sbcB*) gene and gene product from *Escherichia coli* and a Markov chain analysis of DNA sequences". Professor, Department of Microbiology, Iowa State University, Ames, Iowa.

Adams, P. B., Ph.D. (1986). Behavior Genetics, Georgia State University, Co-sponsored with A. Falek. "Statistical analysis of age at onset in Huntington's disease". Assistant professor, Department of Genetic Epidemiology, Columbia University Psychiatry and New York Psychiatric Institute.

Sammons, S. A., M.S.T. (1987). Genetics, UGA, "Molecular evolution of homeo boxes". Research Scientist, Bioinformatics, CDC, Atlanta, GA

Lemke, K. M.S. (1985). Statistics, UGA, "Dispersal models for *Drosophila*". Biostatistician, Johns Hopkins University Bloomberg School of Public Health, Center for Heath Services and Outcomes Research.

Porter, J., M.A.M.S. (1985). Computer Science, UGA, "Inversion frequency mapping in *Drosophila pseudoobscura*". Ph.D. candidate, Botany Department, Duke University.

Goldman, I. F., M.S. (1985). Entomology, UGA, "Selection for resistance to *Bacillus thuringiensis* variety *israelensis* in field and laboratory populations of the mosquito *Aedes aegypti*". Molecular Entomologist, Center for Disease Control (CDC, Atlanta).

- **Reviewer**

  ad hoc reviewer, NIA grant in longevity

ad hoc reviewer, NIAID grants in fungal genomics
ad hoc reviewer, NIH Nonmammalian models of Biomedical Research
ad hoc reviewer, NIH GCAT study section
USDA grant proposals
NSF grant proposals
United Kingdom grant proposals
American Journal of Human Genetics
American Naturalist
Applied Mathematics and Computation
Bioinformatics
Bioinformation
Biometrics
Biophysical Journal
BMC Bioinformatics
BMC Genomics
Bulletin of Mathematical Biology
CABIOS
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FEBS Letters
Fungal Genetics & Biology
Genetica
Genetics
Genetics Research
Journal of Applied Gerontology
Journal of Forest Science
Journal of Gerontology
Journal of Invertebrate Pathology
Journal of Molecular Evolution
Journal of Theoretical Biology
Mathematical Biosciences
Molecular Biology & Evolution
Nature
Nucleic Acids Research
PLoS Computational Biology
PLoS ONE
Proceedings of the National Academy of Sciences USA
SIAM Journal of Applied Mathematics
Statistical Methods in Medical Research
Statistics and Probability Letters
Theoretical Population Biology

- **References**

  Joan Bennett
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